



PCT/AU98/01023
09/581286

REC'D	12 JAN 1999
WIPO	PCT

Patent Office
Canberra

5

I, KIM MARSHALL, MANAGER EXAMINATION SUPPORT AND SALES,
hereby certify that the annexed is a true copy of the Provisional specification in
connection with Application No. PP 2911 for a patent by CSL LIMITED filed on
9 April 1998.

**PRIORITY
DOCUMENT**
SUBMITTED OR TRANSMITTED IN
COMPLIANCE WITH RULE 17.1(a) OR (b)



WITNESS my hand this Fifth
day of January 1999

KIM MARSHALL
MANAGER EXAMINATION SUPPORT AND
SALES



.

AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

P. gingivalis sequences

The invention is described in the following statement:

P. gingivalis sequences

FIELD OF THE INVENTION

5 The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*.

BACKGROUND OF THE INVENTION

10 Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated
15 with a subgingival infection of a consortium of specific Gram-negative bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically
20 cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of
25 the disease. The progression of periodontitis lesions in non-human primates has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

P. gingivalis is a black-pigmented, anaerobic, asaccharolytic,
30 proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence
35 factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes. In

particular, proteases have received a great deal of attention for their ability to degrade a broad range of host proteins including structural proteins and others involved in defence. The proteins that have been shown to be substrates for *P. gingivalis* proteolytic activity include collagen types I and IV, fibronectin, fibrinogen, laminin, complement and plasma clotting cascade proteins, α_1 -antitrypsin, α_2 -macroglobulin, antichymotrypsin, antithrombin III, antiplasmin, cystatin C, IgG and IgA. The major proteolytic activities associated with this organism have been defined by substrate specificity and are "trypsin-like", that is cleavage on the carboxyl side of arginyl and lysyl residues and collagenolytic although other minor activities have been reported.

P. gingivalis trypsin-like proteolytic activity has been shown to degrade complement, generating biologically active C5a, impair the phagocytic and other functions of neutrophils by modifying surface receptors, and abrogate the clotting potential of fibrinogen prolonging plasma clotting time. The trypsin-like proteolytic activity of *P. gingivalis* also generates Fc fragments from human IgG1 stimulating the release of pro-inflammatory cytokines from mononuclear cells and is associated with vascular disruption and enhanced vascular permeation through the activation of the kallikrein-kinin cascade. *P. gingivalis* spontaneous mutants with reduced trypsin-like activity as well as wild-type cells treated with the trypsin-like protease inhibitor N-p-tosyl-L-lysine chloromethyl ketone are avirulent in animal models. Further, it has been shown that *P. gingivalis* grown under controlled, haemin-excess conditions expressed more trypsin-like and less collagenolytic activity and were more virulent in mice relative to cells grown under haemin-limited but otherwise identical conditions. The increased expression of the trypsin-like activity by the more virulent *P. gingivalis* has led to the speculation that the trypsin-like proteolytic activity may be the major determinant for infection or disease.

There has been considerable endeavour to purify and characterise the trypsin-like proteases of *P. gingivalis* from cell-free culture fluids. Chen *et al*, (1992) [J Biol Chem 267:18896-18901] have purified and characterised a 50 kDa arginine-specific, thiol protease from the culture fluid of *P. gingivalis* H66 designated Arg-gingipain. A similar arginine-specific thiol protease has been disclosed in JP 07135973 and the amino acid sequence disclosed in WO 9507286 and in Kirsbaum *et al*, 1995 [Biochem Biophys Res Comm

207:424-431]. Pike *et al* (1994) [J Biol Chem 269:406-411] have characterised a 60 kDa lysine-specific cysteine proteinase from the culture fluid of *P. gingivalis* H66 designated Lys-gingipain and the partial gene sequence for this enzyme was disclosed in WO 9511298 and fully disclosed in WO 9617936.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly active proteases (University of Melbourne International Patent Application No PCT/AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO. 1331 and sequences complementary thereto.

In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO. 1331 and sequences complementary thereto.

In a third aspect the present invention consists in a nucleotide probe specific for *P. gingivalis*, the probe including a detectable label and a nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO. 1331 and sequences complementary thereto.

DETAILED DESCRIPTION

Preparation of the *P. gingivalis* library for sequencing.

To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (1961)(1). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (1995)(2). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and was treated with Bal31 nuclease to create blunt ends then run twice on preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed on a 1% agarose preparative gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated

to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20°C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below.

As will be understood by those skilled in the art open reading frames (ORFs) may be readily identified. ORFs may be determined using two methods, for example, alignments from FastX search results may be used to define the start and end positions of coding regions if sufficient protein homology is present. Alternatively, protein coding regions may be identified using the ORF identification program GeneMark (3) using a training matrix based on published *P.gingivalis* sequences. This matrix may be further refined by adding ORFs identified from the results of homology searching and ORFs identified by GeneMark. The program PSORT (4) may be used for the detection of signal sequences and the prediction of protein cell

localisation. A UNIX version of TopPred (5) may be used to identify potential membrane spanning domains.

- 5 It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this 9th day of April 1998

CSL LIMITED

Patent Attorneys for the Applicant:

F.B. RICE & CO.

References.

1. Mamur, J. (1961) A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J. Mol. Biol. 3, 208-218.
- 5 2. Fleishmann, R.D. et al. (1995) Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd. Science 269, 496-512.
3. Borodovsky M, Rudd KE, and EV Koonin. (1994). Intrinsic and
10 extrinsic approaches for detecting genes in a bacterial genome. Nucleic
Acids Res. 22:4756-4767.
4. Horton, P. and Nakai, K. (1996). A probabilistic classification system
for predicting the cellular localization sites of proteins. Intellig. Syst. Mol.
15 Biol. 4: 109-115.
5. Claros MG and G von Heijne. (1994). TopPred II: an improved
software for membrane protein structure predictions. Comput. Appl. Biosci.
10: 685-686.
- 20

(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

tcttcgcgtt	tttttggaa	actcattcgc	atcgaaagct	ctacagagct	caaggatgcg	60
gagaggatta	gtttgacacc	cgctcaaagc	tattttgcga	gcgggtggtg	cgctttctgc	120
ttgcagtcca	ataaacctga	tgcccttccg	gcgtctatct	aagcataaac	gacaaaaaca	180
cattagtcaa	actttagaaa	acattgtatg	aacaaagtgt	ggaaatacgt	gacgggagcc	240
tttgatagc	agccgtcagc	gcagtagcat	cggtggcaac	agtggctgct	ttggaccctt	300
ccgaggggtg	aattcttcat	aaccgatggt	acggaaaacg	aatcggattc	aagcagacat	360
cttacacaac	gacatccgga	gccttcgccc	cttgcccaat	ttggtcggag	ctgcagaagc	420
atcggtacac	gccgtagtac	aatcaaagt	gagtcggagc	agcgaatgga	ctcttcagca	480
gtacttcgat	cgttctgaat	tcttcttcgg	aggcgaatcc	agaaactttc	agcgtcccca	540
acacggcagg	tagtaggcta	cggttcgggg	gtgatcatca	tgcacagagg	atatatcatc	600
acgaataatc	atgtagtaaa	gggagcca				628

(2) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

gacttcttta	ccccgctaaa	agtaacctta	ctgatgcgag	gacgttcagg	acaatgattt	60
tcagatagac	tttattgccg	acatatattat	ccgcgatggt	cgcacatttg	agaagtagcc	120
ctgacgcata	attctattca	cggcagcgac	atggcatctc	caggaatcag	gacttcatca	180
cctacagcca	agcctgaaga	ttgcgcaaga	caaagtcatc	gaaagacctc	attccctcga	240
tctcatagat	gctatggctt	tatgaatagg	cttggcatag	gatatttcag	ggcttatata	300
tggatctccg	tgaggggtca	gatccgagga	ctgtcccttc	aggtccttat	gctggcgag	360
aagagagctg	ctacggcaat	aatctttttg	taatagtctt	tctcaaata	ttcaatattt	420
atcttctctg	agagcgattt	gtcgctggtc	ttgccgaatc	gacgtccct	cgatgaatat	480

tcttctatgg	tgccttcaga	cagtcggcat	caaagtcggg	ccaaagcgta	tccgtaaaaa	540
caattccgta	taggccattt	gccacataag	aaaatgctga	tacgcttcct	ccacctgtac	600
gaatgaagag	atccggatcc	ggaatgcccg	cggtggaaga	tgatcagaaa	ccaaatcgac	660
atztatatct	tcaggctcca	cacttcaccc	cgaacctttc	gagccaatct	acggatgaca	720
tccgtcattt	cccaggagaa	ctgtagctaa	gggccaaaac	caaagtcagc	cccgtgtttc	780
cggcgtctct	cgaataccct	tttctaacga	ttcacggaca	tcttcgggga	gccactgaaa	840
tcgccgatag	ccaagaggcg	aatgttattg	gtcatcaagt	cgcacatctc	ttcatgataa	900
gctgtaacga	aaaggcccat	cagcgccctg	attcctcttt	cggacgattc	caattcttcg	960
tactgaaagg						970

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID: NO:3

agccgcacga	ttggaaaaga	aactggagca	actcacagcc	taacggcgca	gagcctgtgc	60
ttgagacgct	gcagaagacc	gggatgattc	tccggatccc	tgagggtcaat	gtctgggaaa	120
gattcttttc	ggatacgatc	agtagcagtc	tcccacttgc	aagtgcatac	gccctttcgg	180
tacacgataa	gccctccctc	ttcgtaccag	gatgacaagc	tcttcacac	gaagagaaaag	240
attcacagca	gatcgccatg	ggacagcatg	gaagcatcca	ccactctctc	ctccacttgg	300
ttcccgtctc	ttccggtatt	tccacaccga	acaggctacc	tatggcggcg	aaggaatata	360
cagtcggagc	caacgtgcta	cctggggagat	cgactcccct	gtacgagcag	agagagtatg	420
gtaatgaaga	agacgacatt	gaaagctgat	ccgctccggg	gatattatcg	atcatgggat	480
aggtggcaaa	atgataggaa	cggctccgcg	caatccgacc	cagctgagaa	aggtcttacc	540
ctgaatgata	ttttgcggaa	gggaatcagg	cagaaa			576

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

gctttcatct	ctattctcct	tttttattct	attgtgtttt	tttcatattc	tcttcgggaca	60
tagccgtttc	cgcatacaag	gcttctcttt	cccatccggc	atttccacaa	actccccctc	120
cgcacagcc	ccgcgatcga	gacaatatcc	aatagctcca	tggcgtaggc	cgtttcccg	180
acggcttcgt	cccgatgaga	gcgatcccg	tctgttgga	cgaaagtcgt	cccaccgtat	240
tcagcccacc	gccacaccta	tggccagtgc	caaagccaca	caagctacag	cccctagcgt	300
accaaccgaa	gcgacaaccg	ccttgaagga	tgccggacac	gatctcccaa	ctcgccatct	360
tttccaagag	aactttgtcc	gaatcatctt	cctngcccg	ttcacgctca	ggaagaccga	420
tcaaagccc	caaaagctgc	agtccgaatg	atagggagcc	ggatccggca	atcccttcag	480
caagcaatac	gctccaactc	ctcttgcgga	aaatggtacc	ggcataaaaa	ctttncagtg	540
ccggtcgatt	ttattctctc	ttacgcatca	tcttatcacc	tcttagct		588

(2) INFORMATION FOR SEQ ID NO:5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

aacacaaaaac	tttagaagg	agtcttacac	ttcgtcccat	cgagtgtctt	cctttaccgg	60
tagtttcatg	agtggaaga	ccgctgccct	gaatgatgtc	ccatcaaaat	caatagcaaa	120
cagattatgg	ccggagattt	atacgacgat	cccgtctggag	tgtaggaggt	atgttccgtt	180
ccaaatactt	ggatctcgta	gntgaaatac	cttcgaaggc	aaagacgatg	acatgattag	240
taaggctttt	acgtcacagg	gtaggacga	ttgttcaaaa	acctcgatat	catcgatcat	300
atgacttcat	ggatttgtac	gaaaggcaac	atgtctcata	atataccgcc	ggccttcaag	360
tactggttct	tcccaaagt	tcgtttgcag	gccagtatgt	attgagcaat	ccgaaaggcg	420
agtacaacaa	cacacacgct	cgctaacaca	ggtgcaggta	gcattctgac	agc	473

(2) INFORMATION FOR SEQ ID NO:6

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

ggggatttgg	ggcaagataa	gttactttgt	agagcttgaa	tggcaaacag	ggatttctgc	60
ctattttcca	aaaatctgca	tcgtcgattc	ttgaaacggg	tgagagccaa	cgggggcgca	120
aggagtttgt	tctgggtggc	cacccgagag	cttcgtctcc	ggggagagtt	ttaattatct	180
tatcgggcaa	cttaaagcag	ctatcagttc	ttgagcatga	cagagttgta	tgatcagagg	240
ctaaaatagg	cacaaagaaa	ggcgtcaagg	atactcataa	gcccgaagaa	cctgcccaga	300
aggaccatct	ccagagggac	ctgaagctgg	tttgtaatta	gttatagaag	ctcaccaccag	360
tagaggtagc	gagttttgct	ggggtgagtg	tcacatctgta	ttgttttagtc	attacgaccc	420
aatagatggg	tattatcaaa	atccatatta	gatattgctta	atgcaattta	tttttaccga	480
ttgtctcatt	gctttatcgt	catcatatcc	cgatattgcc	aaagttaatc	acattgctct	540
cttctctcatt	tataatagca	agatacctcc	tcaagctaaag	ataggcaagg	atctaagttc	600
ggttatggag	ggataagtgt	tgtggtacat	catgactggg	gataggagaa	aattgtagta	660
ttggtcacgt	tgttactata	ggaggagtaa	ttcgaagtat	ccaggagtcc	ctgttatagg	720
aaataatgtc	cagatagccg	aggaagtgtg	gtttttggcg	ggataacccat	tggtataaac	780
gttgatatagg	agccaatata	gtagtttaatt	ttcctgtccc	agacaatgct	gttttgagg	840
caatcctggg	cgtattgtgc	atattaagga	aagtacatgt	tacatcattc	ctcaaacctta	900
aaacctattg	ngaacaagaa	ggcttcaaag	gtgggatccg	tacgatggat	tgaactccag	960
gg						962

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...3307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

cgaaaaagaat	attttccacc	cgtggaaaag	atgtttttccc	gacctggaaa	tattttttccc	60
aggccgggaa	aatttatgtg	taaaactgaa	aaatcacaa	cgttgcattg	cagtcgttta	120
tgtggaaatc	cagaagagag	ctttttttgc	tctgatggcg	gtttatggtc	gggtaggaaa	180
atgggtaccc	atcgggcacc	gatgaatcga	caatctccaa	acgatacggg	cgcggcggca	240
ggctaagagc	agggaaatctt	ctatagtagg	aatgtgtgca	gaggctaagc	aagggcggtc	300
ggaggggcta	tcgccatagc	cataggagat	cgaatctcgc	caagcggcaa	ggctcgatcc	360
aacctgtgga	ttttctcttt	tcccttgtag	ttttgcttcc	gaaccgaccc	gtcagaatgc	420
cggattttat	ctccggaagg	gagcaatgac	ggtagaaac	cccgctcttt	cagccccatgg	480
ctccacacaa	gcagaagcga	ggctgtcagt	agcaccagcc	gatgtccttc	gctgcgatgc	540
attccaaaca	gcgaagggtc	tcgggacgaa	gaatgctttc	gatagcagca	cgaatcgctg	600
tcccattgcc	cggcattcca	cctccctttt	tccttttcaga	ctgtggaaag	gatggctgct	660
ttcgtccggg	cggccggagc	cagccgagtt	tgtagcacat	ccacatggcc	agatagaaag	720
gcagtctgag	ccaaagagaa	taaccggctg	ggcttgccgc	agaaagggaa	gcaaagaatc	780
gcatgggtca	gcgtaccgtc	gaaatcgaa	atggctatgg	gcctatgcga	catagggctt	840
atcgaataaa	gaatgatcca	cacaactacc	gaaagctgga	gccgtgggtcc	tgatagagca	900
tatcgggtcg	attgcaatga	cagcctttca	catcacgtgt	ctcagataat	ggaaaagtcc	960
ggtggcaacg	ggaaagacag	tacgtacaga	tacggggccat	tcctcgatat	gacttcgctg	1020
tctgtggcaa	gaggggtatg	agtataatga	tcgtagccga	gagaatggcc	agtaggactt	1080
gaggaatcca	ctcgtataat	gtttgacgac	aggacgcgat	gaaagagcgt	ctcctgcagc	1140
agacgcaggt	tctctttcct	cttgccgaag	gcgagcgcaa	ggataggaag	agcgtcatca	1200
aagccaacca	atgggaaatg	ggtacccgct	cactgctccg	gccgcataca	atctgatcag	1260
aaagccgaaa	gctagaggaa	agcatccacg	atgggaatgt	gtttgccttt	cagtgaatag	1320
aaagattcag	cagaagataa	agcactatag	agatcagggc	atagacggca	aagggaatc	1380
aaggagtgc	aatatcactg	cgcaagccaa	aaccacaagc	aagctatcag	tatataagct	1440
ttggagagac	tccatgctcc	gctggcaata	ggcgtctcga	tttgacggga	tgcaggcggt	1500

cgatcgctct	atcgcaaatt	cattgaagag	atagactgca	ctcgatgccg	aacaaaatgc	1560
tatcaggata	tggtcagcct	tagcaaggct	tccgtatcac	caatcctgtg	tccgaaaaca	1620
ggggtaggaa	tacgatcaga	ttcttgatcc	actgcttagg	tctcatgagg	gagaaatgtg	1680
atcatgtatg	caatagggaa	agctccgatc	cgatgtttct	cgcagcatga	caagggtttt	1740
ctcttcggct	gcacgcattt	gggctcatcc	tttttgctct	tgtctttcaa	tccgcaaaga	1800
tgcagtatgc	cgtgataatg	acacgatgca	gttcgtcttc	gtatcgaaga	tcaagagcac	1860
ggcatttcgag	cgtacggtat	cgagactgat	aagcaggctg	ccattcaccg	ttccgcttcg	1920
caggaatcga	aggtgatgat	gtcgggtgtag	tagtcatgat	gagaaattcc	tgattggctt	1980
tcaggatata	ttcgtcatca	cagaaaagaa	ggagatttct	cccaccgctt	tcccatatcg	2040
gctgcatact	tcggctatca	cttaccgacg	atccgtcttc	tgatccgagg	aaggctgacg	2100
ccttcagata	gaaattgatt	tttgccattg	tcttaattat	cgttttgctc	ggtcacgtac	2160
cctcaaccaa	agaaaatata	agtgcacaga	atggctgtca	gcgctcggcc	aaatcggcca	2220
aaaggggaata	gctcaccgta	taacgtgtat	tgcgattttg	acggctccat	agtagagggc	2280
tacgacgtag	aacgtggtat	cgcgagagccc	tgtacaatac	tgcatagacg	gccgacaaag	2340
ctgtcggctc	cgacgtctgc	atggcatcga	ccatgagccc	tctggctcca	cttcgctaa	2400
gggttttcatt	agcatggctg	ggattccttc	cacaaacttc	atatctcctc	ccaaaagccg	2460
accagtcgcg	gcaagccttc	agtgatcaga	tccatggcac	ggaagctctg	aatataccga	2520
taccgaccag	catggcccagc	agatagggat	gatggtcaca	gccgtaccga	aaccatcttt	2580
tgcccccttcg	ataaaggatc	atacacattg	atgctgtcac	gcagtccact	aatgacgaat	2640
ccgcacttat	tccaaacaga	agaatggatg	caaatgcagt	gctgatacaa	ctaaagtttc	2700
cggaggcaga	gtccgtcctg	catagattac	ccctccgata	aagaaaagaga	ggaaaagaaga	2760
aaaagaagaa	gaggtttttg	gaagaaatcg	atagctgctt	gatccctact	gcaaggatgg	2820
cgaccaatgt	ggaagcaaac	gtgcaatcag	aaccgggaca	aagatgtcgg	taggatttgc	2880
cgccccgacc	ttaggcgata	ggccatgatg	gaagagggaa	tcagcgtaag	tccactggca	2940
tgatggccaa	gaacataatc	atggcatcgc	tggctttatc	tttttgctgt	tgatcgtttg	3000
caaaactctcc	atcgaacgga	taccgagggg	ggtagcagat	tgtcaaggcc	taacaggttg	3060
gccgatatat	tcatgaagat	attgcccggt	cgggatgggtc	cttaggtaca	gaagggaaca	3120
atcggcttag	aacagggaac	tgatctgtgc	cagcttgctt	ataaggccac	ttcgttctgc	3180
tatttcacat	gaccgagcca	cagagcgagt	acactggtca	gtgcaagggc	tatccaaagg	3240
cattcttcga	ctggctgaaa	gaagcctgca	ccatcgcac	gaaacggaca	catcgccgaa	3300
agctatc						3307

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

agcagccggc	cggccaacgg	aaagcttcgc	cccccatggc	ggcacgaata	tttcgataga	60
cacgtaagaa	gggcttttga	aagacgagcg	accacgtact	tgataatgtt	ggctccccc	120
ttcacgacac	gctgtttcag	ttctgccact	gctcgttggt	cagcttgtcg	gtaccgatca	180
gatcggtcag	aggcgtccgt	ttaccttggc	cgtgctggcg	aaaacagcca	tctgctcgcc	240
atgactccat	aagtacgcgt	gttggtcacg	agactttgtt	tgatgccgaa	gtgctagcca	300
gttcgctttg	cagacgtgtg	ctgtccaaac	cggccaaaag	agtacctgcg	aaggcttcag	360
cccggagtag	ataagcgtaa	caagaccggt	gagtcagccg	gattgaagat	gatgatcacg	420
tgcttacagt	cgggacaata	gtcttgatgt	ccttgcccag	ctgagcagcg	atttcggcat	480
tgcccttgag	agatcctcgc	gggtcatacc	ctctttgcgc	ggagcaccgg	ccgaagaaat	540
atatatttgg	catctgtaag	agcctcttga	tgtcngatgt	aaaagtcaat	tcaggccttc	600
gaatc						605

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

cctgagccac	acactggtct	ataatggcat	tggacacttc	ggccagacgt	atacgttggc	60
ctcgcgagca	cgatagtcac	ctcctttgat	cgtatcgtga	agagtcgata	aacggagtcg	120
ccgtcgttct	ggtagttctt	ggcggcatga	tacctccctg	tgcagcgatg	gagtgcgcac	180
ggcgaggaga	atcctgatgc	agaagttaaag	cacattgaag	cccatctcgc	cgaaaagaagc	240
agcagcgaag	caccggccag	gccggtaccg	accacgataa	tatccagacg	acgttggttg	300
ccgggttcac	cagcttctga	tgatccttat	agttggtcca	ctttctttca	gcgggcccgc	360
gggtattttg	gaattttattg	tagccatagt	gaaatacttt	gaattagggt	gtactatcaa	420
ccgatgaatg	cctgacaagc	aatactatca	ggaccaaagc	gaaaccgcct	accaatacgg	480
tagaaaccac	ttagagatgc	acttgacacg	attecaccag	atggtattgt	tccatcccag	540
gtctgcagtg	cactccagaa	tccatgtgtc	aggtggaacc	acaaagcatc	agccatacgg	600
catagagcac	cacgtagatc	ggttggttga	atgtgtacgg	atcagctctg	ctcccttggc	660
cggatggtcg	aaaccatcaa	taccgatc				688

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

tcgggtcatgc	cctccacggt	atgtttcccg	cccagcagta	tcctttgctt	ccggtacgaa	60
tgtggcgcg	gacttcgctg	agatgccgtc	tcagctcagc	aacattgggc	tatggatccg	120
gaagtgtttg	ccaactacgc	taagcacgga	agacacagga	gcctatgccg	gccgaattgg	180
tcaagaagat	tcaggagcga	gcgacttcaa	tcaggcttat	tctatgggag	aaaatcttgc	240
agccgaagcc	tcgatcaggc	atggcatacg	ctcacggctg	aagagncgga	ggccttaccg	300
acgtggccaa	gttcgaagaa	gaagccctgc	gcaaagtcgg	tctacaatc	cgcagatacc	360
tcctcgctat	cgctcctctt	atttccgcca	tactggagca	atggttatgc	atccggttac	420

tacgcttatac	tgtggacaga	atgctggatc	acaacgttta	tcaatggatg	gtgcaaaacg	480
gtggatatgac	ccgcaaaaacg	gacaacgcct	tcgggatatg	attcttttcgc	gtggcaataa	540
caggattttca	acgtgatctt	caccgcgttc	accggtctgc	aaaagcctac	atcagggatt	600
tgctccgcgc	tcgcggtctc	atgtaataca	gcaatagcga	ggctgtgctt	tcaggttcca	660
agatcctgca	agagcacagc	ctctttttat	tcaccctata	ccaaaaacga	aacagctacg	720
atgaaaaaag	gagattactc	atccttctga	tcattatcct	gatgttgggg	cttatgcttt	780
cccctggaca	tcggaaacat	tcaactccct	cagtcgccat	tatccttatt	atacggtttc	840
ctgaagtttg	ccatcttggc	taccatcggt	gaagtactgg	ccgacggatc	aaagcccaac	900
gatacacctg	ccccacctat	ctatgggtgc	gattgtgata	tggggcattg	tcggtatact	960
catcgctctt	aacttcgggt	gtacgaagcc	ggtatacgag	gtatcatcgc	aagaggactg	1020
ctccccgact	cgacagttcg	gtctatacgg	ctttccttat	ctcttcgcgc	atgaatctac	1080
attcggcccc	gccttcattg	ccgcccaccg	catcagcgat	acatatcgga	gaataaagct	1140
acaggacggg	gaggaagcat	ccggctcgcc	gttgaagagt	ggattggaat	cgctttatga	1200
ctttcgtcgt	tggcaagacc	attccttctt	ctggataccg	gcacatacgg	tcaccttttt	1260
acttccaccc	gagtcgcggt	ctttgtggct	gcactcctgt	ccatcgctct	gggactgatc	1320
ttgccttggc	ttcctcccga	catgcaaagg	cgtaaaacat	cagggaccga	caaaggattt	1380
gataccaaaa	tgatgaaaat	gccatgaagg	aactgaaatg	cc		1422

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

ggcagtagcc	tgcttcggcag	cancgcgtggc	ctcagcatcg	cgcaggtttc	caccataccc	60
tcgtattcga	gtgctnccac	acgattggcc	agctctattc	gcgtaccta	tcggttgtag	120
ctgctccgat	gctatccaaa	tacctttgct	ctggagctct	gctcttcggc	ggtcgttctg	180
catggctttg	accttggttc	gcgtcgcttg	gcgttgagtt	ctccgcggag	ttgtacttcc	240
tgccgtgcag	ttgggtctgc	ttcatccgca	gttcgtcctg	caatttctcg	aactcgtgcg	300
cacggactgc	aagtccagtt	ccaacaaggg	ttcacctcgg	tgtccgaatc	gcctgcattc	360
ttgagcacag	ctatcagacg	cgctgcacc	gggaagtgat	gatctcctcg	aaagccggca	420
ccacttcgcc	ggaagccgag	gagcgatctg	cacttctcct	ttgtccaccc	gccccaaacg	480
cagagaggct	cggatatgga	gccttggtatg	gaggagagca	accaccatcc	gcctaagaaa	540
gaaggactgc	cgaagctgtt	atgattgagg	taaccgtctt	tgcttttccg	ttgagccgtt	600
cggcgaaact	tgtctgtcat	gaatcggttt	cttttttcgg	tgcgagcctt	tggtgtctcg	660
cggcttccga	agagcaaatg	ccatgcaaac	aaatccctgg	ccttattaat	cag	713

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

ggttgtccgt	aaacgtggaa	ccgtgtctgg	cacgtgtatt	ggtcgtagga	aaccgacaat	60
atcgggcgga	gagtacacag	gcgatgtttc	ctgctatgca	ttgatgtagt	accacaaagg	120
atataccctt	tgccgccattt	ggccaaatct	ccagtggcac	taatgaagcc	tatggagaca	180
attcgctctt	tgctgacgtt	atgcctcaag	ttgggcagag	gaatcgatag	ccgccggtgt	240
agcatcaaca	acgtctatgg	gtatgtcaag	gcagacatgt	ttgacaatcc	tgtgcagcaa	300
ccaagatgca	ggagaaaaag	acggacttca	atctgaacca	agtgcgatct	atacaaaaga	360
atcgaccgta	aatcctaaaa	actactttac	ggttatgtgc	cgagagtagt	cttgcgtagc	420
aaatacgttc	ctcatggcat	cccggcgtga	agccggatga	aggctggatc	gaatttcagg	480
gtagaaagat	agtctggagc	agttcaaaaa	atacgtagac	aatccggttt	ctgccggtag	540
gctctggccg	acagcatcaa	gaaggcgaaa	gctgacaatt	cattggtcat	acaggtggat	600
tcgtcagtea	tggaatacag	ttctattaca	aatcgcaaat	tattatgcc	tcctatttcg	660
ccatttcgat	gatgaaaaag	ctcctacaaa	gattcctacg	ggcgtttcgg	cctcgtacga	720
aacaatgagt	atatctctcg	gtaaagtcca	ttacag			756

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

acgaactgaa	aagcggtttt	ctgaaagacc	tctatgacaa	tggcgagaaa	tcattcgaaa	60
ccagcagngg	cagatcgatt	cgctccgaaa	tgtattaact	tctacaaccg	tttctcttcg	120
atggagagtg	agatagccca	agagctgaag	tgattttccc	ctctatcaat	tcggctatgc	180
tggtaccttc	gtccgggtgg	cacagggtag	ggattccggt	ttgctcgtcg	tggtgcgtcc	240
gaaagccgga	taagccagtc	ggaaataaac	aagctaagca	catggatggc	tacggtacca	300
agaccaagaa	agtgcgcctt	atcatagaca	ataatcatag	gtacaaccat	aaacagtaat	360
gcaaatgaaa	ttaaaaagta	ttcttctcgg	agagccctgc	tggtgggtgc	ttaaggggta	420
gccaaagccg	acaaaggcat	gggctcctca	acgaactcaa	tcaggagaa	ctggatcgaa	480
tgctgagct	ggctttacct	cccggtgatt	cgctctacag	tttcgacaag	ccgtccatgc	540
atgcccgtg						549

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

```

gagttctgct tttttagctg aatccaaata cattttcttc cgttttttac gtgttaaaca      60
ataactactt ccgctactac ggctcgtatg ctggccgcaa gataatataa ttccctatac      120
cacagcgcga atctgtttct tcgctctgtt ataacgatgc cgttggacgt acggatctac      180
attgggccaa gcattcagga aagggtgaact cgcccttctt tgcatttttg ggtccaaaaa      240
caagcaagaa agccgagatt ctatttactt ttgtgcactc tttgaacgaa aatncgctta
300

```

(2) INFORMATION FOR SEQ ID NO:15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

```

attacaagga aacctcttga tcgtaagcgg atcggcagac gacaatgtta tcttcagaac      60
acgatgcttt ttacagaggc actggttcag gccaatatcc cttcgacatg gctatctata      120
tggacaagaa ccatagtata taccggggga ataccgcgta tcatctctat actcgcaaa      180
caaagttttt gttcgcatct tttantacag nttttctcag ttgcttgatg gggcgagtgg      240
cgaagggggt tttgttcaact tgctccgttc gacagtgggt tctaatagct ctttttgaaa      300
aaactatggc gcaacacgtc aagaaacccg aatggttgaa aatcgtcttg gtgggaatga      360
gaagtttacc gagactaaaa gcattgtcga ggacattgtc tgcatacgat ctgtacaagt      420
ggcaaagtcc ccaatatggg aagtgtctga gtagggggac tgctaccttc atgatcgggtg      480
gtgatctctg acacgtgcct gtcgattttg caacactttg acggggcgct ccaaaccgcc      540
aatgaagcag aacctactca cgtcgcattg agtatcaaac tgatgggggt aaccatgctg      600
tggtgacgag cgttgaccgc gatgacttgc ccgattagggt gccgcacact gggttaagac      660
cattc
665

```

(2) INFORMATION FOR SEQ ID NO:16

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORIPHRYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

tttttgaatg	tctgccggac	tgagatttga	tcgtaatgct	cttttgggaa	ggtgatattc	60
agacagtcgt	atgtggagcg	aatectatcc	agactctccg	gactgctgca	tcggggagtc	120
ctaccatact	tgagatagca	acctcgggtga	tattgacttc	gacggtaacg	gtaagggcgt	180
ctatgctgtg	cagagcgcgg	caaaggtctt	tactaacata	ataaagaaac	aggggtgcga	240
aggacatcgg	agactgtagc	ttgcacggcg	gctacggata	tttccggctg	tgatcatgtg	300
atagtatatg	gaaggctgtc	tatgccatat	cgctcgagaa	gtgcgatacc	tgcccgatac	360
tatccgatgc	cacacgtccg	ggcaaagcca	actcctgatg	agtttacgga	gagatgagtc	420
cggtgcaaaag	agcgagagag	taggggtttcc	ggctttgtct	ttccttcttt	atctctccat	480
acttttcaatg	tgtagcggta	gtggagtcag	gcttggttcg	gaagagcaaa	agcacatctg	540
tcccctatac	caggaaagag	tgaaagatcg	ctgatcaata	tccttgacag	gaagtcggga	600
gccaaacggc	cgactgcgta	cgacttattc	cggtcaagat	ggaatcaaga	gacgggggaa	660
gccgggtgcat	cgagataaccg	gagcgggaat	gaggtctatg	tcgaaaaggt	cgatttcctc	720
cgctaactctg	tttatccggg	ggcatcgggg	tgggaaagat	agaagtcaag	ggctttgagc	780
cgcatgtctct	gaaggctttt	gctttggagg	ggaagtcggg	ggttcggaga	tgacctgata	840
gcgatggatc	tcttcttctg	cagtttgcat	gaactcgttc	aggtggcatg	tgtacttcct	900
cctttttattt	taggcaggag	gggtttggctg	gatcgagagt	gattttaata	tcttctccct	960
tttcaggata	gagccgaagc	cgttattgcc	ctcgttgaaa	tataatagaa	tgcgactaac	1020
atcgcccttta	tttcgtgtcg	aatctgtgcc	ttggcggaag	taacgtgtat	ctcttctggc	1080
gaaaggagcc	ttccccttca	attcgcagag	ccagaaccga	atcgccctggc	tgagattgga	1140
gagattcagt	ttgaggtggc	aaacatcaga	tgctctctgc	atgaaagaga	aaggagcagg	1200
acaaaacctg	ctactatata	atatatatgt	tggttggtct	ggacattggg	acggagtgtt	1260
tcattgattcc	gtagaagtcg	gagcagggtat	tcctctacag	tttccggata	gtgtgcatat	1320
tccaagcgtg	gattcttttg	gccagcgtat	ccggagtatc	ttccggaagg	acggacagac	1380
tgcttgacgg	aggattttgc	cggtggtcata	atgtccatcg	aaagatgaat	ggtgataccg	1440
ctttctttttt	cccttgacgc	aaggacggct	cggtgtacgtg	atgtccgtac	attccttttc	1500
cgccgaactt	gggcaataag	caggatggat	attgacgatc	ctgtcgggga	aggattccaa	1560
gtaggggtggg	ttatataaca	catatagccg	gccagcacga	tcagggtctat	ccctaattctt	1620
tcaagagggc	aatgggcttc	gatccttcga	gcattctctg	ggtagtaacg	aataagccgg	1680
tattttcagc	cgatgggcac	gtgccataac	tcctgatcgg	agtgattgct	gaggatcaca	1740
gccaagcttg	ccgaacctct	ttggcaaacg	aatgacacag	attttctgca	tttgagccat	1800
taccggaagc	taaaccgcta	cttttctcat	tttatttact	atttttgctg	cacacaaaga	1860
gttgattgtg	cagattttct	ggcgtgata	atggactaac	acggtatctt	cggtgctaat	1920
ccgctaaaaca	gcgctaaatg	aagcacaaat	ataagtaaga	gattattagt	aataaccatt	1980
ttaaagaaca	agactatgtc	tgaagtagaa	aaaaagtgtat	cgacctcgta	gttgacaaat	2040
tgaatgtaga	agcttctgag	taacgcgtga	agccagtctt	tcaaattgacc	ctcgagacca	2100
gactctctga	tcagattgag	ttgatgatga	atttcgaaaa	ggaattcaac	atgtcttccc	2160
tgacgaccac	gcacaggaga	tcaagactgt	cggcgacgct	atcgatatat	cgaaaaaac	2220
ctgaagtaaa	atactccgat	ggaactgaaa	agagagtgtg	aacaggggta	ggagccatta	2280
ctccgcttgg	caactctgct	cccaaactgt	ggaaagctta	gtggcaggca		2330

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 557 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

ggggacacgc	atcagtctgc	atagctcggc	agagaagggt	tcacgcgctc	gcgaatgccc	60
agcgatccgt	ccgaagcgat	gagtgcgggc	gccacgcctt	ggcctgagga	tagatgatgg	120
tcagcggttt	ggtcgctcagc	tcgatcaatc	ccaggccaac	tccggcactt	cgtccatgag	180
gccttgagac	ttcgcgtccga	atcgatgaag	gaccaagcat	gctctngctg	tccgctcttt	240
ctttgcggcg	taaatccgct	ggacggcttc	ttcgttcgtg	gcacgcagc	ctatcccca	300
atggatatctg	tcgggtaaaag	gatgattccg	cctttgcgca	tgattcggcg	gctttcttcg	360
cttcactttct	ctgaatatcg	ttgagcatat	cgtgggtata	tctctatatt	ttcgagagag	420
ccgagtgcgc	tcactccttc	agggcaaaaag	tatgaatata	tgccgtatca	atgctttaat	480
atgtcatttc	tagtcttcat	cggttatttc	tgtctgtttc	tttattttat	aaatgatcat	540
tccggccgga	gaaagtt					557

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...7455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

gtacaaaaac	tcttgcaatt	tttttgtttc	catatatgaa	gtattatggt	ntgttaagtc	60
atcaatgttt	atatacagatg	gtaatgcgtc	atcgttttaa	cgctgttcaa	atctcgttgt	120
ttctcattct	ctgcagaata	cgcatgttgc	aattagaaga	ttctttgcaa	cagacaaaatc	180
tattttctccg	gtaatgtctt	ctccatgaaa	agcaatgcct	cttttgagc	ttcattcttt	240
gataacttcc	tgctaaaatg	aggatttgag	caatgagagc	atctcctcgc	tttgtgcata	300
aatactgctc	tccatcatca	ctaaaaattt	agctttttct	tcaagatatt	tcctggagag	360
attcatgaat	cggcttcttc	ttttgctgca	aatatgcaac	ttgggtgagc	ccaactaacc	420
caatatctgg	gcagatgcaa	tacgtcagtt	tttaatttct	ccatttttgt	aaaaaacatt	480
tgaaataata	tttgatttga	tttgatattt	ctactctgga	gctaaaaaag	tcatacgaaac	540
tgctttattg	aatgattgta	aaaaacgatt	ggtgaaaaag	tcaaatcgtc	ataatcggtg	600
tccccataaa	ctcttttttc	ttttttatag	agccgactat	aaaataagct	atccactata	660
gagtgtagtt	tcccctcttt	tgctagtcta	ttatataatg	atgaaacgta	aatggaattg	720
cattgccgta	tgtaacagat	acaaggttga	tcctttcaat	gaatctagca	ccttttgagc	780
aagattgaaa	attctgcagt	cttggaacat	tctcctatag	cccctaacaa	cgcattgctc	840
caattctgtc	acttttgggt	gaattagga	aattccctcg	aagatttttg	gacgatgagg	900
aattccttta	ttatctatgt	ttcctaacat	tcctctcctg	ataaatgagt	gatttgcatt	960
ttgtcaaaga	gagctatgaa	tcgaccattt	gattgagtg	gatatacagga	atgatgcaaa	1020
aattatcttc	ccgacttgca	atgcaggctt	taagggcggt	agtgtagtaa	taagtccaat	1080
gtttgttctt	caacagatat	ttttgcagag	cctcgcccag	tatcttttcg	ccaaaagtca	1140
ggtattctcc	ggatatcggg	atattagaca	tgctcaattg	tcttttttga	gtaagccttc	1200
tcgttcattg	tctttgccta	aatagctatt	tcaagaaatt	tagatgcttt	tgtccaaact	1260

ttttgggctg	gcattctttc	gtgacaatat	gtggggagag	aaatattccg	ttctttgtgt	1320
ttcatctttt	cttttgacaa	aagagaaacg	ggcctttgat	cctggggaaa	aagctcctgg	1380
gcttggatcc	taaaagagga	aaccgctttt	tcaatgctga	actcaattct	tttggagtta	1440
gcctttccct	ctctgatata	tgattatcat	cagagttatt	gcacatccat	atcggatata	1500
ataatgattt	gtattcatgc	ttttcttcaa	ggtaaagtgt	aacccaacct	tcgctgttgc	1560
ccaaataccc	atgttttgtt	gggggagtgt	ttttgatagc	aaatcaacca	gttgagggtc	1620
attttaatta	cacattcata	atttccttca	aaaaataaat	attcccattt	gtaggagtgg	1680
tgtagaagaa	agatattcta	tcaatatttt	ctcgtaaaat	ttttcttctt	tttgatctgt	1740
cttttcttct	gtttccaagg	ttcttcattt	tcacacataa	atctaaattt	atccataact	1800
agcgtatagt	caaattttga	gtgcctccga	aatggatttt	ccctgcatct	ttcctcctaa	1860
aacacgcttc	cataaatcgt	tataaaaaaa	cgggctatcg	gtggaaacaa	tcgaacacta	1920
tctaactcga	agaaatcggg	taataatggt	atgaagatcg	gcggatagtg	ggaggagtgt	1980
atcctttttt	tgtttttttt	cttatattct	tatctctttt	gttattattt	ctcgggtctt	2040
acgactaaaa	tgccacccaa	aacattctcg	aacaaaccac	aaagaatatg	cttgtcaggg	2100
tacaaaaagc	cttgtagtat	gatcccgga	gttcgcttac	catagagatt	ggagcgggtg	2160
ttcaatgtgg	agctttatcg	acgcagataa	atccgggtct	tttccagtat	ggatagatct	2220
atatttttca	tatttatattt	cattttatgg	caccaagccg	atgccggttg	agttgccgat	2280
gcccgcgttc	catgccaaca	gctggtctcg	gcattcccta	ttatgaggat	agggcaccaa	2340
ctggctttgt	tttcaactcc	cggtaatcgc	taagcatcac	cttggtcttc	ccctgatcgg	2400
gacaaaggat	gcggtggcag	tagggctcat	gattcctacc	gcctgaagtt	tttgcgaaga	2460
ttttctgtca	gtagggcatt	ggctgcttcg	tccttatagc	tatatggctg	aaccatttgt	2520
cctcgcgcca	acgcttcagc	aggataggct	ggcaggaaaag	aaaatttcgc	gatcgggtcat	2580
gtcgggatct	tcgataagggt	cacttcccgg	acgcagaggc	ttttgaacat	ttcgggatct	2640
tgacgatccc	tgccagcata	cgtctgataa	gctccggatc	atgagcactg	acaaaatatt	2700
ggcccaatcg	gcaaagagaa	tactgttgag	ttctgtatcg	agttgcccc	attgagacga	2760
gaaaatgaat	aggagatact	tttgccgtgc	atacgttttc	tcgagcccat	ttttgaagag	2820
tgccgcagag	caaattgttg	tgaaaaaaga	gactaatgaa	tcgtctgcct	tgatggatag	2880
ttctattcgc	agtgggtata	gcttataata	tatttaattg	cctaaagtta	ctctaaaagc	2940
gtaattaata	cgtatttttt	tatgcttatt	tgcgaggaaa	tcggatataa	gcacccatcg	3000
ttccgaggaa	ttttgcgaaa	accgcaactg	aaatagaaaag	gggcgagggc	ggggtataaa	3060
atacgaaccg	aaaaatgctc	gattgtgtgc	gtgttttctg	aaaaaccgga	acaagaagtt	3120
tttctgtgtg	gcgcgaaaatt	ttttatttct	cgaacccaaa	cgaaaaagtt	tacgcgccac	3180
gttttctggg	gcgcagacac	agagaagtgc	gttcgtgaat	gaaccgggta	taacaggtgt	3240
gccttatcgc	tttatgtgaa	cctttaacaa	gagatcaaga	cagcgtagca	agtctgtctt	3300
tcaggatatt	catcttgtga	atagagaagg	gaaatatcct	ctttcggagt	attgggtaag	3360
tgggcgattc	gaggagggtc	gtcataagct	cctatgatta	gagatacttc	ggttttgaga	3420
taatgttagc	agaccgaat	agagccaatc	atgaataaaa	ggtttatccc	aagatggagt	3480
tcctacatgg	aactctctcc	gattgcgata	gaaaggaggt	aggatattac	gcgatagcat	3540
atccttcac	accgattgca	gcattacttt	ggcgcgttag	cgcgttggtc	ggcaagtggg	3600
gcttcgtgtc	catagacaat	cttgctcccg	caaaatcgta	gatggtagtt	ecttcagaag	3660
tcgccatagc	ctactaaccg	gggaaggaga	aataagcgaa	atgggggctg	tttctccgaa	3720
aaactctttg	gagaatacga	attcatcatg	agtaagccct	aattggggca	gcacgtggca	3780
ggcaaatcgg	antgcgncac	tacctcttcg	aagcgtatcg	gtgtaagatg	gctcctcctg	3840
cccacagcat	cacaatccca	tagcggccgg	gtgatcgggc	atagcttggg	cggcaggata	3900
gggataacca	tgatcgga	ggctatgatg	agtgtattct	tccattgagg	agactgctgc	3960
ataccacgtt	atagtcgcca	aagcagctgt	ccgtatagaa	gacgctattg	agatacggtc	4020
aggatgatgc	tgagaaggga	catcgaatgg	ttcatggctg	gaaagtggag	gaagctgtag	4080
aagtaagggt	tcttttcttt	ctccaatcgc	cgacaacgtc	caataggcgt	gggaaactga	4140
tatgatccgg	cgtaccccat	ttgctaacct	cgttttgaac	ggaaagctgc	taacgtccgt	4200
tacctcgtea	tatcagtgcc	gtataggtag	ctacggacat	ttgtaaagtc	agcatctcct	4260
ccgacagggt	gtgggtgcta	tagccgacgg	tgcgcaatga	agcagctatg	ccggcagggt	4320
gcgcacctta	ttgggggtatt	tgatgatgga	tgaattcggc	tcgaagggtg	gccactgagc	4380
gtggctactg	tgctctgtgc	tgttcgaaag	tgcttgcgaa	ggcttggcta	aagagaatcc	4440
cattctgtgc	cagcgaatca	tgagggtgtg	atgccccggg	gtaccaccga	ggcatcccac	4500
ggcattagcg	agaagctctc	cagcaggatc	agtacaatgt	tcggcctatc	tgtactcata	4560
tcctctctgt	gctatcagaa	gccgattctc	ttactctcgt	tcctatcgaa	aaccgtataa	4620
acgaagtgtc	tcgaaagctt	tgatacagtc	ttctttgaca	aaaattgata	gttcgaatag	4680
tcttcttcgc	tatgcatgca	ggtaatatgaa	aactgaaaac	aggattgacg	gcagcctgat	4740
tgtgtagctg	cttggaactgt	gaaagacgga	tcgcacattg	agcgtagcca	ctccactctc	4800
tctctgatca	ggaggaatag	gaaagctcca	cccacaaccg	gtttccatat	gcggcgatat	4860
gcggatgtgc	aactactttt	gtcggaaggt	acctacgggt	aatcgatgta	gaacgaaagc	4920
cggtatgcaa	acgaatacaa	ccgtgatcag	agaccgatca	agagttgcgg	tgctgtaaaca	4980
ctggccatgg	cttccgtgtc	tggcgtagat	aaaaaagtcg	tgtggcatcg	aggcggaaac	5040
cccagtaccg	aaaagctgca	gatccgcctg	gtagatcagg	ccgacaaaga	agcttagagt	5100
gtgtaataat	gcttaagaat	ttgtctcagt	attcgcccga	ttttctttct	ccccagccgg	5160
caatggcatt	gatgccggcg	aacaatagag	gaagactgtc	aggtaagctg	ctacggctgc	5220
atcgtgcctg	agtccataca	ggaaatggcc	gcaatatctc	cgotgggaagt	gcctatcccg	5280
gcaagccggc	caagtacacg	agcaggaata	tgactttctg	aaagaggaaa	tagagcagaa	5340

aagaacaaat	actcctatta	cgtagcagaa	accgcttctt	ttccgaaaca	aagctctcct	5400
cggtcgaaca	acgtcttcat	atgtcaggct	gtcggacgct	tccgcgcaag	aagaaggggc	5460
gtgctatcgc	ccacacaatc	cccagcagag	tagtgccaga	gctgtcttgg	ctatagcttc	5520
tgtgatgtgc	aggctctcgg	atcaaaacga	aattctattt	tatgacgccc	ggcaggaacc	5580
tccagtcacg	gagtatatag	ttggcacgaa	tgatcggtag	agcttgggta	tcgatgtcgc	5640
tgtccagcca	tgaggatagt	atatctcgga	aaatatgccc	agcagggttg	tgtgctcaca	5700
gcttcgtaca	cctgtctggt	cggagcatat	tcttcagact	tatagaggca	gtgctatcag	5760
tcagagccgg	tagccttttt	aggattcggg	agagaatcgt	tcgtccacga	cagcgatgtc	5820
acgcgtcagt	cattgctgtc	caaagccatc	atttcctcat	tggcatttcc	taccagcg	5880
tactgccggc	cggccatgcc	ggaccgtaag	cgcccggtt	cgacatgggg	agggccgggt	5940
gttttctccg	gggactatga	tatacttggg	gttgagcaat	tgactacttc	gcgattgcct	6000
ttgctcagtt	ggtgttcgat	caaatccgat	aacgctggag	tttggcagcg	tggatccac	6060
cgatgctccg	tgtgccacgg	tcgtgggtgg	atcattataa	gtgtccacgg	tgagattcag	6120
aacgcgtacc	cgagcgactt	gtctgcaagg	atttgcttgt	ctgcttctgt	cagagtgcag	6180
cacgttggct	gacgagttcg	ggatctatga	aatgctcatc	gttagatagc	gtttgtccac	6240
cgcccataga	tcgaccagcg	tgatcacggc	caagatacca	gtagagcagt	tgctttgagt	6300
ctcttttgaa	agaagagcca	cacaggatgc	cgcatacaac	caatatgccg	aagctacgcc	6360
atgcatcaga	gctaatatgc	ccgagcgaac	attcacgagg	gtagtcttga	tagctgctgt	6420
tcagggtgac	ctgctgcttc	ttggaacata	gcttctcctc	gcccgtctcg	aaaccgagca	6480
gggagggcac	aagggcaaaa	agaagcgatg	ccccaaaggtc	agaagtgtag	ctgcaaccga	6540
agcagtacgt	tcgcgcttaa	ggaggggttt	ccctctttga	ttatttccac	caaagccata	6600
acggccaaaag	ccggtatcgt	aattcggcga	tcacaaggat	ggacgatacc	gtgcgaaact	6660
tatctacaga	ggaaaatggt	cgatgaagaa	gctcgtcagc	cacatcatat	tatcccccaa	6720
gagagtagaa	tagacaggat	ggtggctgcc	agcaaagccc	actgacaggc	cctttgacga	6780
taaaacaacc	caagacaaaag	agaaaagagaa	caaagctcct	acataatacag	gccttgccgt	6840
gaatggttgg	tctccccagt	gcgattcata	cgagctatcg	cctgagcata	ggatggattc	6900
acggtttctc	caccttttct	tcataaccga	agtaaccgga	ggatcctcct	ttaatatcgg	6960
gataaggagc	gaccaagtct	cacctatacc	ataactccat	tgtgtgaata	ggccttgctc	7020
agtcgcgttt	tattctcatg	cgtcacttga	tccgtgggtg	tccgctctgc	ttgagcgcta	7080
gttcgctacc	tccacgcagt	gtctcttgcc	gtattggtag	gtgtggaaga	ggttggtact	7140
attcacagct	ataccaccag	acctgctatg	acgactactg	ccgaggaaaag	gaagaagtgt	7200
cggttcgttt	tgttcgaatg	gcttctgcca	agaaaagccaa	caccatgaaa	aatgacgaa	7260
caggaagtaa	tagctcatct	gtacatgatt	agccaagact	tcaaagccgt	gaaaaaagcc	7320
atcacgctac	cgcttgccaa	ccacctccca	tgtagatcca	gatcataacc	gcaagagtag	7380
gaggaataaa	acacatagcg	tcagcttcca	tatatgtccg	gccataatca	gaatcaggaa	7440
gtaggaagaa	aggcc					7455

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

ggctgcaagt	atcgcgtccg	gatcagtgc	caacggatatg	gtttcattcc	atcgaatgct	60
gttgttttac	ccggtcatca	gggagacgat	ttgggtgggc	acagctgatg	tattcccgtt	120
tggcagaaag	caaaactttcg	cccaacggct	gtcgcgtatc	ctctactccc	acaagcagat	180
gaatcagcag	ttcgacggaa	gcaaaaggaa	cgattactat	ccatacaggc	aaagctgttt	240
tcctctacga	caaggaacaa	caacctgctt	atcgcacttt	cgagcagtat	atgcgtggga	300
aaacatccct	aagtatatgc	tcaacagcca	gcaatcatgg	ggatcttcgg	attagatacg	360
gtttgtatgc	ttctcgataa	ggaattgctt	gatttgcccta	ctctcttccc	ttcgaataacc	420

gctacggaaa	gcgtatctat	gtgatatttg	tcgtgaactg	tatggcgaga	aaggcatttc	480
tttttcggac	atttgaacct	gcatggcatt	atctcttctc	ctgtttaccg	actcaaactg	540
ctctaaagcc	tttgcttcga	ccatttatac	cccgtccttc	gatttggaag	gcgatattat	600
cggttttgga	acggatcatg	caacctgtat	taccgcaggt	agagcaagga	cgacgtttcc	660
accgcacatc	ta					672

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

gcctatctct	gtgatgacaa	agtcggtact	gactcttttg	tcccaggagt	tgacgttgcg	60
cttgatctca	tccgtaatat	gaggcaccac	ttgcacggct	tgcccaagta	ctcgcccttg	120
cgttccttgc	ggattacgtt	ctgatagtcc	tgccctgtcg	gatattattg	gcacgagtag	180
tgggcgtatt	gaggaacgct	catagtggcc	gagatccaaa	tcggcctcat	gtccgtcctc	240
ggtgaatagc	attcgcctgt	ctcataagga	ttgagcgtac	cgggacgat	attgtatagg	300
ggtcgaactt	ctgaagagct	acgttgaaac	cgcgagcttg	gagagtttgc	cgagagatgc	360
tgctacgatg	ccttttccaa	gagaagaaac	caaccaccgg	tcacgaagat	atacttagta	420
tctgccatag	cgcgaaaaga	tgtattgttg	atactttgat	cgataaatca	ggggtacgga	480
aagctacccc	aacggaccag	cctcctccga	ttcgtgcgca	aatatacaaa	aagaacgcgg	540
ctaaaagagg	caaatacgac	agctcttgcc	cgatgcgggc	acatcaaata	agaaatgagg	600
catccgacga	accgcgataa	ggctatccga	ggcaaattac	gcgcgggaaa	tgctccgatt	660
gcggttcgta	aattctcgaa	aacacggcga	gattttttcc	gttttggttc	gggaaacaaa	720
aaattttacgc	gccaaagcgaa	aatttttctcg	cgccacgttt	ttacgaacga	caatggagcc	780
gatttggaac	cgagacggca	atatgagcag	catgccccac	gagtcgtttt	ttctctcgca	840
ggataaggta	tttccttagc	tggataagaa	ggaaatgaca	ccaccgatcc	atagcaaaaa	900
gcatggtttt	cattccgaca	acaaggtgtc	aatgatgagg	gcaaactcga	tcgtaatgct	960
gccggcacgt	gtttcgaatc	gcacctgcga	tcaaagattg	gctgtttggg	aaaaagcata	1020
taaatattgga	ggaaatttca	gagtttcact	cctaatacta	catcagaaca	tggtgtgtct	1080
atcaatgaag	tttccaggac	gttcggcgaa	tatcttctta	ttcccggctc	actacagaac	1140
agtgcactcc	ccaaaacatc	tctcttcaga	ctcctccatt	aagttcaatc	gcgatgagag	1200
tccccgtatc	aagctgaata	tcccgttggt	tcggccatca	tgcatgctgt	ctccaatgat	1260
acgctggcca	tcgattggca	cgcaacgggg	gactttcggt	tatcttcgga	tcgcagagca	1320
taggagtcag	gccgaaatgg	ttcgtcgtgt	aaagaaattc	aaggccggat	tttcaccagc	1380
gattccaatc	tcagaccgga	caatacgtct	gccgatgtat	tgatctggtc	aaaaggacag	1440
gacataataa	tataggtatc	actcacgacg	ttcgtccaat	ggccgtctga	tggttatcgt	1500
cacgagcaga	gactatcgct	cagcacggac	tcacctcoga	agccggtcaa	agattttatg	1560
acgccgttga	gagacttacg	gtgggcaagg	tcggtattac	gctgagcgaa	gccaaactgt	1620
tatttgggaa	aacaaactca	atacgttgcc	gatcatcgac	gaaaatagaa	tctgcagtat	1680
ttcgtcttcc	gtaaagatta	cgacagccac	aagaaaatcc	gctcgaactc	tccaactaca	1740
cggacaagac	cctcctcggt	ggtgcggtat	caatacacgc	gactataagg	agcgagtacc	1800
tgcaactggg	gagccggtgt	ggatgtgtgt	tgcatcgact	catcgagcgg	ctattccgac	1860
tgcagagcaa	tacgatccgt	tggatcaagg	agaaatacgg	ggacagtttg	ccgtaggtgc	1920
agggaatgtg	gtcgatcgcg	atgggttcaa	cttcttgacc	aggccggtgc	ggacttcatc	1980
aaagtaggga	tcggaggagg	ctccatctga	tcacacgtga	gcagaaaggg	atcggtcgcg	2040
gtcaggcaac	ggctgtaaag	acgtagccaa	ggcagctgac	gactattacc	gacgaacggg	2100
cacttacttc	ccatctgtag	cgatggaggg	ctcgtacatg	actaccacat	ggtgctgcat	2160
tggccatggg	tcgccgatttc	ctgatgatgg	gacgctatct	cgctcattcg	acgagtcgcc	2220
gaccaagaag	atgaagatag	gcagcaatat	cgtcaagaat	actggggcga	aggatcgaac	2280

cgcgctcaga	actggcaacg	ctagacagcg	gcggcaccga	gacgctcaag	ttcgaagaag	2340
gagtggacag	ctcgttccat	acgccggtaa	gatgaaggac	aacctgctca	tcacactcgg	2400
cagatcaagg	ctacgatgtg	cagttgcggt	gtcattacca	ttcccagagct	caagagaaag	2460
ccaagattac	cctcgtgagc	agcaccagta	tcgtcga			2497

(2) INFORMATION FOR SEQ ID NO:21

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

cgaggtagcc	ctgctttgtc	tgtccactca	ttcatatcat	tgagggaagt	ccatcgaaga	60
taggtgtagc	aaatttgaca	ttcatcttgc	gtcccgccag	gcaagtaccg	cttcgaatat	120
ctgtcccagg	ttcatacggg	agggtaccca	agagggttta	ggcatatgtc	taccggagta	180
cogtctgcga	ggaacgcata	tcctcttgac	gcacgatttt	ggacacaata	cctttatttc	240
catgagtccg	gccatcttgt	cgccaacttg	gatcttccgt	ttcttggcta	tataactttg	300
gccatttgaa	caataccggc	aggcagttcg	tccccgatgg	tctatctaata	ttgcgacgcc	360
gtagttcagc	ttcaatctcc	ttggagtgc	tcgataattc	accgcaacag	ccttaatcaa	420
ctcgttcgta	tgtgcatcat	tgtccaatca	cttaattgga	tcacattgaa	atcaagagct	480
tcaagatctt	tttggcgaat	ttgctgccgg	ccttaatacaa	ctcaacattc	aagtagtcct	540
tacgccacag	caggttttgc	ctttggtcaa	gttctggtag	cttgctcgaca	gacgcttcat	600
gaagtgggtgc	tgcccttttcg	cgtatgtttc				630

(2) INFORMATION FOR SEQ ID NO:22

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...454
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

catccccggc	aatcccagcc	acatatacca	gaacataggg	gctacaactc	atcgctcaga	60
ttctccgaca	aagtctccaa	agctgcscgc	ctgacttctg	gcgccacaga	gcagccgtat	120
cgcgccctac	gattcgcgtc	acctgtttgcg	cccttcttca	agcgaacgat	cgactgtctc	180

gaataccata	cgtactcagc	aataagggtg	gtacctgcca	aacagaagaa	aatggccgat	240
agccaaataa	gagaagccac	agcaaatgca	acagcaatcc	ggaaaaaatc	gtccgcaaaa	300
tggtataaac	acagacaaaa	acaagtccca	agaggatcaa	taggtcaaaa	gaaaaacggc	360
aacgatatag	aacaccgaca	tgaaggcgcc	ttcacctgcg	gtagtttcct	ttattcaatc	420
tttctctccg	atgcaatcat	ggaccgaagc	cgac			454

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

gccgtctggt	tgaaaagggc	aagatgtctg	ccgatgagca	gcaagccgta	tggctcgtat	60
ccgtacgacg	atggacttca	atgacctgaa	agatgccgta	tcgtgattga	agcgattgcc	120
gaagaaatgg	aaataaagaa	acaggcctca	gtgctgtggc	ggaagtggta	agcgagcaat	180
gtatcatcgc	taccaaacat	cttcattgag	tatcacagct	ttggcaaccc	gaactcccta	240
ccccactcgt	gtgatcggaa	tgcaattctt	caatcccgtt	cccgtgatga	aactgtagaa	300
gttatcagtg	cccagcaaac	ttcggacgaa	gtgatgaagc	aggactggac	ttgtgcgaaa	360
tgctcaagaa	aacagccgta	cgcgtgaacg	aactccgggt	ttcgtcgtaa	accgtcttct	420
cataccgatg	atcaacgaa	gatcggagcc	tatgcccagc	ggtgtggcca	gcatagagga	480
aatagatcag	ccatgatgct	cggtgccaat	cacccgatgg	gccctttggc	tttgggcgat	540
ttatcggttt	ggatgtctgt	ctggctatca	tggaggtatt	attcacccat	tggtgatgcc	600
aaatatcgtc	ctcatccttt	gcttcgcaag	atggtcggca	ggacagcttg	gccgaagacc	660
ggcaaaagctt	ctacgactat	agcaa				685

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...3273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

acaccgctgg	aaagcatcgc	tttcgggtatt	ccgacgggtga	cgaccgacct	tcgggcttcg	60
------------	------------	-------------	-------------	------------	------------	----

gcctttgggc	tatgcaggag	cgcggtagtc	ggaacgactc	agtacgggcg	tagccgtcat	120
caagcgtacc	gacgacaatt	atgcagagcc	gtacaagcca	tcgctgacct	gctatatcgt	180
tggccggccg	aaagtaagac	agaacagcct	gccgggtggc	agccatgcaa	acggcatccc	240
atgcaagtgg	cgtttgtttt	acaaccggta	tgaagaagca	tactctgaat	tgctagtcga	300
gattgaaaac	aaccgataat	gaaaaaaacg	catctttgta	gtcattccac	gaacaaacag	360
ctattataaa	acaatgatat	tgaacatact	gctctaatta	tcggattggc	tttagtcggt	420
ggcggagcca	attttctcac	catggcgcag	cctccatagc	caagcgattt	cgactatcgg	480
atttggtcac	ggccttaccg	tactggcctt	cggcacatcg	gctcccgaac	tcaccgtcat	540
ctgatggcag	ccttgaaagg	aagtggcgat	atagctatcg	gcaacgtctc	gggagcaata	600
ttttaacat	tctggccatc	gttggcatta	cggctctatc	atgccgctga	ccatgtcgaa	660
cagtacgatt	cgtatcgaaa	tccttcaacc	attctctcct	cgcggtctt	gtttttcatg	720
gccaacgacc	gcctctcgac	atggccggag	agaatgtgat	cacccgtaac	gaaggtttcg	780
tattctggct	ttcttcttga	tatttctatt	ctacactttc	aatatgtcca	aagggaaagaa	840
tcccccgggc	aagtgaggca	gtttgcccta	cccctatcca	tataatggta	ataggcggtc	900
tggtagctct	cgtcttcggg	ggcgatctgt	tgtggacaat	gcagctatgc	ttgccggacg	960
catgggagta	agcgaatcgg	tgtcgccatc	accatcgtag	caggaggaac	ttccttgccc	1020
gaattggctc	cactttaatg	gctggcatca	aagaagcgtc	cgggcatggc	catcggcata	1080
tcgtaggtag	caacctcttc	aacatcctgc	tcctcctcgg	atcagtcgt	ccatcagccc	1140
catacggatc	caaggcatta	cggctcgtga	ctatggattt	tcattctatc	ggcaatcctg	1200
ctctacgttt	tcggcctttt	cttcgagaca	aaacgatcaa	acgcttcgaa	ggcagcatcc	1260
tcttatcgct	cttctatgct	atacggctca	tttggctatg	accgcctaaa	gaaagccata	1320
cgggaaaaat	gcgcaagaaa	aggctcgacg	ccattcgccg	gcataattctg	cgagcgaaat	1380
ctccacccaa	gaggaaactg	aaacagcctc	gctgtccgaa	gcattcccgt	atcgcaggcc	1440
acaactttcac	gcgatctgga	aatcctcggc	tagaaaaatc	ggcctcgcc	tcagggaaaa	1500
aagtgtacat	cctgcctcgg	acaatcgtcc	accctcctct	cgcggtgaac	ttcgtatcgg	1560
acgcaccgag	ggtttatcgg	accggtcgat	acaggagaga	tgcttctgct	caatacgtcg	1620
agggccatgc	agcccgtatc	gcacgcgaaa	tagaggagct	gtctgccccg	aagtggcgga	1680
cgtattcttc	ggcccgcacg	acatcgttgt	catcggcaga	aaggaaccac	acgtcaggct	1740
ttactctcgc	ccattgtccc	ggccttcccc	aagtcctcgg	ctgaaaaccg	acacacctcc	1800
tctcggcaaa	cctaccaaac	ttcctacact	gtatagtcac	gaagactgaa	cgacaattgag	1860
tgtgacagga	acgacatttc	catgagatcg	aacgaatcaa	caagtatttg	cctctctcaa	1920
aagactattc	ccctcgcata	tcaaaaacac	atcactacaa	caaacttaaa	cgggagcatt	1980
ttgaggcggt	tgccccctga	ggtctattgt	taatttcac	tatgcagcaa	tatttttaca	2040
tatctttgtc	gcgttttcatt	gaacatcttc	aaagaacaca	ttccgacacc	tttgacatt	2100
acatactcta	ctatgactct	ctaaacggta	tacaatctca	atccaattag	cctcctgtct	2160
acgaatgtta	cttataaatc	aaagtcatta	gcaatatacaa	aaaatctatg	atcgaccttt	2220
tttcaaaaatt	acgcaactcg	gattgcagtc	ttcgcagaat	gcctctaaca	cctatgtcca	2280
cgcctgctg	agccgcagct	atcgctgttt	ttcctggcct	ttttacagct	tattgtcaat	2340
gaatcctatc	gcgagtattg	gtctcttgga	atatggaggt	tcgatttgcg	gatattctga	2400
tgccccgatt	gtttggagct	tggtcgttta	tttattactt	gcagccatcc	gagccgtcgg	2460
ttatatcgag	gcattatgtg	gcccgtgatc	ctgatcgcac	gcttatgtac	gtagtcgaga	2520
tgtacctgct	caggtgctac	gggactgttt	tatcccctat	atagctactg	catttcttgc	2580
tactacatca	gccgaggcag	tgcatctctg	cgagaggctt	tctcttgagg	cgatattggt	2640
catgtccagg	ttggtatgcg	atcgtttggc	ttgtgagtct	aaccctcggt	cggctctaca	2700
tctactccca	agcagacctc	aatttctctt	tctctactct	cttcgtttct	tagcccaata	2760
ctctatgcag	cagtttggca	ctatcccaaa	gctttgatca	gctctccgaa	gatagaggct	2820
atgctttctc	ctatccgaca	gcgcaccttg	tgagagggtg	gtatggagca	tctcgaaaag	2880
cttgatggaa	gcaaaagagat	caatgccctt	ttcgatcgca	ttactccag	tacaaagaga	2940
atatggttac	caaagtctcc	cctaaaagcg	cacacacggt	agtgtctgtc	tgggtgagtc	3000
agcccgacct	gatttatatg	atagctatgg	ttatcctcgg	agaatacccc	ccgattggat	3060
agtctgcttg	catccggtgc	tgctgtaaat	tcgacgatgt	ggtcagtgcc	aagcctaata	3120
ctcaaggttc	gattgcgcga	tgatgtctat	tggagaaaag	cgtgcaggag	gaaaatggta	3180
tgacgtccta	tgctgatacc	gctactccgc	tccgcgggtt	actatacctt	ctggtgagtg	3240
ctcaggaaaa	actgggcttt	gcagtgcata	atg			3273

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

ggacttatgt	ggtgaacgaa	agcttcgata	cgcaaacgct	tcctaacggt	ggacaatgat	60
cgatgctgat	ggtgatggtc	acaattggct	atctacaaaa	acgtttacaa	cactgctact	120
catacagggtg	acggtgctat	gttttagcaat	catggacagc	tagcagtggg	gcaaaaattg	180
atttgagtc	tgacaatatt	tggtaaactc	taagtttacg	gttcctgaga	atggtaaaact	240
ttcttttggg	tttcatctca	agagccttgg	actaatgagc	attatggagt	gttctgtcca	300
caaccggaaa	cgaggctgca	aactttacga	taaagctgct	ggagaaaccc	tcggatccgg	360
caaacctgct	ccgatgaact	tggtgaagag	tgaggagtaa	aggctccggc	accttatcag	420
gaaagaacca	tcgatctctc	tcctatgccg	gacaacagggt	gtacttggca	ttccgtcatt	480
tcggctgtac	ggtatattcc	gtctttatct	tgatgacgtg	gctgtttctg	gtgaagggtt	540
tccaacgact	acacgtacac	ggtatatcgt	gacaatgttg	ttatcgccag	aatctcacgg	600
caacgacatt	caatcaggaa	aatgtagctc	cggccagaca	actact		646

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

cggcaacgct	tttcatcgta	ttagggacgc	tgaccaaact	gtatgggatg	ttggcttggc	60
tttcttcccg	tttgtgaaaa	gaaaaggccg	ctatttgggt	ggctttttgc	atggttccgg	120
ctgatcggta	tcttgccgat	ggtgtttgag	gaggttctta	tgcccttgag	cagtatatga	180
attggtttgc	tagcctggca	cgaagaatgg	ggagaatctg	ttctccctgt	atcaaaacgt	240
ttcccgcctc	ggatgggttag	gaaaatgacc	ggtattgccg	gctactccga	cttgtgttgt	300
tagtcccccg	acttatccta	ttcgtctctc	ctttcctccg	attagtcagt	acaaggctcc	360
actctttcgg	atgagcatat	tggttcgac	tcgcttttca	ccgtttttatt	cagtaccggg	420
agcgaatcga	gtacttatat	ctagcgttgt	tgggtgtcgg	tatctggttc	atacatcgcc	480
ccaaagggaa	cccgaaccgg	tgatattac	actcttagtc	ggaacactat	tcctctcctt	540
ttatcgccga	ccgatctgtc	cctgcggctc	ttcg			574

(2) INFORMATION FOR SEQ ID NO:27

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1057 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

gactctaccg	cgaaactata	gactttttacc	ccattcatat	cgtataaaga	gcttcctgcc	60
ctaaaagaga	ctcggggatc	tcgacgagcg	catatcttct	accggattgg	gatatactct	120
gacagtggga	gcattctactg	ccaagttgat	gtcggacttc	cttcgtagtg	aagcatattg	180
tcagaatcac	cgttgagtca	aatactcgcc	agttcttact	tttagctttt	tccacatcct	240
ttacgtacag	atattcttct	catcagtgtc	cttgaggtgt	tcnaaacgac	gaaattgctc	300
tgagcgctg	cgccgggaga	tagtgtgggc	aaagcattca	ccatttcgtc	atttcttcac	360
ctgcgactcg	attggaatga	caaacaaaa	catcagtc	ttcaccccg	acagattcaa	420
ggatgtaagt	ttgttcgatg	acaccaaagg	taagcaacgt	ccgaattctt	ggaaagatcc	480
aaggtcgaaa	ctcattgtca	ctgcacaaaa	gtgttaacaa	tagaggattg	gcactcagac	540
gagtttcgtg	atccgattac	cgaagcacca	aagatcattg	agacgaggtt	ggcactgagt	600
tccaactccg	tcaggttatt	atcagaacac	caaagagggc	caacttgggg	ttgttatcgg	660
tcttcagctc	agtcagctta	ttcctgcaca	gccgaggatg	atcaaagccg	gattgccact	720
caaggcccaa	ccttcattcg	ttagagtcgc	accaaactcg	cagcagcttt	gggttttgcg	780
tcaatccaat	gatttcagat	tatttttcgg	gcatgcgaga	taggtcagat	taggtttttc	840
gttacatcga	cagccgttgc	accggtagat	cgacagccca	atgggtcgta	ttaccataga	900
tagtgagggg	ttgcgtcccg	atcgtgtatt	ctggtagtgc	tcacgaata	cnggtattcc	960
tctccttgtn	ggtaagtggc	tccccattga	gatcgatcca	gatgcctttc	ttctctatgg	1020
aatgaaccac	aattcgattt	tttcgcctac	ggccttg			1057

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2349 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

ctttgggctt	caaaaagata	cgaggaccta	tctgtaggta	tattttatcct	gtttttcttg	60
ttttattgag	tggtagtacc	tattttttgtg	atgagagtgg	actctcgtca	tgtcgattaa	120
aaagaaaaca	gaaatgaata	agagtataaa	ggctcaaaga	cagaaaagca	tttgctcatg	180
gcatttgccg	gagaatgcaa	gctcggtcgc	gctatacttt	ctttgcaagt	gttgccaaga	240
aagaggttat	gaacaaattg	ccggagtttt	catggaaacc	gctgagcagg	aaaagagcat	300
gccaaaagg	ttttctcttt	cttggaaggc	ggcatgcttg	agaaaacggc	tcttttcttg	360
caggaataat	cggttccacg	gctgagaact	tggcgcggcg	gntgccgggtg	aaaatgaaga	420
gtggacagat	ctctatccgg	ctttgctgaa	acagccgaag	aagagggatt	taaggagatt	480
gcagccgtat	tcgtcagata	gcaaagggtg	aagccgagca	tgaacgtcgc	tatctggctt	540
tttggctcat	gtggaagatg	gatcggtctt	cgagcgaacg	gaagaaatgc	atggcaatgt	600
cgcaattg	gctatgtcat	tacttccaag	aaagctcgaa	gctatgtccc	gcttgcgctc	660

atccgcaggc	ttacttcgag	ccaatgaaac	gaattactga	ggatcacatt	catatagaaa	720
cgaagtaatt	atctgtctca	tgtttttgaa	ggaggcaccg	ctcgggagag	tcgtgcctct	780
ttttgctctg	ttattccctg	cgaaaagcgt	gtgcgtcatt	ttgttttttc	gaacaagtat	840
agagaccggt	cctgtaaaag	gggactctca	cggtttttcc	ggcatacagc	cggattgaaa	900
agtgtctaatt	cgatgaaaaa	accgtacttt	tgccgaaatt	acttaataac	caaacaagta	960
acctaagata	cttatggaat	gaaaagattt	ttatcacttg	gtcttctgct	tgtgggattc	1020
attccgatga	gctttctgcc	caacaggctc	agccactccc	tacagatccg	gctgttcggt	1080
cggtaagttg	gacaacggat	tgacttattt	catccgtcac	aacgagaccc	gaaagatcgt	1140
gcggattttct	ttatcgca	aaaggtaggt	tctattttga	agaagatagc	cagtccggtt	1200
tggctcactt	cttggaacac	atggcttcaa	cggtagcaag	aacttccccg	gtaagaactt	1260
gatcaactat	ctcgaacgat	cgggtgtacgt	ttcgggtcaga	acctgaacgc	ttctaccgga	1320
ttcacaagac	ggaatatacg	ataatggatg	tgccgactac	acgtcagggg	atatcgactc	1380
ctgcttgctt	atcctgcatg	attggagtaa	caatattacc	ccgacgggca	tgagatcgac	1440
gaggagcgcg	gtgtgatcca	ggaagagtgg	gtgctcgctg	cgatgccaac	cttcgtatgt	1500
tcgaggctat	acttgccaag	ctatgccggg	taataaatat	gcagaacgca	tgcccatcgg	1560
tctgatggcg	tcgtgctcaa	cttcaagcat	gatgagctgc	gcaactatta	taagaaaggt	1620
atcgtcccgga	cctgcaaggt	ctgggtgatcg	tgggagatat	cgatgtgact	atgtggagaa	1680
caagatcaaa	gaactcttca	aggacgttcc	tgctccgtga	atccagcaga	gcgtatctat	1740
acgcgggtag	aggacaacga	tgagctatcg	taccatttgc	taccgatgct	gaggctacta	1800
ccacgcagct	ctcatcagct	tcaagagcga	ccccactcct	caagaagtgc	gaggatcgat	1860
atcggacttg	tggaagacta	tatgaaacag	gtgatcacta	cagccgtgaa	tagcgtctgt	1920
ccgagattac	tcacaagcct	aacgctcctt	tcctcagtgc	ggagctttct	tctctaactt	1980
catgtacatc	acccagacta	aggacgcac	aattttgttg	cctcggttcg	tgagggtgaa	2040
gcgagaaaag	cgatgaacca	ttggtggcag	agatagaaaag	cctccgtcag	ttcggttattc	2100
accaaaagcga	atacggatcg	tgacggcnc	gaatgtgctc	aagcgatacg	agaatcatac	2160
aacgaaaagag	acaagcgtaa	gaacaatgct	tatgccaatg	aatacccacc	tacttcaccg	2220
atggcgggcta	tatcccgggt	attgaggtgg	aatacagacg	gtgaatgctt	ttgctcctca	2280
ggttcctctg	gaagcattca	atcggctatt	gcccaaatga	tcgatccggt	gaagaatgct	2340
gtcggttacc						2349

(2) INFORMATION FOR SEQ ID NO:29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

gcaaacctcc	gacaaagaac	tgcattctgca	caatgtgaaa	ctggctatgc	aagggtggag	60
cgacatagct	ccattaccct	cagttcgctt	ttccttgagg	agcactgcat	ggcgagttca	120
cattgtccaa	gctgccttcg	atgctcgagg	agtggttggc	gcacatcttc	ctgcacttgc	180
gggcatagag	tcgcagcaag	agtgcgcact	gaggatgtcc	gtctgcggtt	ggcgttggac	240
ggctcttgcc	caaggaagtg	tgcagcttct	tccggttgcc	tttggccgaa	gcggttctat	300
caagatcagg	gcagcctatt	ccgaattgct	tcgaagcctc	gattgcacat	tcgtaccgac	360
aggctcatga	ctatgaacaa	agagctacgg	gaacggaggt	gaccttgaac	tcattccaccg	420
gcaaggccga	actcatctgt	cgtccgactt	gtatgtgaat	ggcgatgcca	cgacacgaga	480
cctcaacctg	aagcatcagt	ggcaaacgac	agcatccgtg	cccgactgga	tatgggacag	540
acaagcgagg	agcgaaaaac	ggatttatat	cgctgctcac	aaacttcctc	gggacgagga	600
ctcatcgctg	aatactcata	tcggtctcga	tcgctctcgg	cacgcacgcg	cggatagagt	660
ggcagatagc	c					671

(2) INFORMATION FOR SEQ ID NO:30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 724 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...724
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

```

ccgaatccaa agtctcaagc tctgcaatga ttgctttctt gctcttcagt tttcgcatc      60
ttcggagcgc atatctccct gttcggtttt tttacgttga agaatgcac gcacgcagtc      120
gtaaaacgct tccatatctc atcactaacc gatgaggaac ggctccgatg gttttccatt      180
tcttttggag ttcggcaagc gagtagaggt ttctttccag tcggaactct cctgaaggct      240
ctccgttctt ctaccatggc cagcttcttc ttgtagttat cggtcagctc ttcagtttgc      300
ctttgaagaa agctgttttc ttattgaaat aatcgtcaca tgcgcgcgga aacgctcgta      360
gatcttctca ttgtcgcttc tgcgagcata gctatagtct tccacttggc ctgaatctct      420
agtacggcct tcgtttgctc gcccatattg ccagcgagtt cagaccggag gtatctatcg      480
cttccatttc tcacaaagca atgttttcgc agccagattc tctgtctcgc gcattctttc      540
ttttcgaaat gttcctgata cttcttattg atagcaagta gaagcagctt gaatctcgcc      600
cacacctctt cgcggagttc gcgagctacc ggtcccatc gcgccattga tgatgcagtc      660
ttgcagtacc ctgaaagaat ggatgaatcc gcattctcag tcagcacttc ggctgatgg      720
atca                                     724

```

(2) INFORMATION FOR SEQ ID NO:31

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2863 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2863
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

```

attgttttgt gtgtttatgg tatgatcaat gacacaaaat gatggcacgc aaggaaaatc      60
atccaacgag aagaggtctc attcagggac gtcattgtcac gaatcgatac aggaaagccc      120
ggaatgtatt tttgacccaa gtcgatagct tacatgagag gatactatgg tctcctatga      180
gaggatacta tggctctacac gagaggatac tatggctctca tacgagagga tactatggtc      240
tcacaaagag gatactatgg tctcacatga gagaatacta tggctctcta tgagggatac      300
tatggctcta cagcagagga tactatggtc tcatatgaga ggaactatgc tctcacatga      360
gaggatacta tggctctaca cgagaggata cttgggtctca tatgagagga tattatggtc      420

```

tcacatgaga	ggatactatg	actattgatg	gaagatgcta	tctgctctgt	gtcggatggc	480
aggttcgggg	gtgggaggtt	ccgtgcgagc	tgtaaaccg	atagatgaga	ttgtcacacg	540
cattttccgg	gagatttcgt	tgtcaattga	ctgtttttca	gtgtctgtta	tagacataaa	600
gtatcaaatc	aagagtcggt	tgtttggctt	gtcgggctat	gaatttgtcc	tgaataaata	660
gaacagggtg	aagagaagg	tgagccattg	gggtgtagct	cgcaatgagg	gaaaagcaaa	720
tgctgtggtc	agccttgga	gagcgttcgg	cgatggctgt	ctcttctatg	atacttcgag	780
ccattccaca	ccttggtgaga	tacgatgtgc	catacctatt	cccccatgca	tatgccaccc	840
aaatgcaagc	ccggccagcg	catttccatc	cgccggatga	tgccctgccga	agttccgtat	900
cggcgtagta	ttgcggtatg	gcatggcggt	gcgtgagatg	tgcagcagat	ccggcttaca	960
ggtgtgaggt	atgcgcagca	atcgcgtagc	tcttccattg	caatcgtgct	gatctcctcg	1020
tccgaaaggc	tatgagcgaa	gcatttcgca	ccccacccat	gaatatggaa	tagagtgcgc	1080
cccttcagg	gctctgccac	ggaacacgtc	cgaagggaac	aggatgcgag	gatgcgacga	1140
ttttccctcg	aagggtacag	gcacccgaaa	gcccggcggtg	tgtggcaaca	tttcggcgga	1200
acctacacgg	aacctctatc	atggggcata	atagagctgc	tcgaacacgg	ctgattcatc	1260
cgcagggaag	tggtgaacag	tgtggggata	tggtgcgctg	ccaccgtact	caccaagtgg	1320
cgaaggaat	ggtgtgctcc	tcttccgaag	catccgtata	ggtaaggccg	aagtgtgtgc	1380
tcccggtga	ttgatgtatc	ggatttgcgt	ttccgtcagg	agtgttcgcg	tccgatgtag	1440
tccgccaag	cttcgaccag	aagaccgagt	ccccttgtag	ggaaaagacc	ttgcgcgagg	1500
ctttgcggtc	gcgttcgctt	gcggctgtcg	ggcttttcga	acggcaccca	gtacgaagct	1560
gccgtatcct	gctccagatc	gtatagtttg	ggcagggcaa	agcgagtaac	cagttggcgg	1620
gatctcctgc	ataaatacct	ccgaggaaa	gatcgactgc	gtagtcacaa	aacttttgcc	1680
cagccggcga	cgagccaagg	ctccgaccgt	ctcatgggtt	gtccgcctct	cggcggaag	1740
ggttcgcca	ggatacgcca	tttgcccaca	gggaaaagag	aggagttagc	actgcctcgg	1800
cgatgttcct	tggaggggat	acagtttggt	gcctttccat	atcagacggt	tagaggccgc	1860
agagtggcta	tctcaggttc	caatccgagc	agttcgaata	gctcggccac	tccggagagg	1920
agatcgtgcc	ggtattcggc	cctgtctcga	acacgaaccc	tcctctctgt	aggtgcgtat	1980
ctgtccgccg	atatgagcag	ctcgctccaa	ccagaacagg	cctgccggca	agctctgagg	2040
aaagcggctg	tggtcagtcg	gtgagcccg	ctcctatgat	gacggtcaga	tgatccatga	2100
atcaggctcc	ccaccttcaa	aggcaagagc	atagaaaagc	atctgcttga	gcatgggacg	2160
aggccgttgg	agcgtgtcgg	cgagagatga	tcttgcaacc	ctactcgca	atgaagtaga	2220
gatcggacga	aacgatgtct	ttcggtttct	ggcttccagt	atccgtagta	gcagagccac	2280
tatccctttg	acgatgaggg	catgctatcg	gcccggtagt	gcaccttgcc	atcttgagg	2340
gaggctgcta	tcatacgcca	ctctggcaac	cttcgataat	gttctccggc	accttatctg	2400
cgcattccagt	tccggtaggg	cactgcccac	atcgatcagc	agttgataac	atccatccaa	2460
tcattcgaaa	cggagaattc	ctcgatgac	tgatcctggt	ttcgtttata	cttggcatgg	2520
gataagctaa	tgagtgaata	gtcagtgtaa	gcggctttca	cctgttcgct	caaatatcga	2580
atgacggttt	gcgccacgca	tcgagtaac	ttttgtcgat	gatctgcata	ttgtccctct	2640
gggtatccag	tggtcgccga	agccatgttc	gttcttgagc	gagtaattga	taatacga	2700
caagggatcc	ctaaattctt	gatcacagg	acatgatcat	ctgtagagcg	cctccgtcgg	2760
cttgatgaa	gtagttgcca	tatcctaatt	cgggtgccgtc	tgccatacgg	cagagatcaa	2820
ccccggggca	tagctcttgg	agagtactcc	caatagaatg	tag		2863

(2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

aaagtccaag	gaagagttgt	ctgcttttct	cggtgtgag	catatcgagg	ctgcaaatgc	60
ttcgtcaagc	aggagcaatt	gcgggcgttg	gagaaatata	gtgccagtgc	cacacgtga	120

```

cgttgccctc cgcttagatc cttcggaacc gatgcaatat gtccgacaag ccgaggggtgt 180
gtacaatgct ctcaaattccg gcattctctat ggcttccttt cgcaggggtat atggaagtac 240
gatatctcat gcaactcgttt ccatggcaaa agcccatatt gctggggaac tattctatgg 300
aaaaagattt cggattcaga ggtttcccat cgaatagcac ttccctcat actctgtcag 360
tacacctgcc aaaacgtgca ggagtgttga ttgccacagc ccgaagggtcc cgttatggca 420
aaaatctctc ctttgggaat atcagtgaat gaccgtccaa tgctttcact tccgtactcc 480
cgtggcgata gtaacggcca gattgcgaat agagatcatt tgcctaattg aggaatctgg 540
tttcgtccgt ctcttgatta tgccggactt tacggatcag atccttgcgg ttagtcgctc 600
gggaccaatt tcttggcatg taccagtc 629

```

(2) INFORMATION FOR SEQ ID NO:33

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

```

tacaaactgg acgttgtagt tattccgaca aacaagccta tcgcccgtag gatatgaatg 60
atcgatatcta taagacggca cgtgaaaaat atgcagcatt atcgaagaga ttgtacgtct 120
tgctgaagag ggcagacctg tacttggtgt actacttcgg tggaaatata cgaattggtg 180
agccgtatgt tacgctgcgt ggcattccaac cacaaatgta ctcaatgcca aattgcatca 240
gaaggggccc agattgtagc tcaggccggt cagaaaggaa ctgttaccat cgcacgaaca 300
tgcccggtcg tggtaacnac atcaagctct ctgccgaggt taaaaagccg ggggtatggc 360
tatcattggt acggaaggc acgaatccag acagtggaca gacagcttcg tggtcggtcc 420
ggcgcgtcagg gtgatcccg tgcgccatat tctatgtttc ctttgaagat catctgatgc 480
gcctctttgc acagaaaaga ttgcattatt gatggatcgt ttaggtttca aggaaggaga 540
gtgctcgaaa actacatgct nagtaagtcc gtggagcgtg c 581

```

(2) INFORMATION FOR SEQ ID NO:34

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

gtgctgatga	cgtagccgt	ttactcattt	atgcctctga	tccggacgaa	cagatctcat	60
tgtgacgga	gtgttcgac	gcctttcgga	aacactctcg	tcggggaaca	acgactgacc	120
atcaatacgg	ctacagaact	gaatccgtga	ttatggattg	gctctctgcc	ttggacacca	180
atgttgctat	cctgctacac	tgatgggatt	ggtcggaggc	ttcacgatga	tagcccggtc	240
tgattttttg	gtcatggaca	aaacgcagtt	tatcggcatg	ctcaaagctt	taggtgtgct	300
gaagggtcgc	ttcgccgcat	attcctctat	ctggctatga	tgccgttggt	cgtggtatga	360
tctggggcaa	tgttttggct	cttatactct	gctcctgcag	caacatttcc	gctggttgcg	420
tctccttcga	tcctgatatt	tctacatgga	ctatgtgcct	gttcaagtgg	actggctcgt	480
atggattctc	ttattttggg	taccttcctc	gttaccttct	tgatgtcctc	tgctccatcc	540
atattatttc	gagaatttcc	cccgtaaag	cccttcgctt	cgagtaatgc	ttcaccaggg	600
aatagggtag	gtcatctgtc	cattcgagac	cat			633

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...4047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

ggcaacgtcc	tccgcagtgc	cgaaaacacc	tgcatgtccc	gatatacctc	gaggcatgca	60
gcagcttcgt	cgtccacggt	accgcggacg	atgcctttcg	tagaaatttg	tcgttctgtg	120
ccggtgcaat	gcgcgaaacg	gaatattatc	gagtgggaaga	taaccgagcg	aaccggctcc	180
gatggggcgg	aatatagttc	ttcgacaaaag	acgttcaagc	tcttgcccga	tactttttcc	240
acaattgctg	tagcaggata	aaccccagat	ccgaataactt	gtagcgtccg	actcattgcg	300
aggggtagaa	gcgatggtat	tgaggacaat	ttctttgacc	tcttcgatag	atacagattg	360
gaagaaaaac	gaaacggata	gtccggccga	aatgcccgga	aaccaaactc	gagcgaaatc	420
cgaagaatgg	attgccccac	aattggtatc	tactcgaacc	catcccgaac	tcgcgcgggg	480
agagagcaac	tgccgtccaa	actgctactg	tctatcagag	attcgtagaa	attgatcgag	540
gccgaaggcc	tgcttcatga	agtagaagct	gctgtacggt	gatgtcttga	ggtctgttcg	600
ggcaaaacga	ggcaatagcg	ttccgagccg	gtcggaggct	tcaattttcc	atcctgaacc	660
aatagcatca	cagccggagt	agtggcacga	ccttggtgac	ggatgccaa	tcgtagatgg	720
tggaagaaga	cacctgcctc	cacgtgccga	tcgctcgaga	gtgccgaagc	ttttgtcata	780
tacccttgt	ctcgatggac	agcgaggata	cgacaaccgg	ggaaagcccc	ttgcttaggg	840
cttctttcgc	tatgcggtct	accgcgggca	tcgggatgag	gcggacgaca	attcggtcgg	900
cggcatcatg	ttcgtctgctg	gatcaagtgt	ctcctcttcc	tgaacgaccg	ggatcccaac	960
gcccaggat	accacaactc	gtcccgaatc	ttggaggctg	ccattcgagc	agcctccttt	1020
acgttttcatt	gccacgacta	tagcccgagc	tttgtccata	gccgcgggaa	tcctatcgct	1080
acatagggcg	atgtgaagaa	gacgatggca	gtgtgggttt	gttccgtagc	cggtggagaa	1140
acgttcctgc	ccagtcgggc	tgtgtatgtc	gaactggacg	atcacagcat	cgtaaccctt	1200
gagtttgag	agcaactctt	gtgtagtgtg	ctgttgctgc	ccttggcata	ggaatagcag	1260
tccttgctcg	taagcccagc	tcttggtgtaa	aagtattgga	ggctgcacca	tctagattga	1320
cgctgcaata	cggtttccct	ccgagagggg	gaggaagtgc	ttcttggttt	tggaatcgta	1380
atggatgcct	gccaaagatc	ttccgacatc	cgttccgctt	ccggtctgtt	acctgtcgta	1440
ccacttcctc	tgccggtagc	tccttgata	tcctttacaa	atgatgagcg	catacttgaa	1500
ggccagaatt	ttgcgacatt	ctcgtccagc	aattctttgc	ttatcgttct	gtcttccact	1560
gcggccagac	ctcgagagaa	gtcttgaccg	gggccaccgg	accgaggagg	atgtcatgcc	1620
ggccaatatg	gcacggacgg	agatcggttg	agaaccggct	gtctgtctcc	ctgcatggcc	1680
agtccgtccg	taaagatcag	ccccttgaaa	ccattcctcg	ccgaagcaga	tcggtgcaga	1740
tggcatgact	gagggaggag	ggcgattttt	ctttgcttcc	aaagccggaa	cattgaggtg	1800
agcggctcct	actcgctgag	gccggctcgg	aaaaactcct	tgaaggggaa	caattcagta	1860

tttccaattc	ctctcgggag	gcaaagaccg	tgggcaaggt	cttgtgcgag	tctctgtggt	1920
attgccgtgt	cgggggaaat	gcttggccac	ggccatcact	ctccgtcctc	caatccttgt	1980
gcataggcaa	tccctctttc	tgctactcgc	gtgggttgtc	gccgaagctg	cgcgtgccga	2040
taacagggtt	cttcggatgt	tgttcacgtc	cagcaccgga	gcaaaattga	tatgaatccc	2100
catcagcggc	attggcgcg	tacctcccga	ccatagttgt	agaggagctg	attgtctttt	2160
ggtgtcccaa	gcccataattg	cgagggaagc	gtggggcatc	tttcaacgca	tgtgcaaacc	2220
ccactcaccc	tccatgtcta	tgaggagagg	ggtgcggctg	cttcttgcaa	gcggcgagtc	2280
atcgtgtatt	gctccgagag	tgctccctttt	ggaagagtat	gccccgatg	tggcaggtgc	2340
gcaccagctg	ttggcttgc	ttactttttc	ttctctgtaa	gagggataga	cgatcggcat	2400
ggcagctggc	ctactttttc	ctccgtgctc	atagccttca	tgcggtcgtc	acccagcgtt	2460
tgacatcttt	gctctcgact	cccccgaa	ggagaaagga	tagtctttgg	actgctgggc	2520
atgcatggca	cccattgttcg	tgcgggccgt	gccgtagctg	tgtacagcac	cgagagagag	2580
agtattgtga	tggcggaata	agaaatcggt	tcatacccta	caaatgtaca	taaaaatggt	2640
ggccgatccg	agccttccct	tctacaagaa	aaagggaagg	gacggacaaa	agaagtttgc	2700
ttccgttgtc	gtctccttcg	ctcgaaagag	agtaaaaggt	agagaagttg	ttatgcttgt	2760
tcttgtacga	tgatctcgcc	atcgcgagca	gagggcgtag	cgtctgccct	ttctcgatct	2820
gtccggagag	gataagatcc	gtaggcgatc	ctccacttcg	ttctggagtg	tgcgcttgag	2880
cggctcgtgt	cgtattggag	gtcgtatccc	ttcgtcgcta	tcacatcctt	ggcttcacgc	2940
taaggacgag	gtcgtatccg	gcacgatgga	tgcgcgccaa	gacggcttta	gctctatgtc	3000
caccatccgg	cgaatctccg	tcttgcccag	ttggctcgata	ggatgatata	gtccaaacgg	3060
ttgagaaatt	cggggctgaa	cgtcttgtca	gagctttttg	gatcacggaa	cggctatgct	3120
ccttgttcgc	ttcctctctt	tttccgaacg	gaaccgcata	ccctgcccga	agtctttgag	3180
ctggctgtac	ccacgttgga	ggtgatgatg	atcacgggtgt	tcttgaaatt	cacggccgtc	3240
ccagactgtc	ggtcagctga	ccttcgtcca	tcacctgtaa	gagagattga	agacatcggc	3300
atgcgccttt	tcgatctcat	ccaagagaac	caggaatagg	gtttgcgtct	tacgcgctcc	3360
gtcagttggc	cgccttcttc	aagcccacat	atcccggagg	ggcaccacag	agacgcgaaa	3420
cggagaactt	tccatatact	cgtcatatc	cacctgatc	atggcattct	catcctcgac	3480
aggtattcgg	cgagcttctt	ggccaaatag	gtcttgccca	cccccgtagg	ccgaggaaaa	3540
ggaaagaacc	gatcggtttc	ttttcattgc	gaagtccaga	cgattgcgct	ggatggcatg	3600
caccatcttt	tcgatggctg	tgtcctacct	actactttgg	tcttgagatc	atctgccatc	3660
gtgcgcagac	gttcgcttcg	cccgtgctca	gccgctcagc	cggaacgcct	gtcatcaacg	3720
ccacacatgc	gccactacat	tctcgtccac	cgtctcgcgg	tgcttgagca	tctctcttcc	3780
cattttttct	tctcttcgc	tatctgtctg	tgagtgcgcc	gccctgatcg	cggaaggagg	3840
cagccagttc	gtagttctga	gcctttacgg	cgagagcttg	ttctctcgca	ccgatgccaa	3900
ttcggcctcc	agtatctcga	ttctttcgga	gccaccacat	tggtgatatg	gacgctcgcg	3960
cgggcctcgc	catggcatct	atcgcccttat	ctgggaagaa	acgatcggat	acatagcgtc	4020
ggtcagttcc	actgccgctt	tgatcgc				4047

(2) INFORMATION FOR SEQ ID NO:36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

gtgttttttg	cgataaggtc	tgaccttgaa	aaaaaggatt	ctcaaattgt	caatatatatt	60
tcctctatgt	cttatcgatt	ctgatataata	acacaacttt	tcttttgaag	tgggtatcag	120
gcttatgttc	tatcctttta	tgttcatttc	atattgatcc	ctaattgctta	tgtattgtca	180
gataaaatat	ggcaaaaggt	gtgatttttg	ctatttttgt	tgtgttctca	ttctttatgc	240
ttaagatctc	agcagtcacg	ctgaaccata	cgctaactat	aaagtctatac	tctttgaaaa	300
atactgttta	gagaattatg	atcgtgcatt	ctcccttggt	caggtgctta	ttcctccata	360

caacgtggag	aaatcagaaa	tcgagtctga	tttgaaatag	cctacttgaa	tgtagctaaa	420
atgttttatg	acaaagctcc	cgcaatcaat	ataagacgat	aagggaatac	aggccactga	480
atccgaagag	atcgccctcca	tgcaatacca	ttcggttaatc	cgatttaggt	ttgcttgta	540
ttgtcagact	cttctgttct	gagatattta	ggatattttc	tgtgtaaaaca	gaacagaaga	600
taaaaagaat	gatgagagcc	tgactttgtg	ttgccacgtc	tttttcctac	aaagtaattc	660
gacataatat	gataaccgtt	gcccattgat	caataacatt	ggccaatcag	gaccggggat	720
agtcatgcgc	gacatattcg	acacatggat	c			751

(2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

aggtttctccg	tctcacacag	atcgatgtgc	acagttttggg	tgagctgcgg	tcaatcaagc	60
actgcgcaat	atcgaagctt	tctacgaagc	tttcaataac	agcctactga	taagatgtat	120
ttggaacccg	aaaagcgtgt	agtcgtttgt	aagctgaccg	acactcctat	acgggaaaag	180
aggctacgtt	ccgaggttat	tctttggaac	gcagcctctt	tcgttagaaa	aggaacctaa	240
tcggaaggaa	agagcataag	gaggggttat	aaactcggcc	tatcgctcat	cagataatga	300
gaccaattcg	agggacgctt	ggtaacggct	gccaccaata	cacgatcttg	gccgcaaagg	360
cttctgccaa	tggtctggcc	gcagcttgta	cctagccccg	gtagtcagca	catcgtccac	420
caaaagaaca	cggataccgg	cacgcgcgta	ttcggggaga	gggcaaactt	ccctttcatg	480
gctgactttc	ttccgaatag	gactgtccgg	tctgactgtc	cgtatatacc	tttctgcgca	540
accttcttga	acaggtattc	ccgttacgcg	acttaatect	tgtgcgatag	gagtgcctga	600
ttgtagccac	gcttacgttg	tttgctgtgg	tgtaaagaac	cggcactatc	agatcgtaat	660
ccttggaacag	gaaaggatag	gatcggcgcc	cattcgtccg	agcatttcgc	cgatctcact	720
gtatcctcca	tatttagtgc	gtgtatcata	ggccttacac	ccccgtcctc	tttgaaaata	780
aaaagctgta	cagcgcgtcg	atataaacat	ccccattcag	acgatctaata	ccaattgcat	840
cccttcgata	taccnggca	ttctcaccat	gcaacgagga	caaccccgat	ctccgtctcg	900
gcgagcaagc	t					911

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

tgggctgtcg	tattccaacg	tgccgaaggg	gaagtctggg	ctgccaccgc	catcgctctt	60
ctcagagact	ctatttccgt	cttgccggcg	acggactcgt	atggcagaaa	acggttactc	120
actgttcacc	gagcgagata	gctggggagg	gacgctgttc	tctttttctt	gcgttggggg	180
tatacacctg	ctgatacaca	ttgatccgcg	aaatacggaa	acttcccccc	ggccatgccc	240
tacgcataga	gtcggagagg	gtattacgac	cactgcctat	gacacagtag	accgtatgcc	300
cggttngaca	gccatttttt	tatcttatga	aggaggntta	aagagtnnct	gaacccccgc	360
cttattcttg	ccggcaagag	actcgttcgc	tactgaatgg	cagatcggcc	atacttcccc	420
tttccggagg	atttcgactc	gggatgatag	cctacatgct	gcacgtcttg	aagtaccac	480
atgtctat	tatctcctat	ggcaaagagg	aaa			513

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

ntccccggcc	cacatcgctc	aaacgggcag	cagcccttcg	ttttgctcac	gaaagcgacg	60
agactttctg	ccatatcggc	tgcacgttcg	ggaaaaagat	ggtgtacaag	gggtgggcag	120
ctcggtaggt	gtcccagagc	gagaaggact	gtagtgtttg	cgtgccgtct	ttagcgtatg	180
gatctttttg	tccgctctct	gtaacggcca	tctgcatcgc	tgaaaaccgt	cgggcagagc	240
agacttgata	gagcgcggtg	tagaaaatag	tgtccactcg	gggcgatatt	ccttttccgc	300
cactatacgc	gacaaggcac	gttgccacag	cagcgatgct	tcccacggta	gcggtcgaaa	360
tcgtggtggg	gagcttcttt	cgccagattg	ttgccgctcc	cttttcgtcc	acgcccata	420
gggcgggtga	gatcgtcagc	ggctgtcgga	cttggctatt	aaaaacgaaa	ggtgggctac	480
aaggccgtaa	caatgaattg	cgtcgtatcg	ttattggcat	attggggtac	actgtctatg	540
tgaactgctc	tatcggaaga	gaaaatctgc	tgcggaagaa	tatgcgctat	cccgtgcca	600
accgtccgag	aagcgataac	cgcttatcgt	gtggctgcga	tcagctgcag	acggcttgct	660
tgctgtcctg	tcccaattca	tcgtgcattg	agatcgaggg	gacttcagta	c	711

(2) INFORMATION FOR SEQ ID NO:40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

tatagctcag	ctgggtttaga	gcattctgect	acaagcagag	ggtcataggt	cgaatcctat	60
tgggcccacc	ttttttcaag	ccgtgcaagc	atcgatgac	ttgtgcggct	ttcttggttt	120
cactttaaaa	aaagaagaaa	ataccagtga	aacggactga	ttgtttttct	ggcaatgggt	180
ggcttgctgt	tcaccctgcy	aacgcacaag	aagcaaacac	tgcatctgac	actcccaaaa	240
aggacggact	ataaaaaggtg	tgaccggact	aaatgcctct	cagacttctc	tgacaactgg	300
gctgcccgtg	gagaaaaacac	ggtggcaggt	aacctctatt	tgacatagat	gccaaactacc	360
tgaaagataa	atggagttgg	gacaacgggt	tggtacagac	ttcgggtctga	cctacacaac	420
agccaacaag	tggaacaaaa	ggtagacaag	atcgaactct	tcacgaaggc	cggctatgag	480
atcggcaaac	ttggtacgga	agtgcgcttt	tcactttcct	ctcacagtat	gccaaaggaa	540
tgagaagccc	tcggatcact	tgacaggagt	caagcatatc	tctaattttt	cgctcctgca	600
tatctcactc	tcgggtattgg	tgccggactat	aagcccatga	gaagttctct	ctctacctct	660
ctcctacaa	gggcaagctg	actgtatagc	agacgactac	ctctcaagtt	tgaggagcct	720
cggggtgaaa	gttgggaaaa	gacaatgttc	gaacttggtg	cttttgtagt	gggttcggcc	780
aataaaatct	gatggagaa	gtcaatttga	taaccaaggc	ttcattcttc	tcgcttatac	840
gcacgacttt	ggcaacattg	acatcaattg	ggaggctatg	ctgccatgaa	gatcaacaag	900
ttcctcacgg	ctacgatagc	caccaatctt	actacgacga	tgatgtgaag	atcaacgatg	960
gcccgaataa	ccagttcaaa	aagttgtggg	cgtgggtggt	gcgtacactt	tctaaataaa	1020
gaatttcaat	tctgacaacg	aaggctgcgg	ctgccgatat	gggtggttgc	agcctttgtg	1080
tttttgcttg	aattaacttc	ggtaggggag	caagagggca	accgcataaa	tctttagtag	1140
ctttttgaga	tagtctatat	tcagagcggc	tttgaaaacc	tcttccgtaa	ggatagtttg	1200
tctttgtgcc	cagagacggt	acatcaaatg	ggaactctgc	acaataagca	ggcacttttg	1260
ttcattcttt	ttatgtgtgt	caggcgacta	tttggcacat	gccggatttc	cacaagtgga	1320
aagtatcttt	ccaccattgg	aaaataaact	ttccactagt	ggaaacttct	tttccaatgg	1380
tggaaat						1387

(2) INFORMATION FOR SEQ ID NO:41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

atgtacaagt	gaacaaaaaa	ctcgctcccg	atgagtataa	gatatggcgg	actccgtccg	60
ccgcagattt	gccgaattgg	gaactcctat	tgcatacgcc	aaacggtcaa	tgtgtcgat	120
acgttgccga	ctgcccaaat	atccgcatga	attgggtgaa	tggttcattg	acttataatg	180
ccgtgtataa	ttgggacgtg	gagcgaaaac	gactaccgaa	caaatcattg	ggaacacgat	240
ccggatcagg	caacgctgga	acttcccctg	caactccaatc	tgacatcgct	gtatgcaaat	300
ctgctttcct	caagagaata	gagcagcaca	tcacgaatcc	ggaaaaaagg	atcctgtaaa	360
aaaagcagcc	cagccattga	ccaagaaaat	ccgttgctcc	ccgattccac	ggtaacactg	420
acgcacactt	ttgcgtccaa	gaagtgaag	tgtccgctct	cgggtccggat	ggcaagatgt	480
atccgctgaa	acaaaaatca	aggacaagaa	tacaatcgtc	attttaaata	atgacagcaa	540
gagatcaatg	taacggtaac	tcccccgagg	cagaacggct	ccaatcctca	ttcgggtcga	600
taggcgaaag	gatgggtatac	gccttgatga	tgctcaaagc	atcaacctta	actaccggca	660

```

atcgctccggc ttgcatctgc ccggatcttg cccaacatca aagctgcagg cggacaaggc 720
tccgtggatg gtgtttggca ccgggatggg actttgcttt cggctttacg ggagaagatt 780
tcgtgaaaaa gccgcg 796

```

(2) INFORMATION FOR SEQ ID NO:42

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

```

ccgttcaaca cataagtcgg tttgtcggat gcgggggctt gccaaagtgag gtcactgtct 60
gcccggtatc agaccattgg agattctgta cgggagcgat tcattgccac cttctccggt 120
cactacaacg gacgcagcat cgccgggcct tgctcgttga cagtgaatg ataagtccta 180
ccggcctcta ccacatatcg ttacctttgg agacaccctc tcctactata tatattatgc 240
caggatgggg ttaatgatta catagtcata agtgccggca ggaatatcgg ctgagctggt 300
ccatcaagca cgaaattcgt gggagaaaaa gatgcacgg catgaccgga actttatact 360
cgaaaggatc gtaaagaccg gccgggatcg ttcgttggca aaccaaaaag attcttcggg 420
aatggatgcg ccgtactgat ttgatctgca tcccagagca tttgatagcc tgtgccgtct 480
tcccatacat gtgagcctcc aagataattc gtgccatacc ggcaggaatc ggatctcggg 540
atccttggcc ttggatgttc gaataccttt ctgcaccgct tgggtgcgtac agaaggagca 600
gtcttcggcc ctccctgtgc ggcagccgct tgtccccaca caatagggat aataggacgg 660
cgagcgaaaa taaagaattc aatttttcat accttttgaa agtattaaaa gattaatggt 720
tttcgcaaga atagtctcta ccactattcg gcccgaaaaa aatatg 766

```

(2) INFORMATION FOR SEQ ID NO:43

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2844 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

```

ccctggctaa tgtctatccg atcaatagct tcgacgggat ggctaccgaa gtctcggacg 60
ctttcgtttt acgacgagca gcactttccc gatgcgtccg tggtttcgca tatcaattat 120

```

cactccgata	cgcttaccat	tcggaaggag	atccgatgga	gaacatccgc	atccgcctgc	180
gcgagaccga	tgactaaagc	tctccgaagt	cgctcgtcagt	gtctccgctt	tcgggggtggg	240
aggcagcaga	acaagacggt	gctcaatcct	atggatgtct	acacgaatcc	aagtgtaacg	300
gagatctctc	gatggcgctg	cgtcagacac	ccggcctgca	ggagtgggag	atcgtgaggg	360
ctttttcggt	cgcgaggagg	cctcttgagg	aaggccgtga	cgatagaagg	cattagagtg	420
aagcggtttt	tcggcaagaa	cgattcgacg	ctcctgctcg	ttcacgtttc	gagacaggaa	480
tgttcagcgg	ctttcgctct	ccaccggagg	ctatggggcc	acggaaggcg	gtgcgctgac	540
ggactactcc	ggttgcgatt	ggcgggtaag	tctccctcgt	ccgtcgggta	ggaatatccc	600
cgctttttgt	aaacggtggg	ggtgggcatc	tttccagtcg	aatcgtttct	atatagagca	660
aaatgcctca	gtgagcgatg	ccgccttata	cgctcgtctg	tcaagccgga	gtacaaaactg	720
cccggtagca	accgccctat	gcctacaatg	cacggacgat	atggaacccg	acttcgcaag	780
atgagtgaag	gggctttttc	tcttcgtaca	cgacctttcc	tcttcggctt	tgccataccc	840
tctcctgcaa	ctgcatatat	gctctatgcy	ggacgaaaca	ccatggattc	gggatggctg	900
tttgaggcca	tgacttcgaa	ggaggcaaaa	cacctccacc	ctgtccgccc	gctatagcga	960
agaccacaac	cggctgcacc	ccagcttgaa	atcgagccgg	acatagagag	cactttccgc	1020
accgtagagg	cgatgccaat	atccgccttc	gcttcgattc	tcggattaag	gcttggaact	1080
ctcctacgga	tcgattata	catatagcga	agccaagtct	tctgttcgga	ggataaatca	1140
tcagccttac	ccacactgcy	agaacacctt	gtggcaccta	tgccgaagcc	ctcttccttc	1200
tgtcgaatcg	gatctccgct	acagcggatt	gcgcgccgaa	tattccggac	ttaccgagtc	1260
ggctattata	ctaccogtnt	gtcagccact	tacaagctct	ctccttcgag	ccggatcacc	1320
ttgatgcagg	agggtgtgcc	gccccggcgy	actactacct	ctcccatggc	atgtgcccga	1380
aaagcgcgaa	cactcgcagc	agtacaaact	gacctatgaa	tgcgaccctc	gcgtacacaa	1440
gtgctacgcc	tccaagccta	tgacaaagaa	attcccgact	gaccacgttg	gctcccgatg	1500
gcacagcctc	caacctcgga	agggatatgc	acgggggctg	gacttcttct	ggaaagcatc	1560
cggactgaca	gatctttcga	gcattgggtc	tcctatttct	ataccgatgc	tcgcaggagt	1620
atctcttttc	gcccgatcag	gaacgaccgg	atttcgtagc	caagcaactc	tttccaccgt	1680
gctcgaagat	tggtgtgctc	ctatcagctc	actatcaacg	tgtcgtatgc	ctggcggttc	1740
ggcatgacct	accacgatcc	caactagcct	ccccggccta	tttgaacgca	tcgctaccgg	1800
ccaattttcag	catagtgcct	cgtacaatta	cccattcaag	tacaagaaag	ccggcggtgt	1860
actgtcttca	gcgtgcacaa	tctgttcaat	tcggatccca	cctacggcta	tgcttcgggg	1920
acaaaacccat	cggaggcgta	tatccatcgg	tcagaatctc	accccttacc	gacagtttta	1980
tatggtaggt	ctgttcatca	acttcggaaa	gaccgcccac	aagaaatcat	gaacaccgat	2040
ataaaaatca	aatcaagaga	aaactttcaa	aagaatcgcc	ctgctcctcg	tcgcaggctt	2100
tgcaggggtgt	gtgcaacatc	cgcacaaggg	acggcttatg	ccgaagtgat	gaatcgaaag	2160
tagctgctct	ggacagtgtg	ccaccgacgg	aatatgccac	actggtgcgg	acttttcccg	2220
gatagcagcc	gtggaaggat	ccgactggat	ggctcttatt	ataccgccta	ctgccggata	2280
atccccggcct	tcggcaaccc	ctcgaggccg	atcggctatg	cgaagaagcc	gaatccatgc	2340
tgagcaaaag	ggatccctcg	gcggagatct	gtccgaaata	gcctgtttgc	gtagcatggc	2400
ccctcggcac	gccttttggg	caatccgcaa	gaacgctggc	agacatatgg	gcagagagca	2460
gccgacagtt	ggctgtcgcc	cttgaagcca	accctgctat	ccgcgagcct	acttctcgca	2520
ggcccaaagc	ctgctgtaca	ccctgcgag	ttcggagggg	gcaaggacaa	ggccctccct	2580
tttgccgaga	agagcggttc	tgctatgctg	cggccacagt	gtcgctcgcc	tatgctccgc	2640
actgggagag	cagcaagcac	gccaactcct	aatgctttgc	aaggcagaaa	cccaaagtga	2700
ctttgcggcc	atcggtctcc	tgatcgagaa	cctctataac	ctgcatcttc	gaaaacacga	2760
accgaaatcg	ttccgattgt	ggcacgtgtt	ttcgagaaaa	tggcgcgaga	ttttttcgtt	2820
gtggcgcgta	aaatttttgc	ttcg				2844

(2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

```

cggctcgtgc aggacaatac atgcttgtct gtacgggcga tatggaatcc ttatggaaga      60
tgcctcatgg atagagttgg cttccataga agtagcaggc atacgagcac ccattcatcg      120
ttactggtgg cctccaaccc acagatcatc ttctcacagt tcatcggggc aatcccgaga      180
cattgccgac tttcagatta caaatgaagg tgggtgctact ttctccggga aaatcgaaat      240
agtggataaa aggcctttctc ggaaactttc ttccaagcga aagaagaaca catggtctcg      300
cccaagggga aaccaaagta ttgtctccgg agctgactgc gaatcttctc tctatacaaa      360
tgccgaactc tttcccgatg gcacctatta catgtcatca gagagcaggg attttgggat      420
ccgatcgatt tgtttgggga cattactatc gtatccgtct cattacggat ctatcctctt      480
cggacatcgc ggtaaggatg tttctactat agtactttat cccaatcctg ctcacgactt      540
gtccatgtag ccattcctcc cacatatgcy ggcagcacac ttcgtttgtc gatattcaag      600
ggcgaatgca gctctccacg aagatcgaat ctgccgaatg cg                          642

```

(2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

```

ctttgaaggt cccctctaga ggatccccgg gctgtteget ttcttttggg cgggcccatt      60
tgaggactga ataggaaata aatgttttat aagacaaaca ataagatgca gatgagaaca      120
tttcgtgtcg ttgcgatcgt ttcgctgtct tttcttcttg gatgacgctt acggcgcaaa      180
agaatagttg gtgggtggtg cccatgccgg acgcgagtac ttcaacaaca caagtgagga      240
tatgagaaag gatggaatac cggagtagtc ctgcgctact atttctccga tcgatatatt      300
ctttggc

```

(2) INFORMATION FOR SEQ ID NO:46

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

```

cggcagaaat aggaaaaaag gaacggatgc atgtcagact ccggttgag agcttaagct      60
cggagtcggy acctacatgc tggcagaacg tctttttccg ataagctccc cactcaaata 120
cgccacttgg gtgctatcga tattatgcag ccgctaacgg ccggctggac gatctgcgcc 180
tgaaaactcg tgtggaacgg atgccggagc tttgaccata cagggcagca tcggcctcga 240
ttctcctggc gacttgccga tgtagatgct catgcgacta ccgaaagact ggaatcaagc 300
tcatggcaga ccggcacgat tggcctgaac atgtggcggt cgactgaaga tgaaggcccg 360
actggctgcc ggcaatctcc tctcggaag tgggagggac gcgtgtcgca cctgactttc 420
cgaggctata cctatgagga ctgacgatcg acttacaggc cgacaagggg cagtggtcag 480
gcacccgtaa atgaacgacc ccaatggcca tatccggcta tctctgccg gagaggggag 540
cctttctctt cgagttcttc ccggttcgaa tggaaatctga cagcgacaa cttcgtcccg 600
atcgactttt gcccgcctcg gactgccatc ggccgatctc ttctgatttc ttcc      654

```

(2) INFORMATION FOR SEQ ID NO:47

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

```

cgtattcaga gogatatgct gctttctact gcccaaaagt ccaagaacac tggttcggca      60
actcctatat catgggtata atcaagaaca attatctgag tttgggtgcc gtttcgagga 120
tctctataag cccctgcccg gacatgacc gagatggggc gtggcggtcc tcacatgtat 180
gtgaaggga gctatcttgg gcggagctga ctatgggaga cttctacgat cagttcggta 240
gcggttggtt ttccgcaccc atgaagagcg caacctcggt atagacaacg cggtcgcggc 300
ggacgtatag tactcactcc ttttgatgga gtgcgtgtca aggtattgca ggacagcagc 360
gtaactactt cgaccgcacg ggcaaggat tcattccggc cgaggctacc tactgggttc 420
tgatctggag ctgaatgtag acgttggagc agtgccatgc gcgacaatga ctatcatttg 480
gctatcgggg atcgttcggt tccaaacacg aagcagacga agatataatt gtgggtgtag 540
cgaagatcgc aagcgactca acctgcccgt caatgtccc attatgggct gcgcaccaac 600
tttcaaaaag gaggtctcgc cctctacgca gagtatgata caaatacaac gatac      654

```

(2) INFORMATION FOR SEQ ID NO:48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

cgatttctgg	agggctatca	tccgatccag	acgggatagc	tttacctctc	gggcacatcg	60
tccgcgaggt	ggcgagcagc	ataagtaccc	ggccgttcga	atacttgaac	atgaaggcag	120
agtcgtaacg	cacctcttcc	atcaggcgag	agtggcttcg	aagtcttcct	ccgtctccga	180
atggaagcca	cagaagggtc	gctgctgatg	gcgcagtcgg	gtatggcccg	gcggatagct	240
gctacctgtc	gagataccac	cggcgcgat	agccgcgctt	catgacgcgg	agcacttgct	300
gcttcgcgtc	tgtgccggca	ggtgtatatg	attgcagata	ttgggtatcg	tgccatgacg	360
gcgatggcct	cgtcatccat	atccttgggg	tgggagaggt	gaagcgtatg	cgcatgtcgg	420
gcacagcttc	ggccactgct	ggagcagatc	ggggaagcgg	atgatccgcc	cgttttgttc	480
gtatcggtag	agtttacatt	ctgccccagc	agcgttacct	cgcggaatt	cttggcttta	540
gatcccgcac	ttcgttgagg	atgctttcta	tttcgcggct	tctttctcgc	ctcgtgtgta	600
gggtacgatg	cagtagctgc	agaagttggt	gcacccagca	tgatggagac	gaatccgttg	660
atatgtacgc	ca					672

(2) INFORMATION FOR SEQ ID NO:49

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...4127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

tttcgtagcc	atgcacttag	tgcggacgaa	tgagagagag	atcttcttgt	ccgtgtaata	60
gatacccggt	ctatactgag	agccgacatc	gttccccttc	tattgaggat	tgtaggatct	120
atggtcttga	agaaaagatc	gagcagcgag	agagcgatag	ctcactcgga	tcatattcga	180
ctcttaccgt	ctcggcaatc	ctgtggtttg	ggaacagacc	tcttcatacg	aaggatcctc	240
gacatgccgt	tggcataccc	gacttcggta	gccacgacac	cacgcacttg	tttgagaaat	300
gctcgggtacc	ccagaagcac	ccaccggcaa	agtatattgt	cttgtctcgg	gaatactgtc	360
attatgcttt	cgcgaagaag	agcaactacc	ggactaagag	aaaaactaaa	agaagccata	420
ctgataagaa	taagagaaaag	aacttcataa	caaatcggat	tctcttttca	tgagaatggg	480
gaagagacag	ctcgaagtag	tggcaggtcc	tattcatgat	gatagggttc	atggttgaga	540
tagtcatggc	acgatacacc	tgttcggtga	agaagaggcg	gatcatctat	gagagaaaat	600
cattcggctg	agcgatatcc	tatcggttac	agcctccgca	ctgcagggtc	aaatccatat	660
gggcctccta	tgacaaagac	cattcgcggg	tgccgatcag	cattttcttc	tgcaaaaagg	720
ctgaaaaactc	catgcggaat	actctctgcc	tcgctcatcg	agcaatacgg	tgctgtccga	780
cggcgaagac	gagcgagtat	ctcccgacct	tcggcatcct	tttgctgttc	ggagaaaagt	840
tgctacccag	acggacatcg	ggtattacct	ccacttcgaa	agaacataat	ggctcaaccg	900
acgaatgtat	tctccggtg	cctgaaccat	tgtttgctgt	cggtcttgcc	tacaacgagc	960
agtacgatct	tcatcagaaa	gcagatcatc	ccccgcatac	gcgttggaag	cccaaccgct	1020
tgcgggctgg	acggcatgct	cggttggttc	ggttgaaaag	tcggagcacc	ggcggcgagca	1080
tttctgtggt	caactgctgc	tgacctgtgt	gcccgatata	tccgcgcccc	tgcgccaagc	1140
cttcacatcg	gtgtaccaac	ggccggttgaa	ctcacgcttt	caatatcgac	ccagaccgta	1200
acctgatcgc	ctacttgata	ggaagatcaa	tacgatctcc	ccacacgctg	aagtgtatct	1260
tgcgagggtg	ttgacgagcg	tttccagtat	gtactcttgt	tttttccatt	cctttccgga	1320
agcttgccga	ctcccgaatt	gagtggcagt	atctgaataa	gctgcccttg	aactgaatat	1380
ccatatttgt	tttgttctaa	catagttatc	gttgggtttc	cacgcctccg	ccatgggtctt	1440
atcgaaaacc	gatgatgtgg	cgtacttcgg	aagggttcgt	gcagcacttt	cacgagcgcg	1500

ttcgggtcct	tctcgaaccc	tctgtccaaa	aatgttccat	ccgcctgaat	ctctaataatt	1560
cgttccctat	aggagtggtg	aaggcgacaa	tgtctgccgc	caactgcttc	ttgaggtgcc	1620
atagcgaata	gaacagttat	tatagaggtc	atcgaatagg	cgatagcctc	atccgaggat	1680
acgatacggg	gcatggagaa	aagattttcc	accgggtccg	cttcacgctg	ttaggcactt	1740
cgggaccggc	atcgggtcac	gcttcattac	cttcttgcta	atcgttttgg	catcatcggc	1800
caaatagatg	gcatgccttc	gctcttgccc	atccttgccg	atccatccaa	gcccggcacc	1860
ttaaagctgt	tgcacccgga	gagaacgatt	cgggttcggg	gaagaagtc	actcatagat	1920
cgtattgaaa	cggcggggcaa	acttgcggtg	catctccatg	tttgctcctg	atcttttccg	1980
acaggaactt	tcacggcacg	atggatcaga	tgtctgctgc	catcaatgtc	ggatatgtga	2040
gcaggccggc	attgacatgt	tcggctgctt	acgggctttt	tccttgaaa	atgtcgttcg	2100
ctccagccgc	ccaaatacgc	attcatattc	agatagagat	aaagctcgag	cacctcctta	2160
catcactctg	tacatagatt	gtagccttct	ccggatcgat	cccgcagcca	aataattcagc	2220
cagtatcgta	cgcacattgc	ggactatatt	atccgatgcg	gatgtgtggt	cagcgaatgc	2280
caatcagcaa	taaagaaaaa	gcattatata	gatgctgcat	atccagaaaa	ctccgaatag	2340
caccaaaata	atgcccgaat	gcagattgcc	ggtcggcctg	ataccactga	ctacagtttc	2400
ctacacaaa	cctgttttat	ttgttttccg	atggtcgcaa	agatagggaa	aagaaacttt	2460
ttgtccgtaa	ttaaagcatt	ttgcagattc	tgcggattcg	gctatcagtg	caataactaag	2520
gtaaattttg	caagaagcat	tcgagcgggt	tctgaattcg	aattcctttc	ttgggtctaca	2580
cattcgggac	attccgcaac	acaccttcaa	gtctggcaag	acttgctcgg	ccgacagaga	2640
accatcgtct	ctcggaaatt	tcataaaagg	tatcagaagt	ccattctttc	ggatgctgaa	2700
agtcctcggt	gctctatgaa	atatacgtgc	caaaaaagtt	ttcacaacga	agctgagttt	2760
agaatcattc	caataaagta	tcgaaaggga	agcgattttg	aggtgaaaga	gacaagaaag	2820
cgaccttttg	gggcttgcaa	ttgctttgta	ggaggttgat	ttgcgattta	tatataaacc	2880
gttttcgatt	ttatatagat	cgtttcta	ttatatataa	atcgcttttg	attaatatat	2940
gattgattgc	cattttgtata	taaatcggat	agcccaaaag	gcccttatca	gggccataaa	3000
taaagagaca	cgcgccagg	tcactataga	actcggcgg	gtctctttat	tttgagtgt	3060
ttatggagag	gatctgttcc	tttttattgt	ctgatacagc	ctccccttta	ttcaaatact	3120
gcgatgtcga	atgtattgtc	ggggcgacaa	tgcgaccgc	aaagctcgcg	tgtgggagg	3180
aatttagtac	tcataattta	ttatcgttta	gtcgtttatt	aaagtaattc	tattgttcga	3240
aagactgttc	ggtcgcaaca	ttaagctttc	tgtagaaacc	tcttcggccg	gcaaataatag	3300
cgaagccgaa	actacaggga	atcgtaattc	gccattcaat	tatcaagtgc	aacgggtctgc	3360
ccattttatc	cgcgggtcta	ttgttttaga	atatgtgaag	ggtgaaaagg	tgtttaagat	3420
tcggcaaaaa	agtgtagctt	tgcaatctaa	gttttttgag	aatgtccgca	cagacttttt	3480
cttcaagcta	ctgttgccgt	ctttgtctct	ttgcacagga	gtcgtttcgc	acaaaaccaac	3540
gttgcttctc	atgagcctgt	ccgctacaat	ggagaaggat	cgtctatgcc	ctcccacaga	3600
cacgcacgtg	tgtacgggca	caattaaacg	tactatccac	aagcccgga	cgctccatct	3660
ctatgcccaa	aggatttcgg	acaggaggcc	ggcggagaa	cgagcatccg	ttaccgtttg	3720
ggtaagtgtg	agcccaatct	gtgggaatac	ccgatttcga	tcaaaaatat	atatagagtt	3780
ccgtgccggg	acgggtggcag	acttcgtaac	cctcaacaaa	agggtatcat	agtcgggtatc	3840
aatgccgaca	ggcaagacct	gccgtcacca	ttccggacac	tctcttccgt	ttgccgacaa	3900
tacagcccg	catagaaaaa	gtcctgcttt	gcctcaggaa	tataccgtgg	caggcacgaa	3960
aggaaagcag	cggaaatcgc	cgcagcccaa	gtattccgca	tacgtgagag	cctgatgggt	4020
tgctgaccgg	tcaggctgag	aacatgccca	aggatggagc	ggctatgagc	tgatgacaca	4080
agagctgaaa	gcacaggaaa	ctgctctgct	ggaattttct	atggaaa		4127

(2) INFORMATION FOR SEQ ID NO:50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

cccgggtggag	aaaatagaga	gaaagctgcc	atcagctgga	cggacgaaag	atgaagttag	60
tcaccgaagg	agaagaacag	atcttcaagc	tcatcaggaa	aagtaatccc	accaccccc	120
actatctctt	ccgttcggaa	tggaagcgat	aggaaaagag	gatatgctcc	atgcaccgag	180
tgccggcata	tcctctttct	ttttcagcta	ttgctgctga	tgaaacagcg	ccccccgtca	240
gtctacctgc	gagagccatc	gctgataacg	acattgtaca	ccttgggttc	gcggcgaatt	300
ggttccttgg	aatctctnct	nggcattctc	gacaaagaga	tgcacagttc	tttcttgacg	360
aggttgatcg	tacaaccgcc	aaatccgcc	ccatgacgcg	cgaaccggtc	acgccacaat	420
cccgtgctat	gccgttgagg	agtcgagctc	ttcgcagctc	acctcataga	gacgactcat	480
accatcgtgc	tttcgtatat	tttctgtcct	acggtttcgt	agtcgtcgcg	ctccagtgtc	540
cgcacacatc	gagcactcgc	tgcaattctt	cgacgacata	ctcggcacca	tataatcctc	600
ggcagagact	tc					612

(2) INFORMATION FOR SEQ ID NO:51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature:
- (B) LOCATION 1...733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

cggcattatt	ttttttctga	actatcattt	tcttactatg	ctgtatgctt	atcgtatggc	60
tgcattttgc	tgaggccata	cgctaaaaac	atttcaaagt	atgtatttgt	ttggataagc	120
ttttccctat	catatattat	cgctgctgtc	taacctctat	cattgagtat	cgtatcatcc	180
gccagcaatt	cgggttaaagt	tcccgaacgt	attctgggtg	tagaaacttc	ttgtcaggcg	240
gatagtgggg	taagcctgaa	cgtacaagaa	aattatcatt	tgtgggacca	aaaacgtggc	300
gcggcaattt	tttgcttttg	gttcgggaaa	aaataatttc	tcgacaaaaa	cgaaaaaaaa	360
ctcgcgcgta	aattttcaaa	aatacgaacc	atatctcgac	actttggggt	cgtaaaatct	420
ttttggccaa	aatctttcgg	aaaaacaagg	taagcctcat	catctttctt	gttggtggaaa	480
tccgtgtcgg	atggagtttt	acaccggttt	tcctgtcggc	ctcttccatc	aataccgatg	540
aagcaattcg	cagggtctgc	aagtttgaac	cggatacttt	atttttgtct	cattacgaaa	600
ctattttcgg	acagcgatat	gagccaaaag	cctacaacga	tcggaaaatc	atcctcatta	660
ccggcgggca	cgttcgggca	aaagtcctat	gctgagcaga	tggcactagc	gcttgccgtc	720
atcctatcta	cct					733

(2) INFORMATION FOR SEQ ID NO:52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...3401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

ttcataggta	taaacgaaga	cagcacgacc	tccttttcgtg	cccatcgtag	gtacacgata	60
tggttgcgctc	catgcttccg	cctcataagt	cctttatgta	caatactcca	aggattttac	120
cgattggctc	ccttattact	ggcaaggtag	tctcagacta	cgcgatatac	gtacaggata	180
gatctaagcc	ctggaacgat	gtcgtacgga	tggctnattc	gncccgacgc	catgaagaag	240
atacgaaggc	tgaagagagc	ggactccgct	gtacgtcggc	cacggtggac	gaccgctgcg	300
cctctgccgt	atatccatgt	tccgacagga	agcatangga	tttgcagcgg	agacattgca	360
gcggctggcg	gaagtgcgca	tcgaaaggca	tgagggtgaaa	tagtcgggtg	cgaagatagc	420
gaaggggcgtc	tactggctgc	ctcttccctc	cccacgatca	taacacggcc	tacacgattg	480
cttccgggcca	attcgtgaag	gacaggggcg	caatgcccga	gcttttgctc	tgtatgaggc	540
atctggaggg	cttctgagat	ggaaggcatt	catacatttg	acttcgaagt	tccatgttgg	600
aggggataga	gggattcttc	cgctcgttcg	gaggtatcaa	acaccttatt	tccgactgtc	660
caaaggctcg	attggcttat	atggccacta	agacgtaaat	ggcgagcctt	tcatgatacc	720
ggtcagcaaaa	aacagtatga	atactgaagt	aatccactac	atcattcgct	ttctgatcgg	780
agataaagcg	gaaacgatca	gtcctcag	cgcacggtt	atacctcgaa	gcaagcgaga	840
tgtcccgata	cagcattgtc	atccgtgctt	caaacttctt	cgttcggata	tttacgtacc	900
gataaggctt	ttcccttggt	accgctgaaa	gatggggagg	cgtaacctct	ctttttggag	960
agccgaccga	agagctggtg	aagagagcga	cacactgggtg	ctgaatgccg	acattgtcgc	1020
ctctacatat	tctgatctcc	cgctacgaag	aggatgtacc	ggcgtaaact	tcgagataac	1080
acggacgatt	tccgggaaga	gagtccttgc	ctttcaaaagc	aggattttac	agcgtcctgt	1140
agtagatgaa	tacggggcca	ttctggcgac	caaaatcgtc	agatgggctg	gccggtaaaa	1200
gacccagtc	cccatttctc	catgggaatc	tgacgcagta	cgtagacgaa	ccgttcgagt	1260
acagaggatg	gagagtcttg	cccagagcatt	gatcaaaagg	acgcaaatct	cccttcaagg	1320
cttccgtctg	gcttatgcca	atccggcaag	tgatcggttc	ttcacttttc	ccgttttggtg	1380
gattgggata	aaatattgctg	cagcaaaatg	ccggattgct	gcggattatc	ttcttcttca	1440
aagcaccocgg	aaaggcccca	caggatgcac	gaactattcg	ctgagaaaaac	cgctctatca	1500
atcgctccga	cttttggtta	aaacaatgga	atagtgatag	ggcttcacag	caactactct	1560
gccgggtctaa	cccagaactg	atcggaaaagc	agcgcaagcg	acttatgagc	gataccgtat	1620
ggcagtcgac	tgcaacaggc	atcactacct	tgacgctcgt	gagccgagga	catgcaagcc	1680
ctgatctcgg	caggatcag	acacgattat	accatgggta	tgccgatgtt	gcagggttcc	1740
gccttggtac	atcccgctcc	gttccttcat	tatgccttcc	acaagacggc	tgaccgagct	1800
gatcctgcac	ccattacact	gatggattgt	acgctgcaca	ggcaagagta	tatgggacctg	1860
gacgaagcta	cggccataga	agttgggtga	aggaaaactgc	tgatgcatac	ttcatccacg	1920
gaggagaagc	cacactcctt	tggcacaacg	aatatctctc	cgcnacattc	atccctggca	1980
tgcccggttg	tatcgagaag	tactgaggcg	atagaaaacca	tggaggaaaaa	acaagaggag	2040
gaatctttcg	actacgaacg	gccatcgacc	aatgaaacgg	gtactcatct	tcgccgatat	2100
cttccctcgg	cttttgctcc	gagagctgcc	tatctgacca	aatatctgcc	tcgattgggt	2160
gggaaccttt	tgtaataacg	gaaaaaatgc	cgactccggc	atcccgctgc	acggcgatgt	2220
gttttggtga	ttttgcagtg	atattccggg	aacgctatcg	atctctcttc	ggcttcggtt	2280
ctgtctcaag	cgattcgctt	agccgtctgt	tcggcgaaat	gttttgggag	cagaaagaag	2340
agcgattcta	caagaagcgg	cgaaagcttt	tcccagtgct	aaattcgatg	ctgtactttg	2400
tttacctatc	gcaagtttcc	ccttgctacg	gcttgccgct	atgcacaggc	catcgattgc	2460
cctgggtggc	ggattgccgc	gatgtgatcg	aacagtacac	aactacgatt	ttcttccctc	2520
tggcaagcga	ctgccaagtc	tgctgatgag	tggcttcgac	accgctatat	ttctctccga	2580
aaccattatc	tccacaagct	gatcgtgtag	tttcgggtatc	accctggcac	tgcaatctgc	2640
tcgcagaggt	aatcctcgta	cagaattgat	ctacaatgga	tatgatcccg	agctttttct	2700
cgaggatcgc	ttccttggtg	caaattcatc	ctctcctata	caggcgattg	ctgactccgg	2760
aaatgcacga	tcctaccctt	ttgttcgaag	cttggcttct	gaagctcttc	aggaggtgcg	2820
caaagagaga	cgaatagagc	tgactgggat	gtggacgaat	actcccgcctc	catcctgcaa	2880
ccattcattc	gcagtatgct	ctgaaggata	tgtgccgctt	tttcccgatg	gttccggctg	2940
tcaggtagccc	gaaattctcc	gccatagcag	tgtcctgctc	caactgggca	cacagagaag	3000
cccggaggcc	cccattggat	agtatcgacc	aagctattga	gtcactggcc	atggaaaaac	3060
ccatcctgat	gtaaggagc	gatgaagtat	cgtggcagat	attatatcgg	aggccgaggc	3120
aggattggct	gcacagcgac	agaagaggta	gccacattcc	tgagtgatca	atacactcgc	3180
tggaaagcaga	aggggatact	tctcttcgga	acccgaacag	gaattttatc	tccatttttc	3240
gcgtgaagag	gaagccaaac	aatatgctcg	tctactggaa	tcgtcgtcgc	taactaaatt	3300
cagcatcgta	tcatgaagta	ctgtgatttt	acccgttgcc	tctcccttcg	gagcctaata	3360
cgacagtcac	tgccggtcct	tcagtgcaga	aagtgaggag	c		3401

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 627 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...627
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

tggattccgg	cagattttctc	cgtccaactt	tagaagaatg	agttggatat	ttggggtaag	60
aggtgtagat	ggattgttgg	aaacataatt	tgtagggaat	taattgctcc	ttgtataacc	120
aaatcaatgg	gattcattcgc	atttccattt	tgccaatgaa	gtctgcagta	gttacatttt	180
taacaggata	ctgcttcgtc	gcttaaccgc	tcagacatca	atatgatatg	cttatccaca	240
gcagtgaagt	ggccataatg	tttctcgcca	ttttaagccc	cccctgggta	tgtgtcccca	300
aataggagtc	aaagcccgga	ttttttgaca	gagaaaagca	gtgctttggt	aaaatcagat	360
aagcgatgag	gctcatggtc	ataactcaca	aggcgatncg	cacccttctt	gtagccgtcc	420
ccttaggcaa	catttttttc	aaaaacgctg	tcccgatgca	atggcagact	ttaatctggc	480
aatgttttgc	ctcccattga	cgaagactgg	tcgataacca	tcaccacatc	gacaggtacg	540
ttaccgcttt	agtagtgatt	tttagcgtca	catcccaagc	attgggattt	caggatccat	600
tggattggca	accggtaccg	catactt				627

(2) INFORMATION FOR SEQ ID NO:54

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 611 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...611
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

ctgctcta	aaagaagg	atataatag	tcttggtact	tcataacag	atttatgagt	60
ggaaccct	cgatcagaa	agcagatgaa	ggcaaagtca	acttggtggc	ggagatatag	120
agaatg	cggtcaaa	atatgcagat	ggacgacaac	aagattgctt	gtgaagtctt	180
cgggactc	aacggataga	tggtcggaca	agggtttgtg	tttctgacgc	atctgtcttt	240
gatttgagt	gtatgaagat	gaaatatacg	gaggcctgat	atttgacact	ttctctatag	300
cccttggg	aaacttcttt	atgcgaaatt	tggtgggatt	atgtcaggag	taaagagtct	360
tttataac	ctttcatttc	tccgacagtt	gtcaaggagt	ggatgtctat	actttggccc	420
gggaagata	ggatcgaaa	taaactccgg	tgtctgaggt	gttgcttttc	gacctggctg	480
gcaggatg	cttcggcaaa	ccattgataa	taaaatctat	tcggacatag	atactaacga	540
ctaaagcga	agcgggtatt	acgtagtctc	ggtgcgggtc	cttccggaag	gtatcagtcc	600
taagggtgc	g					611

(2) INFORMATION FOR SEQ ID NO:55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

```

cgatggtttg ttattcatag aagagttgcc taagatctta caatatccgt agtgggtgttc      60
tttttcctca tggtaatcaa tagtataaat ctaattgagg aatcgatgga ttggctacaa      120
gtctgggtgct tctggggatg ttatttttat accattcttt atctatgtca atatgtatatt      180
atatgtaata atctgttgtc tgttatttgt tgcttgggag cttttcttcg gatgaatctt      240
tatggacaac tgagaagcga acaaagattt tcatgggaga tacgggatct ttaatttagg      300
ccttcctttg agctttatgg ccttacgctt gcttaccgcc attcaaatac tgctttacct      360
cttccatatg tagtagctcc gctacttatt cctgggttcga tttattccat gtttttgtat      420
tgagaatttt atcaaagaaa atccttttaa acctgataag agtcatattc atcatagact      480
tatggccttg gggtgacgca gagacaaaca ctggttgcat attactatac tctatcgcg      540
ctctttgtta atatcttttg gtacccattt tttaatatca atgtgctgtc tgctggatat      600
cgtcatatgg atcacatcca atatgcttat agccaatttt cgcgcaaa      648

```

(2) INFORMATION FOR SEQ ID NO:56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

```

tgatcgccat attgtcccaa gagcataagg atatggagga gaaagtccga agaaacttca      60
ggaaatgata gcggatacgg atcatcgctc ggatatgcgg atcggcagac cgaccgaaag      120
atcaggatcg gcagaaagaa tgccggctgc cgaagtcggg tgtcatagcc gactggctgg      180
tacgggatat gatgcgtttc agcccgtggc gaaagacacg agtggcaagc ctctgaacaa      240
tagcaggcca acagcaccga ataccgatg ctacagcgcg cctcgcctt tttcgcggag      300
agaaagagcg tctgacaccg tatttccgcc agatgaatct gac*      343

```

(2) INFORMATION FOR SEQ ID NO:57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

ccgaaccaat	ggcttggcta	tatgccggag	gcgatcgtag	aatcaacaag	tggtggggga	60
ataccggcaa	tgctgagaat	aagccgatca	acttcttcgc	ctgacaactc	gcggtggact	120
tgtatatgac	gtgccgatta	ttacgcagaa	ggtgctattc	cgggagggca	gtacttacct	180
tttgccaaag	gcttatggcg	gataagccga	gttatacggg	ttataggaat	cgtcattaca	240
tatatgtatc	aagacgctgc	cggataagat	agaagtgaag	tattctatct	gcgatggaat	300
tttagtacct	aacgatactt	atatgggcta	tggctacaac	gtggagtcga	tgagcaaggc	360
aatgtcacca	ttactaatac	gatgcagaat	tggatcccca	tgttggtgaga	ctcgttgcta	420
aaaatgggtgc	ttacttttggc	tccagcctac	cgatacttcg	gttgagtttg	ctgagttagc	480
caacgggtgct	cgcaaacatt	caaagtaaat	aaagatgctg	tggcggtcgg	ttctgcttac	540
tggagggttta	ttacaaccgc	gatccgaatg	caacagggtc	gttccggaaa	agttttatca	600
agaaatagac	agacttatga	aaaagtattg	gtatatgctc	gttgctaacg	agtgtt	656

(2) INFORMATION FOR SEQ ID NO:58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

aagggtttcaa	tttcgcacaa	tgagagatcg	ttttttttgtg	caaagggtgtg	tttctccttc	60
tgcagatatg	tcactcttaa	ttccattatt	tcgtcttaga	accgaacaaa	ggtagaattt	120
ttaaggagaa	ggataaatga	aaaaacctta	aaaacatgaa	agtaggagat	aagtgtgaga	180
atgagtgcgc	ctgatcttgt	gatcggcgca	ctcttttctg	tgtttggtcc	tatggacagt	240
ctattgtatc	cggatcgat	tcgggttaga	gccctcctcc	tcctgatccc	tgatgccacc	300
accggtttga	gaattgctat	cgcctgcatt	ggcagaagca	actccggaag	cggcttgccg	360
tactcggcga	acttcagatc	cggagcgatc	aggtacaatc	ccgttcgcga	gtgaccgtat	420
tgtaacgaca	ctctgcccctg	aattgaccgc	aacggagttg	aactgggagg	ctttcacatc	480

ctctttcttc	ccactcccga	tcctttggcc	tgtgcaatga	gacggaaaca	accgatgcct	540
cgagcttgat	cttcttgccc	gaagccaatt	cctgcgcat	gacgatgcca	aatcgcgag	600
gataccgaat	acatcgccc	ggctggctcc	cgaaagtctg	agatttggtc	tgcgatgtgc	660
aggggtggagg	caatgctgcc	gttgatactg	tctgcgata	ccacagcttc	ttgcctgttg	720
ccttggtggc	aatacggatt	gtcttctttt	gaagaataac	ataataattg	aaagaattaa	780
tgattaataa	tgcggacttt	ttctgtccat	taatttaata	atagcaatcg	agaatcgatt	840
cggcgccatc	ctcttctctc	tgtttgcaat	gcaaagataa	ggtaaagaaa	ctgatcgctc	900
aaatgttttg	cagaaaaaag	ttttcaacaa	caaggcgct	ttacgcttta	tatataaaac	960
ggcttccgta	tttcttatac	aaggcttcga	agcactcttc	cggctttcgt	aaggggagct	1020
gaaatccggt	attcggcggt	gtccgaatga	tttatatata	aagtattttc	gattaataat	1080
aaatcgattt	ttatttatat	attaatcggt	ttcattttgg	gggatccc		1128

(2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature.
- (B) LOCATION 1...1094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

cgggcctttg	ctgttttctt	cgctgagtac	ggcacatgcc	gatatgccgt	ttggtcttcc	60
gtcatccata	ttctttgggg	tgtcttgcc	ctgggtggtg	tcctctattg	gctgcttgga	120
tcattcggtt	cacgagccct	cggacactgc	cgggcttctg	cgcattcccc	aaatggcttt	180
ttggctatgg	gttaccgcgt	ggctatcatc	atggccaaaa	cgacaggcta	tgtgatggca	240
caaggtccga	cagcatccgt	ttggagctgc	tggttgccgt	gggtgggtctg	cttacttggt	300
gccttgcaat	tggggttggg	cangtggtga	agcaaacgat	attgaaagag	agcattacgg	360
ccggtcaggc	tttgggacag	aaaaacacgt	cgttgccatt	tggtgtgcgc	ttacctattt	420
gaatccgata	gcttctatcg	ccctgcaagc	tatgtggtat	ggcaaaattc	gctcaattcc	480
atccaaatct	gctatacgat	aaacgaaaga	ataaaaccga	cagacaatga	aactaacagc	540
cgatggttta	cttccatcag	tgaggatgag	aagggcaaca	tagtattctc	aatggacgct	600
tggagcttga	cgaattccga	ctgagtggca	agctgaaatc	cgaatcgaaa	tacgctggcc	660
ctacgaagcc	gacgaacaag	gtctgttaca	gaatcggcag	gcaaacggat	cgaagagatc	720
gagctgctca	tccgtaggct	atggaaaagg	acaagttggc	catcatgaca	ggcaactata	780
ccggggcgga	acaaagtatt	gggtctatta	tgcccgta	gaacgagtat	tcgcgaacgg	840
ctcaatgagg	tggttgcccc	ttacgaaaca	ttaccgctgg	agtagaatgc	gaagtcgata	900
ccgactggga	agagtacctc	gatatgctct	catgaaagac	gaaaattcga	tatagccatt	960
atgccatctc	tctgtggcga	gggagctatt	ttttatttgt	caagcttcng	aaccggatcg	1020
acgataggat	gattgcgcgg	atggtaggtc	tcgatttcat	gccggagtgt	ttctctgtga	1080
tatgggtata	gatac					1094

(2) INFORMATION FOR SEQ ID NO:60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

gctcaacaag	agaagcaggt	gtttcatttt	ctgaaccttc	cggctactga	caggctttgg	60
ctgccggagg	caaagctatc	accatcgtag	acgacaatcc	ggactggctt	ttgagaatcc	120
ggctctgctc	ggatatgaat	cgggtggcgc	gcctttcttt	cctatttata	ttatatgagt	180
ggttcgcata	tgggcatgcc	tgttatgcct	cgtccgctcg	agagcgtggc	atgtgggggtg	240
ttggctgcgt	ttcctgaact	acgggtctat	gcaaggatac	gatcagaatg	cgatgccacc	300
ggctctttta	gtgcttcgga	tatagctgta	caaggatttt	acaccatgaa	ctgagcaacc	360
acttccgcgg	tggagtcagc	ctaaaagcat	tgattcttct	atcgagacgt	atagttcctt	420
tggccttggt	gtggatgtcg	gatcagttat	tacgacgatg	acaaaggata	ttccgtttcc	480
gctctgttca	gaacgtaggg	gcgcaactga	aaggctataa	tgaagaacgg	gaaccgctca	540
ttgggatttc	cagctcggtc	tttcccgtag	ttttatcaat	gctccgttcg	cttgccacatc	600
acgttgttca	atctgaatcc	gcactatttc	aagcgtctgt	accacgcgat	ct	652

(2) INFORMATION FOR SEQ ID NO:61

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1402 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

cgacatttta	tatatcgctg	atagaacaag	aaaactcaaa	cctatgaatc	agttcctgct	60
tctgaaaaca	aagggtcaatc	ccgtacagtg	gaagacgacc	gcagtacttc	ggactttatc	120
tcaacctcgc	acgagagaat	ttgatagagt	cgaaagtcac	gttcgcatta	agttcgggaa	180
gaagaaattg	aatgaaagtc	gctcaagcaa	tctcttcttt	gtgatcacct	gctctccgtc	240
gacgtggac	caaagtctat	ggccatagca	gacgctatct	gcctttcctc	catttttcga	300
tccggatagt	cagatcgaaa	aagaccatga	tagcaagacc	ggttggatcc	cgattcggcc	360
caaaggctga	tcagagagct	ttattcttta	ctgatttcct	gcgcaatgac	ttctcgcaca	420
atcggttga	tggcactaca	tcgagcatct	cgaagtcagc	cctgacatca	gctcctttat	480
taccgggaca	actccttggc	atgcggggaga	gcacaatcgc	ggtttgacga	tttcttcaac	540
ccgacgactt	tgctcctggca	aagaacagga	aggaacaatt	gataagcgag	cggacggaaa	600
agaatgcctg	accgttagtg	gccttgccct	tttcattgcc	tcttcctcga	tagggagcag	660
gcttcgggta	tgctgagcag	gattcgggat	tcaaacgaac	cgatgagaat	tgggcacgag	720
ccgtgcacga	gacctctgct	atctctgcat	ccgtcatcct	cacgacaggc	tcgaaagcag	780
caatcgaaag	aagctctctt	gctcgatatg	ctcaacgaac	tgaaccgttg	ccccgcaccc	840
tttacgatat	gctccccgaa	gaggagcggg	cgcaagttcc	tcctgcgctg	gacgaaaata	900
gcatgaacaa	cctctcggaa	aacagcctga	agaagagagt	cgatttgctt	gggacggctc	960
ttcggatttg	gcagaggcac	gaccaagagg	atccgccatc	aggatcgctt	cccctatctg	1020
atgcttcggt	tatcgaggag	atggatctgc	tcaagggtat	acgctttcgt	gtcgatttgg	1080
tgaaatcgag	ctggattctt	actccaaaaa	ggtaggccgg	aatggtggta	cgatcgacag	1140
ataacggatc	atgccttggc	attcggcaag	ctgtcaactt	ccagaatgaa	gaagaggtaa	1200

gtaggatgat	cagtggagag	gcgtctatcc	cgtagcttc	tctctctttg	ctccccgcta	1260
tgccatatac	gacataagat	aggctattgc	catacatccg	accctgtata	tcctaagagt	1320
aagcagggag	taagagggcc	ttgagcaatc	ctcagtcgat	gggattatca	gttgcacaaac	1380
cttcgtaagc	ttctcttgat	gg				1402

(2) INFORMATION FOR SEQ ID NO:62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

ttatgcctca	aaaattttat	attcaaaagt	ttttctccca	tttcaataag	cttttgacat	60
tttcttctgt	tgcaggctgt	attttatgca	ctccaaattt	ttagcgatat	caggagatag	120
tttttagcaat	tctcttcctg	tctgattatt	ccaatgatta	caagcttggg	atatttgga	180
ttggcaacat	tgtctgtgca	agctttgcaa	tattagacaa	acgcaaactt	caaattgggtc	240
aacaatctat	ggaatcctc	tataacaaaa	tttctctcct	cttcaaaatt	actataatga	300
gttgattttat	tntcgtcgtt	tcattctatat	ttcttgctga	caatattcaa	aatgtatttc	360
ttcttttatg	tcagataata	tcttcaaaat	agagaagtct	tccctgttcc	agtttgcccc	420
tctatgataa	ctggcttctt	ttacttggtta	catcaattag	aattttcgta	gtagtttagn	480
ggttcgacat	tgtaagtgc	g				501

(2) INFORMATION FOR SEQ ID NO:63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

aaaagagatc	ggaagacagc	gaaaagagat	tgggaaacga	tttatatacg	aacgaattcg	60
atztatatat	ttatcatttt	cgatttatat	ataaatcggt	tcatttaata	tatagattgt	120
aaagtgtttt	atatataaaa	cgagaggaga	aaaggcctct	tcgaccgatg	aaataaaaaag	180
aggcaccac	ccaagtcg	accgaactcg	ggcgagtgcc	ttagtatctg	acagaaatgt	240
cgggacttat	tcgcgcttgt	acatcacaaa	ttcggcacaa	gcgtcctcgc	tcgacgatta	300

```

cttcatgtta gtcttcccag cgtacattgc gcatgtcgcc gctttggcca attcctgatg 360
gaaagcaaaag cagcagtcca gacccct 386

```

(2) INFORMATION FOR SEQ ID NO:64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

```

gctgtcgatg agtttcttga gtttgagctc gatttgatcg cagagggcag caattcggtg 60
cgatcggcga actccacatc ttcttcgggg aagtccaatc caactccatc agccccgtaa 120
ggcgaagcaa ttcctcacgc agagcatcag ttcttcgcta tatccaccac gcagttgctt 180
catcgccatc tgatgcgtgc cttgctctcg ctggcgatga tatccgccac cggctcggca 240
ctactagggtc catacgcccc ttgaggtagg cagggcgagt aaattcgccc cgnttgccag 300
accgaacagg cctgatttga tcaatgcctt cgagaatacc gtcaccgtat attatatgga 360
gccatggcag gcaatctcga ctggatgctc ggagtgaagg agtgcnggcc atggaaacac 420
gttaggataa cttcgtcaat ggctcgtccg gctccatgaa ttctgccata gaaggcggtg 480
cgaggcttgg ttccgctgaa gtcaatcggc ttggccacga tatagaaaaa gtgggctaag 540
agcggaaagc attccggacc ggacacacga attcaccgga ataccggc 588

```

(2) INFORMATION FOR SEQ ID NO:65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

```

gtacaacggc tcgttcgaag ccaattatct ggtatcgaag tccggcgaca atacgtgccc 60
ggagactaca gcaagaccac cagtctgaat atccgatgac acacagtcag gatccgaagg 120
ccaatccttt gcaaacggtt tcggccatgt caattttgcc accggnagct atttccagaa 180
ttcgctgaat accaccatga tgtcaatgcc cgtactgcta cgacacgaag ttcggccgtg 240
agctatcgcg caagtttccg ggtactcctt ttctgattac gggtagcatg gatacagcca 300
gaacatgcgc gatacgacgg tgagccttac cttgccgaat cttcgattaa tatgtccacg 360

```

```

cgttatcctt tcaagcggaa gacccgtgta ggccggagcg atggtagag aagttgagtg 420
tgggctattc cggtcagctt ccaatagtat cttgacaaan gagaaagatt tgc 473

```

(2) INFORMATION FOR SEQ ID NO:66

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

```

cgggctgtaa ctacaatcctt tctcattggt ctttacttat tgtttttaag ttttgagtca 60
cggtatcacc ataatagcaa tcagtgtgta gtttggcacc gtccttataa caatcggatt 120
cacttttttg ttgtgagttt aatcacaaat tgtcgagaag tttatcggca tgcttcgagt 180
atgcggcgag ccatagcccg tcgacatcca atgcttcgcc atagctgacc cctcgttcga 240
tgaatgacgc tctatttcct ttatcacatc cgatcctatg tgcatttcct ccagcgggtc 300
ttcagtcoga gttcgcggaa gaattcctcc gtccgagcaa tagtgcatct atacgctcct 360
cctctgttcc ctcttttata tcccagattc gtcggcatat tggagcatct tctcccgtt 420
gtgatcgtgt cccaaggtgc gagagtacc ggtagcata tggccagcgt gtgtccgtgt 480
gtgagtcceg cagtgcgta tctcatgacc gatcat 516

```

(2) INFORMATION FOR SEQ ID NO:67

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 889 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...889
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

```

cggcaactcc atccttatca aggtaaacca gattggtacg ctcacagagc cctgaatgcc 60
atcgagatgg cacaccgtca cggctttacc agcgttactc gcaccgctcc ggagagacag 120
aagacaccac tatcgcagac attgctgagc aaccaactcg ggacagatca agacgggatc 180
gctcagtcgt accgacgtat ggctaagtac aaccaactgc tccgcatcga agaggagtta 240
ggccctgcgc tgtatacggc tacaagaaag tgtaagcgcg aaagtacaca caggtacatc 300
tttctgccga atacggaaaa ggggaaaaaga tagtaccact gccaaaaaaa gaatgcccc 360
aaagttggaa acacaacttt gggggcattt atttgccgac ttatttagaa gcgaacaccg 420

```

agacccacaa	agaagtcattg	atacgcaaaag	aagtccttacc	cggagcatcc	ttcaacatat	480
taagcaatcc	tgctcatatc	caatttgtac	gtaataacgg	tcgtagctca	aggcagcagc	540
aagcccaagc	ccaagtcgaa	acggttatat	ccgttatcac	caaaggcact	acagaagccg	600
taacgcctgc	aacttttagtc	ttaatcggtc	cggcgaccca	tatgcgaaat	agggacctgc	660
ttccaatgaa	atagccatgt	tgtcagaaaag	ctaaatctca	taccggcatt	caccgggtatt	720
tgacagataat	gcaaggagtt	gtcgtttcac	ttagtgtatt	catcttagca	cctctcatcg	780
tatagccaat	ccgggggagc	gatagaatcc	atcattgcta	agagcgaact	cagagcagca	840
ccaacacgta	agcctacgat	catcttattg	ttcacgctcg	tggttgcgac		889

(2) INFORMATION FOR SEQ ID NO:68

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

ggttccatgc	cntgggggtat	caggacttcc	aaattttcatc	gaataccgat	tggacaatat	60
ctcgtgggct	gccaagacag	gtacagaccg	gatagagctt	tacaccgagc	cgatatgcagc	120
cgcctatcat	aaggacatgg	ctgctgcgta	cagccctatg	tcaaggcttc	ggtacacgct	180
cattcgctcg	gtctcgtatc	aatgccggac	acgatttgaa	tctggacaac	ctccgttact	240
ttgccaacga	ctgccctatt	tggacgaagt	ttccatcggc	cacgcactga	ttgcgatgct	300
ctctatattg	gactggagga	gactatcaga	caatatcgag	accacttgcg	ttataaataa	360
aatcgaaaca	gtaacaatca	cattgataat	ccatgaatat	tccaagcatt	ccctttctgc	420
aaattcccgt	tcagtcggcg	ggactccctat	cgactccctt	gctaccgtca	ttactcccgt	480
taccacaccg	cagaagctac	cctgtccatt	atggatctgg	ctctcaaagg	cggttggata	540
tgatcgattt	ggctgctctt	tcgctcttgg	ccatctacat	attcgttcca	aggtgatgga	600
gatcagggct	gccggcgagag	aagacaattc	gttcatgagc	ggatcaagga	ttatatccac	660
gagggtaaaa	tagaatcggc	catgcgcttt	gtcaggacag	ggctaccctt	tctgcccgtg	720
tgatagccaa	ggggacaccc	gactgggacg	accgatgaac	gacatactgg	tagccgtcga	780
gaatccggaa	acatcgaaat	tggttaagctg	gaaaaaggac	tgccctattat	tgcaccattg	840
cagccggagc	acctatgatc	ggtttcttgg	gtaccgtaac	ggtatggtgc	gtgctttctt	900
cgatatggcc	aatgccggta	acggcggggg	gacgtagctc	tcctctcggg	aggtatatac	960
gaagccttgg	taacgactgt	ggcgggtctcg	ttgtcggtat	cgtaacgctt	tttgccctaca	1020
actatctcga	gtcaggttgg	ataaggtcgt	caataagatg	gaaaccaaga	ctcttgagtt	1080
atggatctcc	ttaacgaacc	catcaaaaaa	tgagtctgaa	acgtaaaacca	aggtcacaga	1140
agttttttagc	atggcttcta	tgaccgacgt	gattttctgc	tgctcatctt	cttcatggtg	1200
accagtacgc	tcctcgtacc	caatggctac	gcgtatctct	tcctctcgcc	aataaacagc	1260
ctgccccgga	agctcttttg	cacggatcac	catttcagaa	gatatgcgct	atttcgccgc	1320
tttggtcagg	acaaagggca	tgaggctcgt	ttcgaggaga	tacttcccct	ctgcttcagg	1380
agcaaagtcg	caatcccga	atgtacgtag	ccatatatgc	cacgagaatg	tcccgtatcg	1440
tgagatcggt	aagggtgttg	gtatggccgg	gagaacaaaga	tgaagggtgt	ggtggccacc	1500
aaagcccaaa	gtaaaaagta	gttcatgcga	caagagaaag	tcaaacgcaa	tgccgttgcc	1560
atagcgtctc	ggtgggggca	catgtcgcac	tgatcaccct	cttggttcgtg	ctgcatctcg	1620
tgctgctccg	cgcgaaagaac	cggaagaact	gatactcgtc	aatttcgaat	cacggagctt	1680
tcgtccggag	ctttcgagcc	ggcaccacag	gaaacgcata	caatcccgat	gtacaaacgg	1740
aacaaactcc	aacgcagaaa	cagccgtagt	caaaaagcag	caggcaccgg	ccgaatctga	1800
tctgcgtcag	gactagagcc	ggcacctcac	ttggccaaag	ccgaaaaggc	ccgtcaagag	1860
gcgaaatgaa	acgcaagcgt	gaagccgaag	aggctcgcaa	acgggcagag	gtgcggcaga	1920
agccgagcgc	aagcgcaagg	ccgaagcagg	caaggctatc	ataataatgt	ggccggagca	1980
ttcggacgag	gcgcccagca	aggcaatacc	aagggttcggg	cacacaagcc	aatggcaatc	2040
agggcaatcc	cggaggtacg	gttcttctga	ctcgcttacc	ggccgtacta	tcgtgggcaa	2100

tgccgagcatc	cggaaaagcc	tcgctacagc	aaaccgattc	gaggaacggt	acgagtaaca	2160
tcgtagtaaa	caatgccgga	cgtgtgaccg	atgcttccat	ccgtcgcgcg	gtaccaatat	2220
cacggatgct	gccgccagc	gagcagctat	agaacggcca	aaactactcg	cttcaatgcc	2280
atagcgggtg	gtggagatca	ggaggagtaa	tcacctatca	tttcgacatc	aagtaaaaaa	2340
cataaggaat	ataaaaagac	agcattagta	tttctggctc	ccggtttcga	agagaccgaa	2400
gcgtaggcac	gctcgatatt	cttcgtcggg	gagggtgtagt	cgccgaattt	tttccattac	2460
ggattcgctc	tatgtagagg	gagccaacgg	gatcaccgta	aagccgatcg	cctgatgact	2520
gatttgccga	cagtggatgc	tttggtttgc	cgggaggact	ccccggagct	gataatctga	2580
acagctgtga	acctcttgc	gttttctaa	cgagcattat	gcccgcctaa	agcttgtggc	2640
tgctattgtg	ctgctctctt	ggtattcggg	ggtttgggtt	ttgtctgtgg	cagaaagcta	2700
cttgctatcc	gggctttgaa	tccaaactcg	aaggagccga	ttatcgggtg	aagctgccac	2760
acgtgacgga	catgttatta	caggcaaaag	cccgcctgcg	tctttgcatt	tgccatagaa	2820
gtagttcggt	acctctgcgg	tgtcaggtag	ccgatgagat	cgctaccggt	acactcttca	2880
gataattcga	aatcctatac	cgcacaaaaa	gaaagtgtcc	cggactgcaa	ggttcgggac	2940
ctttcttttt	aggetcctat	gcttctcgaa	gcactcgctc	ctttatcttt	aggagagtcg	3000
ggggtaaacc	gcagtgcagc	ccagttgtta	cgtgagcggt	ttccgaaaga	gtcagac	3057

(2) INFORMATION FOR SEQ ID NO:69

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

gactgccaa	ggtccgctca	gtaccgtgat	accataata	tagaatcggc	tcgagcagag	60
gtggtaggag	gtctgcataa	tcgtattgag	catattggca	gacccatgac	atgccctaca	120
tagccgaata	tgccgaagaa	gagaatgtga	agccgagggc	ttcgaagaga	tgacgcctga	180
acgtcagttt	cttgtgtgag	atcttgtctc	catttataat	gatgtatgcg	gtgggtttttg	240
gtgggaaaag	acaaggccgg	agcggagctt	cgttcgggtc	tccgctccgg	tcttgccgtg	300
aggattatga	gttggtgtag	acgaccctgc	ctcctttgac	ggttgctcca	cgaggttcat	360
accgaagtga	taggagagga	atttgtacga	tggtattgga	gtacgacgag	gtcgcccttc	420
ttgcccggtc	cgatgctgcc	gtcgtatcgg	ctcttcctat	ggctgcagcc	ccgttgatcg	480
tgagggctgt	atggcttctt	cgacggtcat	gcccattgtag	agggtggcaa	gggcaaacag	540
agggggacgg	aagccgagaa	gcaactgccc	ggattgaggt	cgctccccgt	gcaacggcac	600
agccggcgctc	gatcatctta	cgggccggag	cgtagtcgca			640

(2) INFORMATION FOR SEQ ID NO:70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

```

acgctcgcta tgcagatcaa ccccatgctc tgcggttctt cgttcaagac aagggcgtac      60
agacactgct cgatgccgta tgtaagttcc tgcccagccg gcagatactc ccacagtgga      120
aggtacggat ccttctgact cgagtaagtg atagagcgca agacctctcc caacgagcct      180
ctctgtgctt tggcgtttaag attgctaccg acccttacgt agggcgctctt tgcttcttcc      240
gcgtaattcg ggcgaattgc ctgccggttc atacgtttac aatgctcggt ctgaaagaag      300
gagcgtatct ctctgtctct ccagatgcac tctaacaagc agaccccaaa gaggtgatcg      360
gttgcggtga catcggtgcc ggtgtaggct tcaggatatt cgtacgggcg atacgctttg      420
cgatgagagt catcctatcg tctcgaatct atggacttcc ccgatccggt gatcgggtatt      480
gccgtggagc gaagacgcag aaggacctcg atcgtctggg tgtaggtttg gccaaagctgc      540
tgaagaagac cccacgttcc gcgttcagac gaacgaagat tccggccaac gggtatcagc      600
ggtatgggtg agcttcacct cgatattatc atagacctct gcgtcgtgag ttttaagggtg      660
aatgcaacca gggacgtcct caggttctta caaggaggct atcaacgata ctgtggagct      720
tcgcgaagtg taaaaagca gaccggtggt cgcggttaagt ttgccgacat tatctgtcgt      780
gtgggcctgc cgatgccgac ttcgaaaggc gaattgcagt tcgtggattg agggaagg      838

```

(2) INFORMATION FOR SEQ ID NO:71

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1088 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

```

gactctctcg ttttggacgt cgctctcgaa agaataccgc cgcggacatt tcccgggcgc      60
agagagtttc cccctgtttt cggatgcgga acgagccggg taggtacgct ctatgtcaga      120
catagtccgc aggccggcgt agagcgagat tggagttcgt tgggccgcgt atggccgaga      180
tggtgcgaga agctcgtccc ttgctgccgg cagagacatc atcctctact gctggagagg      240
aggtagcgaa gcgagagtgt cgcttggtcg ctatccgtag caggacttcg catcgtcgtc      300
tccgtggcgg atacaaagca taccgcgggc atttccccga tatctgaagc tttaccctgt      360
gcgtttcatc gtcttaggcg gttatacggg ataggaaaaa cgccatcct gaacgaactc      420
acccaaatgg ggaacaggt gtcgatcttg aaggattggc ccaccacaaa gggctgcct      480
tcggtgcctt gggcaagagc agcagccgac caccgaacat ttcatagaatc tcttgacgt      540
gctctctccg cttgtgatcc gaatcgtccg atatgggttg aaagcgaggc aagactatcg      600
ggcgcgtatt tcttcgggac gatttctaca aagtcacgt caagctcctt tgatcgagct      660
gtctgtcccc cgtcccgtac gcatcgccat attgccaaag agtacggcgt gtacgatgca      720
gaggcactgg caaacctttc gagcatatcg ctgcgccgat gggaggagcc gctacgcac      780
aagcataact gccctcaagg aaggacgtct ggaggaggcc gtatccttgg ctccgattac      840
tatgacaagg cctatgcaca ctgcgtggct gaattcaggg aagctcctct gctcgactgg      900
cagtagaaac ggatacacct cagcaaacag catcaaacta ctggaactat ctcatataaa      960
agggttacaa tcatgaaagt gtggatactc gggggaaact ctgccccctc cctcttattt      1020
tgctcaagaa gccgttgacg gcactcccg cggagaagaa atctccgtaa tgactgacat      1080
gaaacggc

```

(2) INFORMATION FOR SEQ ID NO:72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

gccataatt	ataaaattca	aacagcctaa	acattcttaa	tgcgatgaca	ctagtaacaa	60
gcaatacaag	agctnnggaa	aaaattacag	cgtaatcaaa	tacatctcat	tctgaaaaaa	120
agagaataat	acggctgacc	aaaataagaa	aggctcaagt	ggtaatacgg	agaaaaccta	180
tttgcacgaa	ttaagcgtag	attgatagat	aaaacagcaa	caacaaaaca	agaccaataa	240
accagctca	gcaagagcgt	tcacaaactg	attgtgtgag	aaaactcgca	tgccgtcttc	300
tgaaaattac	gctcaacaac	ttgagtatac	ccctgtccca	acaaaattca	taaatattac	360
cctcactcca	tccttctatc	ccattcacc	aaaagaagta	cgtccagatc	cttttaaatac	420
cattccttct	gcagaagcat	tgtatgcaca	ttgcgcccag	ttatccttgc	ctgaaactgc	480
tcgttgggtat	atagaaataa	acaagagcaa	caccaactaa	gcctatcaaa	aatgaaaatt	540
aaccaagtga	tgaatagtaa	ttttacgagg	aagcattaga	ataaccaggc	aacaagaagc	600
atcaaccagc	ctgtacggac	ataggcctga	aaaacagaat	taatcctact	acaatcagag	660
aagcattgaa	acccttctga	aatgactcct	aaattttattc	agtctaaatc	cgtttggttag	720
aacgaggatt	gatgcgcgaa	gtangangaa	tcccgcatga	ggagctccaa	aaattccaga	780
ataaaaactg	ccccctcaat	tccaaaagca	tcagcagata	aaaagtcttc	cacggagata	840
caatccccac	aagtactaaa	agtgatgcaa	gaagtacaaa	ttggctaagg	tataaaggaa	900
gaattcgagc	cgatcaactc	gattagagaa	ttaaccaacc	aaaaacgaaa	aa'agagag	958

(2) INFORMATION FOR SEQ ID NO:73

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

ggctccgctga	cattcggcta	ttctaccacc	tatatatatg	atthttgcacg	gatagtaagc	60
gtgctctgat	cggtacgctc	tccacggact	ggacgcgcgt	cctttccgct	ttgccactat	120
catggagtac	aatatggaga	cgggcaagcg	gatacgttta	tcactcgcca	tccttccatc	180

gacgcaatcc	agtataaccc	gacggcaaac	atctgatcgt	aatgggttcg	gcagatgctt	240
tcggcatata	ggactgaacc	tgaaatcggg	agtcactccc	aattcttacg	acaacaattc	300
ttcctgttcg	atctctccac	acggaaagca	acagccttga	ccagaatttc	aacccccagt	360
tatcggcagg	gagattcgac	agaaaaaaca	acactattac	ttcagggctg	aaaacggatc	420
gcgcaagcag	ctctatcggg	tggatctgaa	aacccttgag	atcagtcaga	ttcagaccgg	480
agagggatgg	agtacaatgg	ttcgggtgtg	cagctgataa	tggtgctgtc	tggtacagcg	540
ccagagtgcc	aacaatgctg	acagactcta	tcggctcgat	gggaccaagg	aaaactcgta	600
tgggatctgt	ccgccgagaa	gttggccaat	atcgattcac	accggcacgc	gactggaact	660
atacggctcc	ggatggcaca	gtcgtaaggg	ttggtactac	ctgcctccgc	aattcgatcc	720
ttccaagaaa	tatccatgct	ggtctattac	tatggaggaa	ccagcccgat	caataggaca	780
ctggaggaca	ctactcgctg	gcgatgtatg	ctgctcaggg	ctacgtagtc	tatcgctcaa	840
tcccagcggg	actaccgggt	atggacagga	gtatgcagct	cgcac		885

(2) INFORMATION FOR SEQ ID NO:74

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

gcttcgggttt	gctcgggtctg	tgcagagata	agagagccgg	ttcctgtatg	cagaataggc	60
gcaatccgat	attaaccgac	atttcctgcc	ttttgagaga	aaacttctgc	cacgatcatg	120
ttacgttttc	acaaaagtgg	cgatgaaggt	gacaaaatag	catgccgaac	agcattcgaa	180
tgacttttgg	tctaattctg	ccccatcggc	acggtggcac	tgtatttgta	gectcttaca	240
agcaagattt	acagcccgtg	aaaacggatt	cggacgatgc	ccaaaggagt	attcggcgga	300
cccttcatac	tttatactat	aaacccttcc	gactttatac	ttaaaccctc	caccctttat	360
actataaacc	cataccactt	tatactataa	accataccac	tttatactat	aaaccatac	420
cactttatac	tataaagcct	catactttat	agtataaagc	ctgcgagctt	tatagtcgga	480
agtattaaag	gatgattgtc	gtgctacact	tgtgcaagaa	aaaggatcag	aacggatagc	540
tactgcaatg	tgccaagcga	aattggaaga	aagggttggg	cgtgtgatgc	ccatttgtaa	600
cgccctgtct	gctgaggatc	gtaggctttc	agtccggatc	cagccgcaca	aggaaataat	660
cgaagtcgag	acgaagcccc	agaccgaggc	caaagctatt	tccttgtaga	agcgatcgaa	720
acgaaagaga	ccgtctcctg	attctcatac	tcctttatcg	tcagacatt	gccggcatcg	780
acaaagctgc	tgcgcgaaac	ttccagaaca	gctttgtcct	gtattcgaca	ttcgatccag	840
acgaatatca	cccatctgat	cgaagaaggt	cttgctccgga	gtatcttcat	actccccggg	900
ccgagggtac	ggacactcca	gccgcgaacg	cgttcgatcc	tccggcaaag	taacgtaact	960
aaagggtata	tggcgagcat	gccataaggg	aaagccagtc	cgaaaccag	attgcagtcg	1020
caaagtattg	ccttttcgag	agaacg				1046

(2) INFORMATION FOR SEQ ID NO:75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

gggcctcaac	aatcgaataa	aacggcattt	gagaatgata	ttttctcttt	tcttccgtgc	60
cggagcaaga	gttgcatata	aggactaaag	ataattgcgc	atacagagtc	catcgggcag	120
attggagccg	gaaatcaaga	tcgttcaatg	cctgcgaagc	agatcgagag	aattacggtg	180
ttctatacgg	atggcactat	caagagtttc	gctcaaacia	agagtaagcc	tctctttttt	240
cgtaatttgc	actcgaatac	tgcaactcga	tttctcgatg	aaatacaacc	ataactgcgt	300
gtcgcgacca	atacgaagct	aaacgcacgc	tatttccttc	ttaacttgta	cgggagcata	360
atgaagtacg	attatctctg	ccggaaataa	agccggacag	tttggtcagg	tactgactgg	420
atgtccaagg	ggcttttttg	ctcggcctat	ctctgtttgt	gatgtcgatt	acgaacggca	480
ggaactattc	ttctgggttca	aaaagtaggc	aagggtacac	gtgcttttag	ttcattacag	540
catccgattc	attggatctt	ctatatccgc	ttggacaggg	gtttacgcta	acgatctgcc	600
ggatggagag	tatcgtcctc	ttctcgtggg	tggcggttag	gcactgctcc	tatgctctat	660
ttggcgcggt	gtatcagaga	gaggggatcg	tgccggatgt	tctgctcgga	gcgcggttcg	720
cagatctgat	cgtttagcagg	acagattctc	tcgttttgcc	aatctgcatt	gcaccacaga	780
ggatgttcgt	tgggggtgaa	gggctttgtc	acgagccacc	cgacccttcg	ggagggcgatt	840
tttctcatat	atatgtgtgt	ggcccaaaag	caatgatgat	ggtgtagcat	ccctggcacg	900
tcaacgaaat	atcccgtgtg	aaggtctctc	tgagaatacc	atggcttgtg	gtatcgggca	960
tgtttgtggt	gtgtggaaaa	tcnaaagaag	gcaatctttg	cgtctgtacc	ggaagaccgg	1020
cttcaa						1026

(2) INFORMATION FOR SEQ ID NO:76

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

gggccatgag	tttgtccgta	aaagaggcga	agtagtcata	gggcacagat	agtgtcgaat	60
actgtcctct	ttcggacgga	tattcacata	ggggctcgact	gtttcatgtg	agctttgtta	120
gttacgatta	tagaggcttg	ttcttaggca	agtttaata	tcgggcgaca	aaaaacgctc	180
caacttcttc	acagcagggtg	ggaccaatgc	cttgagagca	ccttccgagg	taccgggtgat	240
ttcggcattt	tttcgtaagg	catctcatcg	tagtaccgaa	ggttgaacac	caacgctggt	300
tatcaggcaa	ttccagtata	gccttttgga	aggtaatctc	ggctcatctc	catcgaaata	360
aacatccccc	gtgaggttgt	cgagcagata	gggttttcgt	ccgtgatcga	tatactcata	420
tcgtcttcga	tctttttctt	ctcaggaaat	tgagtgatcc	gtacatggct	atccgataga	480
gccagggtgga	agttttggcct	ccccacgaaa	accgtccaat	gcactccatg	ccttcataag	540
gtatttttga	gcaagtcgtc	cgtatcgtca	tgactgagca	ccattcgggg	atttgccagt	600
agagtttacg	gttgtagcag	cgtactacct	tttcaaagcc	atacgccgcc	ttgcccggatc	660
tctcagctct	tccagcaact	cttcttcgaa	atcaatagct	tatcagccat	aatgatgcgg	720
taaagatagc	aaaaggtgct	ttatctatgt	caataaagtc	gaagattcag	ctctgatcct	780

gtaggagaga	ccgaaacatg	agagagttat	gctcctgtgc	tttccattct	atgccgactc	840
tatccttttcg	gctcatgcg	caatccaaat	tcaaatacctt	tgagttgcgc	tactcagaca	900
aggtattgca	aatgcctctc	ggctattacc	caaatacgtg	cgaaaaaagt	tttcaacaac	960
ta						962

(2) INFORMATION FOR SEQ ID NO:77

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

ggcgaagagc	atgttcgggc	gtacgctcca	gtcctgagct	ttgccgtccg	aacgtaatcg	60
aagagatagt	tgtagcaatt	cagaaacgta	tcgggggaaga	tctttcgatc	cggctgatga	120
tttcgccgat	ctccggtttt	tcccatgag	ttctcgttcg	aagcagaggg	cattgtacca	180
gagagcattc	aattcgcgag	atagccctca	cgggggatga	cggctttgcc	attcagtttg	240
gcatcatcca	acttaacggg	aagcctgtgc	ctaagacgta	gagaagccca	ttttacgaat	300
ttgtgccgtc	gggtgctggg	cggacagata	ataagatacc	actcgctgac	gaaggagccg	360
aatctcttgg	ctgcttccag	accgttgccg	cggcatactg	ctggatggcc	caaatagcc	420
aaatcccaac	gtccggttca	tcagcccgtg	tatggtgtcg	tcattctcat	gcagtcgcat	480
gtagcggtcc	tcgccggaat	gacggtattg	acgatgccgt	tcgaatcgct	tccggtgctc	540
tacacaccag	agtacagccc	ggtaagtgcc	acgaacagat	cgcgagctga	acgtcgaac	599

(2) INFORMATION FOR SEQ ID NO:78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

cagtattgcc	caatggggtg	atgagcggtta	cccctttcaa	tgtagcggt	cgacagagaa	60
tcgcttcgac	aaagattcgc	ggtgggtggag	tgcgctttt	cggccgacaa	tagttactgc	120
atcggtttca	gccatgtgaa	tctgagtgag	taggctgtcc	cgaactgagt	ggaatactgc	180
tgatggccac	ttccggacat	tcgatacctga	ttactgctgc	tatggctctt	cgctcagtcg	240

agaattgcgc	gcccgggaga	atacaaggct	gtattggaca	aatacgggtat	agatcagccg	300
tgaccgtaac	cgagcggact	gctttgaccg	aatttgcttt	tccgaaggag	aaggccatat	360
cctgctgaac	ctgggacagg	ccctaagcaa	tgatcgggag	cctctgttcg	attcttaaac	420
gactccacag	tcgtcggcag	cggctgatgg	ggacgttctg	ctacaatccg	caagcagttt	480
ttcgctcagta	ttcgtaacttc	aggtgagtcg	gcgaccgatc	tctgccggct	attggaagag	540
cagcctccta	tgacagtgga	agcccaatgg	gattcgactg	cagggaaaat	agcagtacga	600
cggctacagc	gtgagatgag	cgtgatgaca	tcgtgtcgat	ctcgtcaact	ggatc	655

(2) INFORMATION FOR SEQ ID NO:79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

ggggctgatg	gaatatgttt	ttcccgaact	cttagccctc	aaaggagcaa	aacgcgtgat	60
ggcatcgggc	ataaggacaa	tctcactcat	acttataagt	agtggacaac	ttggctcggc	120
acagcgatag	tctttggctc	aggtgggagc	attgctacac	gacataggca	aaccacgcac	180
taaaaagttt	gttggcgaca	gtggacattt	cataatcaca	actttgtcgg	agccaagatg	240
ctacctctct	cttcaaacga	ctccgacttc	cgctggatgc	caaactcaaa	tacgacaaaa	300
actcgtagat	ctgcacatgc	gtccggcgagc	tctggtggac	gaagagttac	ggattctgcc	360
gttcgcccgc	tgctcttcga	agccggtgat	gaatagatga	tctgatgatg	ctatgcgaag	420
ctgacattac	aagcaagaat	ccgacaaggt	gcgcaagtat	atagacaact	atgctttggt	480
acgtcataag	ttaaagaaa	agaggagaaa	gaccacgttc	gcaacttcca	agcaccgatt	540
ccggcggaaga	gattatgcag	accttcggtc	taaaaccatc	gcgccacgtg	gcaccatcaa	600
ggaggcgatc	aaagaggcca	tactcgacgg	ggctatccca	atgactacga	agctgcccga	660
gttttcatga	tcgaagcagc	tgcttcctcg	gtcttcaccc	caaaaaccaa	acatcatgcc	720
acagcgatata	gacctcgagt	gcgccccgaa	gaggctactg	acgaacaaat	actgcgcaaa	780
catgagcgag	acagacaaaa	acagatccga	ccgacataca	tactataata	atcgacgtcg	840
cagtattgac	gctcgacaac	gacagtatac	gtcaattggg	tcgaagctat	a	891

(2) INFORMATION FOR SEQ ID NO:80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...2496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

accatatatc	gctatgaaat	taatccaagt	tcaaattcat	tcttccggag	gaactgattg	60
cattagagcc	gaccaagttc	cgcgacgaat	cgcgaatgtg	gtcgtacatc	gtcgtacagg	120
agaaatcgaa	catcgcgttt	tcaagyaatt	ctggagtgatt	tcgacaagg	tgataccttc	180
gtcttcaaca	ataccctggt	tttctgccc	gtctctatgg	taataaagag	aaaaccggtg	240
ctcagtcgaa	gttttcctcc	tgcgtgaact	gaatgaacga	ctgaagctgt	gggagtcctc	300
gtggatccgg	cccgc aaaat	acgcataggc	aataagctct	attcggcaat	gatgaagagc	360
tggtggcaga	ggatgatagac	aatactacct	ccgagggcgt	acgctgcgct	tctgttacga	420
tggtctcat	gacgaattca	agaactgctt	ttccaattgg	gacagactcc	tctgccgaag	480
tacatcgatc	ggacgtgaac	aaagaggatc	cggagaggta	tcaaagcata	tttgccaaat	540
ggaaggcgcc	gtggtggcac	ctgctgccag	tcttcatttc	agccgcgact	gatgaaacga	600
ctggagatca	aggactgcc	tttctcttac	ataacggaca	ccacgctttg	ggagcttatc	660
gcgacatcga	tgtagaagat	ctgacaagat	caaaatggat	agcgaggaga	tgtatatcac	720
ggaggagtcg	tgcataacat	caaccgttca	tgggacgaag	aaaagaagat	ctgcgccgta	780
ggaattcgat	tcttcgtgct	ttggaacag	ctgtgagcac	agacgggtcat	ctcagccggt	840
cgaagggttg	accaatcgct	tcatctttcc	tccatacgag	ttcatctgcc	ttctgctttg	900
gttacgaact	tccatattgcc	gctctctacc	caactgatgat	gacggccgct	ttcggaggac	960
atgaactgat	tatgagtgc	acgacctcgc	tgtaaaagaa	aagtatcggt	tcggtgctta	1020
tggtgatgca	tgctcatcat	cgattgagta	tggccatagt	gtatctttct	ttgggcagaa	1080
cttaggcgat	cgacacagtt	tgttgtctgc	agcattggag	atgctacaac	gagggtgggc	1140
agactgctca	ccctttctcg	gttctatgaa	accgagcgtg	gggattcgaa	tcgccccatc	1200
ctttcctcaa	tgcggtgggtg	gctttcgatc	ggaactcaaa	ccacaggaca	ttctgcacat	1260
cacacaagcc	atcgaaggga	attgggtcgt	acacaaaaaa	gcaatggagg	ggtctatcac	1320
gatgtccgat	agatatagac	attctattgc	attccgtata	cccgaagta	catcacctga	1380
gctggaactg	ccccacccac	aaatgtggca	acgggatttt	ggcgtatgcc	gctatcggac	1440
gtagctcctt	ggctgcctcc	ggaggctccg	ctccgaacct	ctgactaatg	aaagaaatga	1500
atgtaaacga	cttcgagata	tggctccagt	cggttcgtac	gaatcgctta	tggcagccat	1560
caaggcgag	cagattcagt	ttacttcggg	attgaaggac	tgaatatgcg	tgcgcgactg	1620
ccaacaactt	caccacagaa	gatctgtaca	aaatagccga	gatttgagag	ataaaggcgt	1680
aaagagctat	ttaacgggtga	ataccgtcat	atacgtgagg	acatagcact	catgcgctcc	1740
gtcatcgatg	cggcacaaaa	ggcaaaatat	ctgccattat	agcttccgac	gtagctgcga	1800
agatgtatgc	caacagatcg	gagtagaagt	gcatctgtcc	actcagctca	atatcagcaa	1860
cgggaggccc	tacgctttta	ttcgcgcttt	gccgatgtgg	tcgtattggc	agagagctga	1920
atatggatca	ggtgcgtaca	atccacgaga	ccatcgtcag	gataatatct	gtgggcctaa	1980
aggccatccc	gtacgtatag	agatgtttgt	cacggcgctc	tgtgtatggc	cgtttcgggc	2040
aagtgtctatc	taagcctgac	gaacacaaca	gctccgccaa	cagaggagcc	tgtgcgcaga	2100
tctgcagagg	ggctacaccg	tcaaggacaa	ggatagcggg	ctggaactgg	acattggaac	2160
caatacatca	tgtcgcgcga	agatctgaag	actattcatt	tcatcataag	atgatggatg	2220
ccggcgctacg	agtattcaag	atagaaggaa	gggcccgtggc	cccgaatacc	gtctatacgg	2280
tctgcgcgtg	ctataaagaa	gcgtcgaagc	ctactgcaac	ggcacctatg	atgaagaggc	2340
cataggccgg	tggacgaaca	attggctacg	gtattcaacc	cagggtttt	gggatggcta	2400
cacctcggac	aacggctcgg	cgaatggaca	catcgttacn	gctcaggagc	acgcgacaga	2460
aaatatatgt	aggcaagggg	atcaaatact	ttcagc			2496

(2) INFORMATION FOR SEQ ID NO:81

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

cgcaattgat	cgggatggct	attctgattc	ttctcgttct	ctatgccaaag	gcaatgactt	60
gctcagggct	tttcgctgac	agaccgctat	gattcggagg	agacttaccc	ccacaacttc	120
gaggagaaag	tgggtttcga	tgagattgtc	gccttctcat	cggccattgc	catagtccga	180
tgggcagcga	tcgggtatac	agatgcatgc	tcttgcaagg	cataacgaag	tcagccgctt	240
gcttgcgaga	cggaagaaat	gcanattatc	ctgagagaag	acgacttggt	tcccatctcc	300
gtctggccga	tgtgcgagaa	gcactaaacc	gtatccgacc	tgcggtacct	atctggaaga	360
gcgagagttg	caggatgtgg	ctactgctct	gagacaatcg	aggctctcat	ccgtttcttc	420
catgtggggg	aagaagagga	ggtaaggata	caccgtaccc	ccacctccaa	actcttttgt	480
ccgaggtcat	gcctttccgg	atctggagaa	gcgtatcagc	agcttggtcg	atcggttcgg	540
aaaatgaaag	acaatgcctc	gcccgaactg	atgaatatcc	gtcgcgaatc	tcttccatag	600
agaaaaatat	ctcgcgcact	ctccaaggca	tccttcggtg	gctcagtcgg	aaagct	656

(2) INFORMATION FOR SEQ ID NO:82

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

cgggggattt	tcctcctctt	tttgggcttc	tgccagcaat	gagggattta	ggctatgcc	60
aatcccacac	tgccgtaccc	ggtcacactc	gctgacgagg	ttatcagggt	cgttgcggtc	120
ggatgcttac	ccgaccggg	atcaaggata	cggcatgggt	agttatctgg	tggcggcatc	180
gcttttttcc	ggtaagtcga	tgtatcgaaa	ctgatctctg	ccccattgga	agccacttac	240
ttcggcacag	agtacgccag	cgcccgattc	ggctgcgagg	ttactatcga	tacaggccgg	300
aagcaaatat	atcgatggca	gcatagggcc	ggatgccgtg	ctgaaggcaa	agaccaatgc	360
acgatcgccg	gcgtattcta	tgaagtaact	gagatacgcc	ctacttgaat	ggcaagaacc	420
tctatactgc	accgtccatc	gatctattgc	caaagtata	gcaaatgata	cggatgggtg	480
gcagccgttc	atctcacgtt	ccgatccggt	ggcaataaag	tcgtggactt	ggccaacaac	540
agtaccgctt	ggctctggtc	ttttcgctct	catcgcggtg	agacgagtta	tcggctccgt	600
ggatagcgaa	ctgcttgctg	atgaagtaac	ccttacgtga	ctactttacc	cgaataaacg	660
ttatgaaccg	gcgatatttt	cttttgatgc	ttgcttttgg	agcctctgct	tcctcctgtc	720
ggctcaggag	tcgaagcttc	tgtccggccg	tcgctttggg	agttttccag	cagagtgggt	780
atgctgtggg	agcatccaca	ccggtacccg	tacccaagc	catggagcac	gtcacgcgtg	840
gtatccgcga	ctgaatccga	tggatgcaact	gagtgccttc	cgcgtttgct	tgccggcagt	900
ccgtgggctg	tgaacgtggg	tatagccgta	ggaaaaaagg	catggaagct	actacacgag	960
tgaagatat	gaaagtagct	tcgtgtcgga	ctcgccttat	gcccggcaac	cctgatgaag	1020
aatatccgga	ctattcaccg	gcgacaacaa	tacgg			1055

(2) INFORMATION FOR SEQ ID NO:83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

tcccccatag	aaatctcaaa	caaccgcaaa	gtctttctga	ccaatcaata	ggggttgtaa	60
acatcactga	cgggatggaa	cctccgatta	ttgccggatc	tctgcttcct	atggatcttc	120
cgtcggggtg	tatggtcatg	tctcacacgg	tgggacatca	taggccattg	ctatttggtat	180
atctacccaa	ccaattctat	ccgctcagca	cgaaaccctg	tgcaggagac	gatgagggtt	240
ttgtcaacaa	caaggcaggc	aaatagagat	cgatagcaac	agccccatag	tccagtgggtc	300
gtatacgatc	ttgaggggaa	aagtgttttt	cgcaaaagaa	tgacgaaaac	gcttataccc	360
tatcctttag	agcaccatg	ctcggcttta	tgccatcatg	atcgaaacac	aaaattcgat	420
tatcaataaa	aaacttaatg	tacacagcta	tgaacgaat	aattttatta	ctcagtactc	480
tctgcttctt	gtatcacctt	atgtacaagc	gcagaatgaa	ggttcagatg	cttattatca	540
caaagtgttg	aactaatccg	ttccgacttt	cgaacgga			578

(2) INFORMATION FOR SEQ ID NO:84

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 868 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

gagaatccaa	aagcgttaata	gaaaggtata	caagcaaaat	taggcttcac	ggagttgggtc	60
ttttttctta	catttgttga	ctcaacaact	aaatgcccat	atatgctacg	acttcatata	120
acatcgacaa	acagtaaggc	cgattttcta	tcccacatac	ccactctccc	atcgcgaaag	180
gagagaaaag	aacgctatac	ctatgacgaa	caagcaggaa	taaggctatc	aatagccgga	240
caaaacataa	ggcacgcacc	cgatttcgag	ctgaatcagg	tgcgtgcctt	tctttatcgc	300
ctgtcgaaaag	ggctttcttc	atctacgata	tatatataaa	tggatgacaa	tctatataga	360
tatggaaatc	gatttatata	taaattgaaa	acattaatat	acagatcgaa	aatgatttat	420
atataaatcg	aaaatgggtg	aatacaaatc	gtttttccat	ttcttagaaa	cccgaatccg	480
agctaaagaa	ttcgttttac	caccttttgg	ggttcaaaag	gctcttactt	tcagggtgcta	540
tttagaatca	ttcaaaactc	atcttcggtg	ttgaaaactt	ttttgggtgg	atttttcagt	600
gtttgccata	agctccggag	agcagagaaa	aaggcctcca	cgattgattg	tcttctccc	660
cctatcctac	ccccaaaat	accgcttagc	tacttatcga	tagtatgagt	gcggctccgc	720
tcttgatgcc	ggcagagccg	aaaaagggaa	tcgtgcttca	ttatttatta	cttttgccgc	780
ataagttctc	gtgcagacgc	ggccgatgac	cggatcgtgc	acaggagaag	caaaacattc	840
ttacaggacc	aagcgtacag	tatggaaa				868

(2) INFORMATION FOR SEQ ID NO:85

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

```

cgatcttctt ccagtatgta ggccggagat gctatgtcgt ggtattttgc atctcttagg      60
attagttctc attcggatc agttccaaga acagctctgg agctgtgcct catcaatgac      120
agagggggcg tcgatcatga catcccgccg gcattgttct tcgggaaggc gatgcagtcg      180
cggatgctgt ccaaacggcg aagagcgata cccagcggtc taagcccgta agccaatccg      240
ccgtgggagg tgctccgtac ttgaaggcgt tcatcaggaa gccgaactgc tccttgcttt      300
ctccggcgta aagccgagca actcgaacat tttctgctgc aggcactgtc gtgaatacga      360
atggaaccac ctccgacttc gacaccggtg ataccatata gtaggcattg gcacgcacgg      420
cacctggatc ggtatcgagc aagggatgtc ctccggcttc ggactgggtga aggggtggtg      480
catggcgtag atcgcttcgt ttctcgtcc cattcgaaga gggggaagtc cacgacccaa      540
ggcaggagaa tttaattctt gtcgcgcaga ccgagctgag agccactcg aggcgaagtt      600
cgcacagttg cttgcgcgtc ttcatgaggt cgtctccctg aggatcagaa tcaggtcgcc      660
cggttctgcc tccatcgtec gncgaactct tggagcgtct cttgtgtgta gaatttgtec      720
acgctgctct tgacgtgccg tccgattcca c                                     751

```

(2) INFORMATION FOR SEQ ID NO:86

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

```

cgtggttgat ctgcaaatcc accgattcta cctttctact aagaagaatc ggatttagaa      60
aaagtgtttt tctctatcga tcatgcaaaa gggacaatgt taataagaaa tatatgcctt      120
atggcacggg ttagattctt gtcctaagaa tctcgttacg gatctctctg caaaaaagtt      180
gcaagtagcg gttaatatgg ggagtataaa gattggcata ataaagattc gttgtgggtg      240
cgcgatgtca taccttgcat ttaatggttt tcgacgaaag tggcgagaaa acgaaaagta      300
tactgttacc ctcaatcggt atgattatca accgactacg ttttttggca tatgctcgat      360
ggagtagctt taccggatat caatgcttct ttgtcgatgt tgtaacacat gctgacaggg      420
tttatttggt agcagccaca gtaataagac gctgttgat tcabctgaca ggaaaaatcc      480
tgttcattgg ctttactatc gtcttcgggc ttgtccgggt catgtaggca gatagccgca      540

```


ctgaagatgg	acgcgcttgg	attctaacag	attccggtat	ttatcaaacg	atgacttcac	600
aaactggagt	ttgctcccct	ctgaagtccc	tgtgaccccc	tgctgggtgc	catgggttgg	660
ccacagggaa	gtcatacact	ggcattcttg	ctgaaaaaga	tggtctctctg	ttctttgcc	720
ccaatatcga	tggagccatt	cttggcagga	gcaagctccc	gaaactttcc	ctgttcgcaa	780
tttcgtactc	aactatataa	agcaacaat	catccaatgc	tcggtttagt	cgggggtgtaa	840
cgcgtacggg	tgctcctgcc	acttccggtt	ggatcacgag	catggaaaacg	attgggttgg	900
acttgacttg	gctgcccggag	ccattcccgc	acaatggaaa	aaggggcttt	ggtgcaaaact	960
ccatcgggatg	gtaacttgta	tattatgcc	cagaacaagc	cgaaggata	aagcgagtag	1020
ctgtggcatt	tcgactgata	agggcatcac	atggaaacgt	ggagccgccc	atattatgtg	1080
ccggccgatac	ctttctacac	agccggctat	ccgttgctgt	tcgtctggct	tttgatgatg	1140
gggcttacaa	tatatatcag	ttgggaggcg	ttagctttca	ggaacattct	tttccctcaat	1200
atggaagggt	atcctgaaac	tgaataaaac	aattagtaag	aaccatgcgg	cacggatctg	1260
tgccgccatt	gcttggttgc	agtgtgtaac	ggccggatag	ctgctcagga	ttttctctat	1320
gaataggagg	agggttttgg	gctgctcagt	atgttgccga	tgcaaacaga	ggttggttcgg	1380
ttcatccgga	gtagggttgg	agttggctcg	acgttacaa	ttaatTTTTcg	ctgggctttc	1440
agtaccatgt	tggattggcg	tacattgaga	gcgataccga	taagtccggg	aatgtcttcc	1500
ccgattttgc	tcaagcggat	ttaaagtcgg	cttgactcag	ctccacgtta	gaagcgaatt	1560
taactttccc	cttatagcga	tggctataag	tatcttggt	cagctcggct	gtctcctatg	1620
tagcggccgg	gttgctctttg	ggttttgctt	cgggtgctaa	agggttcgctt	ttgctcccgg	1680
gattactgcg	ggaatgggag	tgaagtataa	gcttaaccgc	ggatcaatgt	cggtatcgag	1740
tattctttca	cggggggttac	ttacgatgct	ttggatgcgc	tgacggataa	aagtgtttgg	1800
ctcgaggatac	cattaagatc	aatgactcct	gggtcaaaaa	caaggatgct	acaggggcct	1860
tatgcttagg	attacgtatg	acttcggcct	gcgtaagact	ttttgtaata	acaatagggc	1920
ctcgaaacat	tctaagggaa	tagacctctc	ttggattgg	gttaggtgaa	atatcttgat	1980
agaaaagaga	tagatggaag	gtgatggagc	aagctccagt	cagcagttat	agtgccgagg	2040
catatcgctt	tggtcatgat	ggtaatggcc	gttgggcaaa	gatacgaggg	aaagagcgat	2100
gcgaaagaca	tgcgccgggt	gtggatgctc	tgcgcgtagc	tttgcgtgca	gcagccgggt	2160
gcggtgtgga	atatctcaca	gcctacacct	tcagtaccgg	agaatggaat	cgtccggaag	2220
aggaagtcag	g					2231

(2) INFORMATION FOR SEQ ID NO:87

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

ggttaccggc	tctctgaaag	tattgcagac	cttttaagat	cagtaagggtg	gtacgatcgc	60
cggttgtatg	gtcaaaggaa	ggtaagggtca	agcgaacagc	aagggttcgtc	tcatacgcca	120
cggtatagtg	atccacaccg	gagagctggc	tctctgaaac	gattcaagga	cgatgccaa	180
gaagtgggtg	ccggaccgaa	tgcggtctta	atctggctca	ctcgaaacgac	atccaagatg	240
gtgattaatc	gaagctttcg	acgagatcga	aatcaaaaag	actctctaaa	gatcaaccga	300
gacgggttac	caccatgaa	cgcgatcgat	ttagccatac	tgaaattttg	gcgataggat	360
tactgaaagg	cctgtttgat	ggtatcatca	aaaggcagtt	tactttatag	ccatagtcgt	420
tgccacgtat	ggttggtgct	tcttgccggt	cccatagaga	cgtggatcgg	accttttttc	480
ggcctttcac	agcgctggct	catacttttg	ctttgatcgt	tgggttcttg	gctattttgt	540
tatcatcccg	atggtcggca	ataaggcttc	gaaaatcggt	ggcaagaccc	tatcggcatt	600
ctcaatcact	tggccggcgg	aatagtcggg	atagggttag	cagctattct	gatgagctat	660
cttttctcga	ttgccgacaa	tgtttttcaa	gagacgaagc	ggacagtgc	aatccgtccc	720
ttcgcaatac	ttcgagctgt	atgacctgt	aaaaaacata	gtcccaactt	ttagcccca	780
tcggtgttta	tgaattgaaa	ttcgtaaaga	gcttactcag	agacttcaaa	tatcaagaga	840

acaataatat	attggatgag	gttacaggca	gtgaatataa	atcgggcttcg	taaccgacat	900
cgaaacagaa	actataggac	gcggaactttc	caagatacag	ttcgtctcat	atctgcgaag	960
aaggaagagc	cggaaatggct	ctcgaattcc	gcctgaatgc	ctataggcac	tggtctctta	1020
tgaagagccc	gactggggcac	acctcaatat	tccaccgata	gactaccaag	atattatcat	1080
tatgcagctc	cgaaaaagaa	aaagggggccc	aagagtttgg	a		1121

(2) INFORMATION FOR SEQ ID NO:88

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

atccccgcaa	gctcgaaaca	cccgaagccg	taacggcttt	cgagggactt	ccatacctga	60
gccggggcctt	gaaccgcgct	tctgcgtacg	cgaaggcggc	aggaagtccc	cgttacgacg	120
agatatacgg	acgaggcttt	ctggcagtg	tgcatttttc	tttcgtcgcc	ggcaagcatt	180
ataccgaggg	ggatgccgat	cgaacatcgc	cgtggcagtc	attaccgaca	ggttggcgcg	240
ccggtcttcg	gctcttcgag	cgaggccgtc	ggccggcaag	ctctgatcaa	tggggcaaat	300
acaccgtctg	cggagtgggtg	cgccatgtga	ccccctttctg	cgattcgctt	acggagatgt	360
gtggatgcct	gtgttcaggc	tgtacgaaga	aaagtgaaga	acaacctatt	ctccagattc	420
aatgtaatct	gtctggccaa	agcccgaagg	acttcgatgc	catcaaggaa	gaagtcgggg	480
ccttgactgc	aagtgaata	gtgtgcagga	gaagttcaat	atcagttttc	ccggccagct	540
gccgatcagt	tcacgacgat	gcaccgcaaa	tttcaccgtg	acgataccaa	cctctggagt	600
atcgccgtcg	cttcattctc	ctcctggcag	tgtttcttgc	atcccggcca	tcaatctttc	660
gggtatgacc	cttagccgta	tgcgtcccg	ttggccgaat	tgggcgtacg	acgctctttc	720
ggagccgtcc	gatccatata	gtccgccaag	tgctggcaga	gaatatgctg	atcagtctga	780
taggggggct	ttcggattgc	ttttgagtta	tctggtcag	gccctctttc	cctgtggctc	840
ctcagcgtgg	ggagccgggg	aatgatgcag	ggcgacatca	acgagccatg	ttcaatccc	900
tcattttctc	gatagctctc	gtcttctgtg	tctgatcaat	ctgctcagtg	cctttatccc	960
tgccctggcg	atatccaaga	acccatcgta	gaatccctct	cccactaacc	tcatacata	1020
gatattatct	gctacatcat	attatcaaga	tcattccgcg	cgaacgtcgt	gccaaccttg	1080
gatatggctg	gagatgctcg	tcgtatgtgg	cctgctttgg	ttcgtcagga	ctatgccgtg	1140
acagctctgc	gtgcttggac	acgcccattg	aactacatat	agaacacgtg	taccgcatca	1200
cgctggcaac	cgtacaaaaa	gataagatgg	aaaatggaaa	gagaggtctg	cggatcaggg	1260
aaaaaccatg	atgcaaccct	cgatctgata	gctgcatatc	cggagtggaa	gcgcttgtct	1320
ccaagtgggg	cggca					1335

(2) INFORMATION FOR SEQ ID NO:89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

```

cctgaaagta atatccggat caaggggtgt gcagaggagc atgtcatcct gtcgcacaag      60
ccatcgaaca tatctaccag atcaccgaaa cgatcgcttt gaggcatacg gcaagggcgt      120
tgatggtgaa gtcgcgacga cgcaaatac ttccagcgta ccatcttcga ctatcggctt      180
acgactatcg tgtcggaact ttccttacgg gcacccacaa attctatctc cagatcacca      240
tgcttacttg agcggtagcg aaattggcga aaacggatag gtgagccttc cgtccagctt      300
cttggctaca gctttcgcca ggtcgatacc gcgcctacg gctctatata gatattcttg      360
gaaggacgat tcaagaatat atctcgacac taccaccac gacataaggt ttccagtcct      420
aactgatctg ccactttctg cataagacgg aatatcggga tgtcgattta ctaagaatta      480
actctttgtc ggcattctaa aaaatcaagg aatggattgg ccgacaaggt      530

```

(2) INFORMATION FOR SEQ ID NO:90

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

```

cagcttggag gctccgagtc cgcgctgaat ctgaatggta ctggcttgat catcagacca      60
ctccaattgc tccaatatac tttcccgctc tccatacctt gacaggaact ccgttgatga      120
gtacaccgaa gttgtaagtg tgaatcacg cacattggta cgaccatcac cgaaacctcc      180
gcttcctttt gtcgtaaggt agagggagtg gatttaacca gttcgggaaa ttcgacattc      240
aacgagctgc ctgaatatca gccacacgga tattggaaac gggtagcggc gtcaacggtc      300
tttgggcacc acagaggcta ttacctgaat ctcatccaag ccgtggcctg gggatcgagg      360
agaatcgtag cgaggtcttc ttgagaacct ctctataga gcgagttacg gtagcataac      420
ctacgcaacg gaaagttaag aagatttggc cgggtact                                457

```

(2) INFORMATION FOR SEQ ID NO:91

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5301 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...5301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

tgctccgggtt	tcttcttagg	cttcgggtcc	acacgtcgta	gtcgaaggca	gggctgaaga	60
ccccggggcg	agcttgcgc	gtgcggggat	gctcttgact	ctgccgaggg	gatgaagacg	120
agcctgtgct	tctggatctg	atctacaaga	aattcttggg	gtcgtccaat	tgtttggaac	180
cgaacgagag	gcggaactgc	ccagctcgcc	gatgcgaacc	gtcttgccgt	tgggcagctc	240
ctcgcgagga	tattgacgag	gcggtccagg	atgcctttga	cgctcgcgga	ggtcgagccg	300
actcctcgcc	tattcgcttg	cagaggctgt	ggaagggttac	agatcttgtg	ccgccggctg	360
ggcataatag	atggctctgtc	cggctttggg	gcgatcttgg	cgacagactt	tttgatcaca	420
tacttttaggg	acataaacttg	ctattattag	tttcttggtt	tttgatgacc	actcataccc	480
gatacatccc	caagtctctcc	gaaaaaaaaa	gtctggacgt	tccgaggaaa	acgtctagag	540
ttccgaataa	aacgtctaga	cgtttcgagc	aaaagggtcta	gacgtttcgg	caaaacgtct	600
agacgttttt	tccgaggggat	attgcagacg	gccacggcac	gtcccggcgt	ttcccggggg	660
aggctctcgg	ccttcctccc	gtgaggcgct	cggctcctcc	cgcacgcggc	tgaccgaggg	720
ggcggccacg	acttgggggg	cggctctgcaa	accgcggcaa	aggtacccaa	atagttcgat	780
tccgagacag	tataagccgg	gagctgggta	ttgccatgcc	ggagacgaag	ggggcggcgt	840
cccgctcttt	gcgatcgact	ctccgcctcg	cccccggtgg	cctagcatcc	gcaggcgcag	900
ccggcctcgg	cgaataaggc	ggaggagagta	aaccatcatt	cgatttattt	cttacatttg	960
cacgacggaa	aacgaaatag	cacctattct	ctatcctttc	gtcctgcggt	atcgagtatc	1020
ctgacagtcc	attccgagat	gccgtatccc	cctatcaaca	cttatcatat	ttctaaaagc	1080
tcatcatcat	ttattatgca	gaagtacacg	atcgtcgatt	tgaacgaaag	gctgaagctg	1140
aactcgctgc	tataagccgg	gagctgggta	ttgccatgcc	ggctcaatgc	ccaaacaaga	1200
acttattttac	aaaataactcg	acgagaggct	atcagtgtag	ccggcgctccg	gaaggaaaaa	1260
caaaaaacga	cggagaccgg	cacaccgaaa	ggcgcaagcc	gggtcgctccg	cgcaaaaacg	1320
ccgggaggaa	gctcccgaaa	gcgaagacgt	cgcagccgct	cctgccgagc	cgacgacgag	1380
gaagctcagg	ccaaacgcaa	gcgtggccgc	cttcgcaaaag	cgcggaagag	atagcggaag	1440
agacccgagg	agatgtgcag	cagctcgttg	tctggctgct	gcagaggaga	caaatgcaac	1500
ggagaaggag	agtgccgggg	gaagccggcg	gcgaaaacgt	ccaccgcctc	ccctgccaaa	1560
gcccctgcaa	agcccttccc	cgctccggcg	agaccacccc	gcgcgtggca	ccgtctcccc	1620
ttccacgacg	cccgtgagcg	agccggccaa	ggacgatgcc	aagcccagac	gcccgcctct	1680
ccccccgcca	tccgagtcct	caccacgact	cctgcgcggg	agccgtcgat	gagggcggtg	1740
ctcgccgcct	cgtattcagg	cacagaacag	ctcctcggtt	ttggatcagg	tgctgccgta	1800
cagctctccc	cagccccgca	gaggcccaaa	cgcgcgggtg	ctccggctcg	cagcagcccg	1860
ataggcagcg	acaggcgccc	ggcggtgcga	ctccccgtcg	cgaacctcag	cacctctcta	1920
caacttcgac	ggcatcctcg	agtgcctggg	tgtactggag	tcatgcccga	ctgactacgga	1980
ttcctccgct	cctcggacta	caactatctt	cctctccgga	cgatgtgtac	gtgtcccagc	2040
agcagatcaa	gcacaacgac	tcaagacggg	cgacgtcgtg	gcaggtacta	tccgtccggc	2100
cagagagggg	agaagtactt	ccccttcgtg	cagctgcgga	gtgtgaacgg	tccgagcccg	2160
aagagatcgg	cgaccgcgtg	cccttcgata	atctcacacc	cctctccccg	aagagaagtt	2220
caccctcgaa	gcaccgggca	tccgtccgct	aaacataaaa	tatccgtccg	cgctcgtagc	2280
ctcttcgccc	ccataggcaa	aggcagcgcg	gcctgatcgt	atcgagccc	aagacgggta	2340
agacgatgct	cccaaggaca	ttgccaatgc	catcgagccc	aatcaccccg	aagtgtacat	2400
gtcgtcctgc	tcacgcagca	gcgtcccga	gaggtcaccc	acatggcgcg	agtgtgaacg	2460
ccgaggtcat	cgcttccacc	ttcgacgagc	cggcagagct	cacgtgaaga	tcccgagat	2520
gctcctgaac	aaagcccaaa	gaatggtgag	tgcggtcatg	acgtagtcat	cctgctcgac	2580
tccatcaccc	gcctggcccg	gcatacaata	ccgtacagcc	cgcacggggc	aaggtgctct	2640
ccgggtgtgt	gatgccaatg	ccctgcagaa	gccgaaacgc	ttcttcgggt	ccgctgcaac	2700
atcgaaaacg	gcggtagtct	caccattctg	gccacggcgc	tgacgacacg	ggttctaaga	2760
tggaaggagg	gatattcgaa	gagttcaagg	gtagggcaat	atggagctgc	agctcgatcg	2820
ccgcctgtcc	aacaaacgca	tatccccgcc	gtggacatga	agtccagcag	taccgctcgc	2880
gacgacttgc	tccaggacgag	accacgctga	accgtatgtg	gatcctgcgc	aagtacctct	2940
cgacatgaat	cctgtcgaa	ccatggagtt	tgtgcgttaag	cagctggaga	tacgcatacc	3000
aatatggagt	tcctcgccct	gatgaacaac	tgatcagttc	ctgccgccgc	ctcctctccg	3060
acaagagagg	aggcggcagc	ggacaggctc	tgagtgcaga	gccgccctct	atccggatgc	3120
agaccggcag	acgaggggag	ggaagtcgaa	gagccgggca	tatcgtcttt	cggtcttctc	3180
cgtgcgctta	cggtttcgct	ctgctatacc	ttattattat	aagtatcaat	cctcatattc	3240
ggtcagcgag	cattcatgac	atcttcacgc	ctctacggct	ttgggtcggg	atactgtcgt	3300
ccgccacatt	cgggcttcat	ccctgtttca	ctgcccgggt	tccggctaagg	gtgcttcggt	3360
cgagcttatt	ctcttctatc	gtttttcttc	gcagccatcg	ccatcggtat	actgcacgc	3420
ctctcggggc	cagcttcaaa	gtcagccgtg	cggatatagg	gccgctggta	ttgctgggct	3480
cttgatatgcc	ggcacggcac	ttttcctctt	tcacggctat	ggctatatgc	cagcgggtga	3540

```

gccaccacca tccacttccct ctatccgctg ttcgtcaggc tctgatgctt cttttctttg 3600
gggaaagact ttcgcccgtg ccattgcccgc cattttcacc gccctgatac gcgtgggcct 3660
gctgatgggc cttacggagg gggcgatcgg gtagggctta ccggctttgt gatagtcgcc 3720
atctggcgct ttgctatgcc ctctatatcg tctttgtcaa tcggagccgg atcgaatcat 3780
gccgggacgg cggctgacgt tctacgtctt cgtcgcagcc gcggtttttg cctgatcaac 3840
gtcctgggtca gacagggcga agtggctcct ctcccgcagc ggcttcatgg ggcaatatcc 3900
tgctcttggc tttggtgccc cggtaatttc caatctggct ttggtagtgg ctgtacgcaa 3960
catcggtcca cgctcacctc tgcgctggga agctatggag ccgcttacgt ccggtattgt 4020
aggtgtgtgg gtcttcgacg aggtgttggg ggccctcgcct atagtcgtat gggctgtatc 4080
ctcatagccg tcgggcttat cgtcttctcc gaaccgtcga actgatgctc cgcaggagga 4140
gacgatagct gccgttcgct accgtcgtct gctgcgatat tgctttcggc caccaagtac 4200
aggggccttg cgacatatct ttattgatct tggatatata ggtaccgatc accccaaggg 4260
atacagctgc actcctccca agaacatgga gcttacgatg acggaagtc atcgctcacc 4320
gtcttatcca gcaggaagtg cgagatgagg gcatagacga tacgaataag gagagcaaa 4380
aaacccaggc acctaatggg gccacccatt aagcggctct ctggaaaatc ccgtgatgcc 4440
gtcgatggcc aaggcaagct ctctctgagc ggatagttcg tttggccgta tttcctttcg 4500
tctctgtcaa ctgcacccct gtctggcggg atcccattcca ggcgatttgt cccctcagaa 4560
cttgtttctg tcgggcatct ctgcgaggca ctgcacgatc ttccggcgat cagccggaag 4620
tcgcccgtat ccagcggcat atcgatagac gtgatttgcg catcgctccg tagaaacctt 4680
tggcgtcgc tttcttgaa caggttcgct ttccgctgtg catagaccac 4740
ttcgtaaccc tcaggtatct cgcatacagt tccggtatca attccggcgg atcctgcaag 4800
tcccgtcgat gatcacgta gcccttcccc tcacatggct taatcctgcc gcacggctat 4860
ctgatgaccg aagttgcgac tcaggttgat gtagaagaaa ggtcatcacc cttgcacagg 4920
ctgcgcaata gctccatcga accatcgcg cgcgctcatt gacaaagatc agttcgtagt 4980
cctccgttat cgaagccgcg ccgcaactcaa ccgcccgcacc agctcgggaa gttccctttc 5040
ttcattaaga tcggcacgat gatggaaagc tccttcgtat aagtcgtatt gacatcatta 5100
gaattgacgt tttagattgt ttccggcact tcaggtgaaa aatgagtgt taggtgacaa 5160
gggtcaggac cgttcctttg tccgcttcgg gatgaaccag cggatcgtac tgtcgcgtct 5220
gaaccatgtc atttgcttgc gggatatacg cgactgttgc gttggatccg ccttacggcc 5280
tctgcccgat cgtcgagccg t

```

(2) INFORMATION FOR SEQ ID NO:92

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

```

agaagtggag gttgatccgc caattgacac gtatgcaagc tacaccgccg gcgctatctg 60
ctggcagatg tcttcgggta attgtggcct cctatttggc xacaatacgc tgcgttacct 120
cacggaagag caagagcgca tatactcaact ctgtccgaat atctcttcaa cgccaagagc 180
ctgtgggttg ggatccctat ctgcttttct ggctctcctc cttcgccctc tcgggatact 240
acaacaaccc atagccaaaa gcogaatatc cgaactgctg acgaccgtgg cgtcgtgctg 300
gtcggatccg tcgtcgtctt tctgctgctc gtgggtggacg acacgtacac gacacggcgc 360
tctacctgcg gctcttcttt atgatgttgg cgctgtgttg cccttgggta tatttcccc 420
gtctatgggt gacgaccttc gcatcaaaag gcgaaaaaag acaaaagggt atcatcggg 480
gctgctcacc ggagcggcac gatagccgaa gagacggctt cgtggctgaa gtccgtaaag 540
acatggccac cagcgggctc cacttcgtcc ctccgacgac gagagaggat tcgagcagtc 600
gctcaagtcc tttgccacgc ttgtcgccga agcgggtgaag agagcaagcc ccatcagatc 660
atcctcgccg tggattgccc cgatgcagct tcatcagctt gctcctttac cagctctatc 720
ccttccatat gccggatgcg tgccgatgcg cagcatgctt ttcgcccggg ccaaagtaaa 780

```

tgtaagggga	tgaaaggaga	gcctatggtg	gacatgacgg	ccaccaacat	gaggaatgcg	840
ccaagagcat	caagtgggtc	gccgaccggc	tggttctccct	ttgatgttga	ttctgctgat	900
tccggtctat	gccgtgatcg	ccgttctggt	cagcgttcgt	cgagaggccc	cgtcttcttc	960
ggacaggagc	gtatcggact	cacggccggc	cgtttacgat	ctataagttt	cgcaccatgt	1020
acctcgatgc	gagaaggacg	gcccgaagtct	cagcttcgat	ggcgattcgc	gggtcacgcc	1080
atcggggcgca	tcttgcgcaa	ataccggatg	gacgaattgc	ctcagtttgg	aatgtgcttc	1140
ggggcgatat	gagcttcgtg	gggcccgcgc	ccgaacggct	ttctacatcc	ggcagctcgt	1200
ggagcgtgct	ccctactact	acctgtgcac	aatgtccgtc	cgggcatcac	ctcctggggc	1260
atggtacgat	acggtatgct	tccactccgg	atgaaatgct	ggaacgcctg	caatacgatt	1320
ttcgactact	gagaatatga	gcctcaggct	ggatatagaa	gtactgttat	atcttgccaa	1380
acgattttta	aaggattggg	gaaatgaagg	ataaggaaac	ggtcgctacg	ggtgggttctt	1440
gcacttcctc	ctttggcgcg	aaaggcacat	aacgaaaggc	tttttctcat	catcttgagc	1500
ctcatcatcg	gtatcctctg	gcttttgccg	ccgttctgct	caagaatacg	atacacatca	1560
tccagcactc	gcattcgacc	gcattcgcg	aacgagctat	ctctatctca	ttttcccgtc	1620
gtgggtatct	tgatcacgtg	gctatttggt	cgctacgtgg	ttcgggcgac	atcgccacg	1680
gggtgacgaa	gattctgttt	gcgatctctc	agcgcaaagc	cgcatcaagc	cgcacaatat	1740
gtggagctcg	cttgacagcca	gttcattacg	atcggtctcg	gcggatcggg	cggagccgaa	1800
tcccctatcg	tacgacggg	gctgccatcg	gtcccaacct	cggccggctc	ttccgcatgg	1860
agagaagacg	ctgatgctcc	tcgtgggggtg	tggggccgca	ggtgccattt	cgggatcttc	1920
aaggctccga	tcacgggggtt	ggtattcgct	atcgaagtcc	cctgctggat	ctgaccatgt	1980
cgtccgtgct	gccgctgctg	atcagctcgt	cagtgccgcc	gccgtatcct	atattatcac	2040
ggggcaggga	gccatgttag	ctttacgctc	aacgatcctt	tttcgatgga	tcgcaccccc	2100
tatgctcgct	actgggtgta	ttctgcgagc	tggtatcttt	ctacttctcc	aaggctctgtt	2160
cgtcttcgag	agcaaaactca	agaactttcc	acactatcgc	caacgtacct	catatcggcc	2220
tttatectct	gcggtctgat	cttctttttc	cctcgctata	cggtgagggc	tacgatacga	2280
tcaacgccct	gctcggcggc	cagacagctc	tttgatggat	ggcagccctg	tcgagccgta	2340
ttccaaattcc	tatgggtgct	gttcggtttc	ctcggattta	tcatcatcac	gaagggtgtc	2400
gttccgtagc	caccaattcg	ggcggaggct	gcgccggact	tttcgcgcgc	gtctgttcat	2460
gggggcactg	agcggattca	tctttgccta	tgcgctgaat	tctttccctt	catcgaggctc	2520
tatctgccac	agaaaaactt	tgctctcccg	cgatggccgg	agtgatggcc	gcggtcatgc	2580
acgcgcgcgt	gacagggtttt	tctgatcgc	cgagctgacc	ggcggataca	atcttttctt	2640
tccgctatgc	tcgtgagtac	gagttcgtac	gccactatcc	gccttttcat	gccgccagca	2700
tctattcgct	ccgtttggca	cagaaaaggaa	agctgctgac	gcatagaaag	acaaggccgt	2760
gctgacgctt	atgacgttgg	atgcggtgat	agaaaaggatt	tcgaaccggg	gagaccggat	2820
atgactctgg	gagatgtcgt	accgtgttcg	gtatcagcca	tcgcaatgtc	ttccccgtcc	2880
tggacgagaa	cacctgctga	tggggctggg	attgctggac	aatatccgca	atatcatggt	2940
cggccggagc	tgtatgagag	attcaaggctc	agccgcttca	tggtttctct	ccggccaaaa	3000
tagtcaatac	gatgtccatg	gagaccatca	tgcgaatctc	gacgacacca	aggcttggaa	3060
cctgcccgtc	atagacgagc	agggatgtat	ctcggattcg	tgccccaaatc	caagatcttc	3120
aactcttaca	gggaggattg	gtggagacgt	tctccggcga	ttgagcttcc	gtacttttcc	3180
ctcttgctcc	tgcccggcgg	cggatccgtg	tatcgtaagc	tgccgggaacg	ggaagctata	3240
ccctgacgat	tgaattcgct	atagattcgt	tcgtttatat	cccgtaaaaca	ttccacaggt	3300
cgtccgtcgc	gcaccacgca	cgtgccatca	cctcacagag	ctgtcggcca	attccttcaa	3360
gaccacgggtg	gggagggggg	cttgataata	cgcggttcct	catcgatcag	acgcagcagc	3420
agcgttttca	ccgatcgaag	tcctcgttgt	actcgatccc	gatgatccat	tcgttccgag	3480
caccgccatg	cggctgtagt	tgatgatcac	attgctgctg	agtaagcctt	ggggatgaaa	3540
atgtacttgt	tctcgaacgt	cattaccgtg	gtgtggaaag	cgtcacgcca	tccacgaccc	3600
cttccacatt	gttgagagcg	atgtagcccc	cactttgaac	ggtttggtca	gcagcacgat	3660
cagaccgccg	gccagttctg	aagctgtccg	ctcagaccca	tcccagacagc	cacaccacc	3720
gaagcagcaa	ggccgcgagc	gaaaccgggt	ggaaacccaa	tgtggagata	atgtgacgat	3780
cagcagcaca	aagccccga	tattggcaaa	ggagcgaagg	aagtacgcgc	tgccggctcg	3840
aacgaacgac	gacccatgat					3860

(2) INFORMATION FOR SEQ ID NO:93

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

```

cctgatactc ttgctattca gtgccctcgg tgtgggtcgca acccgtattc acactttttc      60
ctccgcttgt ccaatgccgt tttgtatggg caggagcggg ctttctgggc cgtatgccac      120
gctatatcag ttatcggtt tttgtcttat cggccgtatc caaagcacat tgttgctctc      180
gatctgttgt ttcctctatt ggacgacaag gggcaactca ccgatttcga tttgtgggaa      240
agcctttttt cttggctttg ctcttcttcc tgttctgttt tgtcttttgg ctgtgaggat      300
gttttatgcc ttgtgggtgt atttctttgc cgatcgtgag actagatgat ctggagaggg      360
ggttatgcgt tgctcgaatg gatgtggggg atctcctttt tcccgttgcg gtcactctatc      420
tttatatgcc acaattatat tgctaagcta cttgttacca gctattttcg tgctgtggag      480
attagtgcct tcgctaaaac gatacgattc ttctcgatca gggaaagtagg ttttttccac      540
tttcttttga cctttgtgcc caccgaaatt taccgttggg ttacttgatg ccttatttga      600
gtgggtcgga aacaataaag agataatggc tctatggagt aaaagtaaaag aagataactca      660
tttcacagcc acaaccgcga gcgggtgggc gccttattac gatattgctc agaaacatgg      720
ctgtgagggt ggtgttcgtcc tttcatccaa gtagaagtcc cgtcagtgcg agagaatttc      780
gcaacaggaa agtgaatatt ctaagaccat tcggccatca tcttcactgg acctaccagc      840
tatcgacat ttttcagt                                     858

```

(2) INFORMATION FOR SEQ ID NO:94

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

```

cgggggattt ctttgtggag tcgccgatca tcttgctggc ggctattatt ggttcctgaa      60
gatatatgag aacggcagggt attgcacctt tccgcatgca tcgagtttct gaacagacct      120
tatgcgcaga tctttccgat tctgactctt acgatgagct ggccaactat ctttcaccct      180
ttatggacgc atgggaggcg gcgcacagga tcaacttcag ggacagatcg cttcggccaa      240
agaatccgct ttcgaggatg atttctccgg cactttactg ggtaatgacg ggcgtgactt      300
ctcgctcgac atcaataacc cgaaagaacc gaaaatcctg gtgtgggcaa caatcccagc      360
cgacaaaata tctattcggc ggcactcggg tttacaacag ccggatcgtg aaactgatca      420
ataaaaagaa gcagctcaaa actcgggtgat tatcgatgag ttgcccacca tctacttcg      480
agggtggat acctgattgc tacggctcgt tccaataaag tggcaagtct gtctgggctt      540
caggatttca gtcagcttac ccgcgattac ggagacaagg agagcaagtg attcagaaca      600
cggtgggaaa tgttttcagc ggtcaagtgc taggtgaacg gccagacgt tatcggaacg      660
ct

```

(2) INFORMATION FOR SEQ ID NO:95

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

catcggccat	cacacgagtg	atgagcaaag	gagcgggtacc	gctggtgcga	acttgaagct	60
atgccctacc	gatccttttt	cttcggaat	caggccaagt	taaaggactg	ctcctcgacc	120
tgtatttccg	gactctcctg	agctgtcgca	acagaggagt	caataggaaa	aggaagaaga	180
gcagccctcg	aaatgtctga	cgatcatacg	ccttgtacta	cttgacagagc	tatgctatgt	240
attctcaacc	cctttgatgc	gtagcgtaaa	ggtaccatcc	ttaccattgc	tgtaacggct	300
atggtcttta	cgaactgacc	cgagcgccg	gcaggattat	atggacgtct	attttgcttg	360
tctgaccccg	agcgatgggc	tctttgctaa	acggg			395

(2) INFORMATION FOR SEQ ID NO:96

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2346 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

ggtaaattatt	atttgataat	ccggaagaag	ttcggcaaga	aaattattca	ttcttcatcc	60
agattttcca	gcagaagccg	aatccagctg	aatcagttgt	cgtcgatgaa	gagcaattcc	120
tcgataatcg	tgaaatcctc	ctgtgtcgag	ccaccgagaa	ggggcgtaga	aattgggtctt	180
tgtegaagaa	tcgggcgcac	gcagcctttt	gactgcagca	cgaagctcct	gcctcattgc	240
ggacgaatct	ccgttcgtcc	ctcttggatc	caatcgtata	tgaccacacg	atgagttcct	300
cgtctttgtc	gttgaatagc	tgtacttccc	ccgcagcccg	atcatttgga	cgaaaagatc	360
actgatggct	atcgggtgcc	ttttggagct	gtgggggtgt	cgatcgggtg	gcggaacagg	420
cgttcgagct	gaatctgtac	tcgttgggtt	tcattgttgg	ctaaagagat	tgtgtatggg	480
gtttatttgg	cgattgcaac	tgattcagac	tgtctcgaa	tggtggcgatt	cgcgcttcgc	540
atcgcttttc	ttcttttgc	ccagttctat	gacagcttgc	ggagccttgc	cacaaagctt	600
tcgttgccga	gcttcttcat	gaccgaagcg	aggaattctc	ctgataggcc	agttcgtcgg	660
acaacttctt	gatctcctct	cccacgcgat	caatgcgccc	atcgggatgg	cgtattccag	720
tgtaccgatc	aggaagaggt	agagccgctt	gtcttttctt	ccactcgggt	gatggcttca	780
aggtgcccac	tttgatgatg	acggcatcga	aagaggcatc	gtgttcgttt	cctcttcgag	840
cgctcagctt	tccttgaaag	gaatgttctt	gcccgtcgcg	atttgcgaat	ggcggctatg	900
atctcccgtg	tcaggtcgaa	ggcttgcagg	agtcctgtgc	cgtctcatgc	gcatcgggca	960
ggaggcgagag	catgatggtc	cgccatcggt	acgcggttcg	agtgcagccc	atagctcttc	1020
tgtgataaag	gcatagaagg	atggagcaaa	cgcagcagct	gatcgaagaa	tccgatcgac	1080

tgccgtaggt	cttcgcatecc	atcggttgac	cgtatgccgg	cttcacctct	ccagatacca	1140
ggaggagaag	tcgtcccaga	acagcttgta	aaccagggtca	gtgcctcgt	cagacgggtac	1200
ttggagaaga	gatcggtccaa	ctccgcttca	cctcatcgag	acgatacccg	aaccattttca	1260
cggccagagc	cgagcttcgg	gctgcgtgga	cgtttctgcc	tgctgccatc	cttttacgag	1320
gcgaaggcat	tccatatctt	attgcagaag	ttacgtccct	gctccgagag	cgttcgtcga	1380
agagcacatc	gttgccggcc	ggagcggcca	tcatacgtcc	ctgcgtactc	cgtcggcacc	1440
gtattttctcc	atcagcatga	tcggatccgg	gagttgccga	ggctcttgga	catctttcta	1500
ccctgaccat	cgcgcacgaa	cgggtcagat	atacgttgtc	gaagggtttc	ttgccacgggt	1560
attcatagct	gccatgatca	tacgggctac	ccagaagaag	agaatgtccg	gagccgtacg	1620
aggtcgctcg	tgggatagta	gtagtccagc	tcttcgttct	cggatcatc	acatcgccga	1680
atacgcttat	cggccatagc	catgaggaga	accactatcc	agcgagtccg	tgctctgtcg	1740
cagatcctct	actgtgagcg	agtcgatccc	gtttgcttac	gtgccagttc	cacggctttt	1800
tcggccgtct	ccgcactacg	atacttccgt	cgggcaggta	gtaggcaggg	atacgatgcc	1860
ccaccagagt	tgctcgctga	tgcaccagtc	cttcacgttc	tccatccagt	gcggtagggtg	1920
ttcttgaatt	tggccggatg	cagtttgatc	tcgtcgttca	tacggcatcg	agagccggtt	1980
tgccacagct	ttccatctgc	aggaaccacg	catcgagagc	ttcggttcga	tgggtacatc	2040
ggtacgctcg	gagtagccac	cttgtttacg	tagttctcca	ctcgtctccat	cagaccggca	2100
tcgatcaatc	ctgttcgatc	ttcttacgca	catcgaatcg	gtccataccg	gcgtacggcc	2160
gccatgttcg	ttgagaatgc	cgttgctcgtg	gaatatgtct	atgcttcgag	ccggtgtttc	2220
tgcccagaca	tatagtcatt	gacatcgtgt	gcggtgttac	tttcagacat	cccgtaccga	2280
actccatata	cacatatctg	tctcgatgat	gggtactgca	cgcctacgg	tgggcactat	2340
cacccg						2346

(2) INFORMATION FOR SEQ ID NO:97

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic).

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

cccgtgcttg	tctctctctt	gctgctatcc	aaatagagga	tggccgaatg	acgaagccga	60
acagactctt	tcgcgactga	agaatcgccc	gcaatttggg	atgaagccga	tgcttatatc	120
gcggaaatcc	aactgttgcg	aggcgacacc	gcgaagcggc	cgaaatagcc	gacagactct	180
tgctcgcgaa	ttcgccatga	gacagcgacc	tcaactcctg	cgtgtggcag	gcaatgctta	240
ctacctttgg	gcgattcgaa	caaaaaccatc	gactatcttt	ccgactacag	cgaaagggtg	300
gggatcgat	cgcgcctgcc	gatgcttatg	cacttggtgt	cactactata	agcaagggtc	360
gatgaaagaa	gcacttcggc	cacttgccgc	tgtaccactg	acgccggttc	tctcggtgca	420
gagtcggctc	tctatctcgg	aaggcacagc	tggccgaggg	gatgacgagc	gaggccctta	480
tggctttcga	aaggctgcga	ctcaggacgt	caatcggccg	gtacgggagg	tcggaatgtc	540
aatatggcta	tgctcatgcg	tagtacggga	cagtcgagct	tcggtcagcc	gtacgcattg	600
cggagaactt	cctcaatgag	tttccccgat	cttcccacgc	gaacagatgg	ctgctattct	660
cgtcgaatca	tatttcaccg	gcaaggtttac	aattcttccc	ttagatcgat	ccaaaagatt	720
gcacagccga	cggctccatt	ctggccgcca	aacagtttgt	gctgaaccgt	atggcagaac	780
aaaagaagca	gcgggctatg	acagtgaagc	actttctttt	gtgtcgagca	gtaatctatg	840
ggaaacaaag	gggaatatatt	ccctgaagca	tatttctctc	gagcaatctg	cggtatagag	900
ccggtgactt	tccgactgca	gctgcggatt	aagagcctat	atctcggccg	ccggtgatcg	960
tgatggcgcg	aatcttccct	aggatattat	cgtctgggct	attctctatt	caatgccgaa	1020
cgttacgatt	ggctttggag	gccttccaag	antatgtatc	ccnatccggt	att	1073

(2) INFORMATION FOR SEQ ID NO:98

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

```

ccccgtgatt atgatgaatt gcttggttct tccgttggtat cggacaggag gagaggacca      60
ttggattctg ccgatagcga cgacaagatt agaaaaattg ctgacatatt ctattcaaaa      120
gtagtgcgcc gatcggttaag gtcgtccaac agctcagtaa cgtcgtccta acagatcggg      180
aaggctcgtc taacagttgg taacgtcgtc ctaacagctc agtaacgtcg ccctaacggc      240
tcagtaggtc gtcctattcc gatgtgaggg tcatcccttc tgcttatatg gggttttgtg      300
cttgtaggaa gacatgccgg aggtcgtttac cttatcattc gaaaggctcc gtaattttcg      360
agagaggata tgccggagag atctccccgt acgactcgga agcattgata ttcaccgatg      420
ccgtgccact gacggatact tggtagcttg ggtaatgaaa tcggatgcat cacaaccaac      480
agctccgctg atgagagcgt gaactcctcg ccggagcctt tcagtttgat accggaagcc      540
ccgaagcgtt tatatccaat gctctgagac ggccggtgag gtttacagag aagcttcccc      600
acagg

```

(2) INFORMATION FOR SEQ ID NO:99

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

```

cgcaatcgga gtgttttttg ctcgtaagaa caaaagcaac agcttcgcga tattgattcg      60
atggatcaac atcgaaactc catggcttca tgcgggggat agcctccatc tgaaaaaatt      120
gaaactcgcc ctatatcgaa tacagattat aattgctaaa cgacaaaaat tgcctctcct      180
tttgaccgat gcctgccctt actgtttggc tattatcgag agaccttgca aaaggctcat      240
gccacgaaga ggggaaatat gaaactactt gtgatttacg gatttgact atcttgcgga      300
cgcttaattc ggaatcaaat actactataa taaagaatca agacaatgga ctctaaaatc      360
caggaactaa ccgacaaaat ttatcgcgaa gggtcgaaaa aggcaacgag caggccgcga      420
aaattatcgc tgaggctgag gcaaaagcgc agagacgata aataatgcca aggctgaagc      480
tgaacgcatt tgagcgatgc aaagaagaag gcgacagaat ttcagcagaa taccgaatcg      540
agttgaagct ttatgctggt cagatgctgg agtcgctcaa gaggaccatg tggatcaaat      600

```

ttccggagag	atcggtttcgg	ccaacgtaaa	agcggcacga	ccaaccccca	attcatgcaa	660
cagatgatgc	tcgatatggc	caagaatggg	cttcgggcga	gagcatcatt	atctctacac	720
aaaacgccac	tgcactcagt	cctattttcga	aagcaatgcc	aaggacttac	tcaacaataa	780
ggtgcgatca	aagaggtgaa	caaccaaccg	gtggccctata	ctatccagcc	caagatggct	840
catacaagat	agaattcggg	gaggaagagt	tcataaatct	ctcaagaggt	tcttgcgccc	900
caggctgggtg	gaaatgcttt	tctaagtcac	gccaaatatt	acgccactgt	agccggctctg	960
cccaacatca	ctgtggaaga	cggaaattgc	cgtttacgtc	cttgacgttt	ctgcaggagc	1020
ttaggcctac	ctgagtcgaa	cggatagcaa	gctcttcgat	ctcctgcttt	gggagcagag	1080
aatcagttcc	ttcttcgcta	tctggaggac	agcgaagagg	ccaaggcgag	gagtcccggc	1140
cgaactcttct	tctcttatga	tacgctggat	ggcatctagc	tgcctatcgg	gagaaacgtg	1200
tcatgccccg	tatggattcg	ttgccgagca	tttccgcact	tttttgtcgg	aaaagctgac	1260
tgagatgttt	cgcgggaaga	agaaggagac	gttggaacaa	tgctccctgtc	ggacactgaa	1320
gccaagaagg	aaaagcacgc	ctgccaatct	ccgacgaaga	tcgtctggcc	attactatta	1380
tgaatatgcc	atgaaatgcg	gcaacgactt	cctggaagaa	tggttgccct	gaatctgcat	1440
atcaagaaca	tcttgccgcg	gatcacgtgt	gcaagttggg	ctggaatccg	atcaattata	1500
ttgtcggtag	cggcgaaatg	aagacaaatt	gcgtacgtca	cgggctcgcg	acttcgactt	1560
gggcgaagac	tgccctatct	gtccacactc	ttttctgtcg	gtgaggagac	ggacattcca	1620
aacgcgaacg	tctgcttgat	gtgattcggt	gggagtgggt	cgaagatcgg	tattcaaccg	1680
cgtattcacc	gtagagcgtt	tgctctgcta	ttattggagc	tggcgatcat	cgagcggttg	1740
gtgaagttgg	acgaaaagac	gggaaggaga	ctttccgccc	catcgtcaag	actctcaaac	1800
acgagagcgc	agatcttttg	acgagttcag	aagaaatcaa	aagaaataaa	tcaagataat	1860
ggtacaaaag	gagttgttaa	ggggattgtg	tccaacctcg	tgaccgtgga	gtcgacgggc	1920
cggtttccca	aaatgaaatt	tgctacatcg	atgtcaatgg	accaagctga	tgagcgaggt	1980
gatcaaggtg	atcggcacaa	atgcttatgg	caggttttcg	aaagtactcg	cggtagtcac	2040
gtaggagatg	aggcagaggt	accggcagta	tgcttgaggt	aacgctcggc	cccggtagtc	2100
tttcgaaaac	tacgacgggc	tgcaacacga	cttggacaag	atggacggga	tcttcccaaa	2160
cgaggcgatt	atactccgcg	tctcgatgac	gacaagctgt	gggactcaag	cctttggcca	2220
atgtgaacga	caatgtgac	gcaggctcat	ggctggagag	gtgacggaaa	atttccaacc	2280
ggacaagatc	atggtacctt	tcgtttcgaa	ggcaattacc	aggtgaaaaa	tctggccaaa	2340
gccgggttcgt	acaagtgaac	catgtgatcg	ctgtggtaac	ggatcaggac	gggaaagacc	2400
aaatgtaacc	atggtgcaga	aatggccggg	gaaacgtgct	atcacttgct	tcgcgagaag	2460
ccgcgtcctt	tcaaactgct	cgaacggggt	atccgtatct	cgacactttc	aacccccatcg	2520
tagagggtgg	tacgggattt	atccccggcc	tttcggtagc	ggaaagacgg	tgctccagca	2580
tgctatctcg	aagcagggga	agccgatatc	gtgatcattg	cagcctgtgg	cgagcgtgca	2640
aacgagttgt	ggagatcttt	gcggaattcc	cccacctgaa	tgacccccac	acgggcgtaa	2700
attgatggaa	cgtaccatta	ttattgctaa	tacgtcgaat	atgctgtggc	ttcgcgtgag	2760
gcatccgtat	atacggccat	gacgatagcc	gagactatcg	ctccatgggc	cttcgcgtgc	2820
tgatgatggc	agactccact	tccgttgggc	acaggctctg	cgtgagatgt	ctaaccgtct	2880
ggaagagcct	ccggaccgga	tgctttcccg	atggacttgt	cagctatcgt	agccaacttc	2940
acgctcgtgc	aggatacgtt	tacctgaaca	acggttcggc	cggttcggta	cgttcacatcg	3000
tacggtatct	cccgcgggtg	gtaacctcaa	agagcctgga	cggaaaaacac	caagaaagtg	3060
gctcgtgctg	tctatgcttt	ggagcagatc	gtgccgaccg	caaacgttat	ctggctgtaa	3120
accccatcga	tagttatcga	agtacatcga	atatcccgaa	ttcgagagct	atatatcgaa	3180
ccacacagtg	cagactggac	tactaaggtg	aatgagctgg	aagatccgct	tgacacgggt	3240
aaagaat						3248

(2) INFORMATION FOR SEQ ID NO:100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2612 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

```

aggaccgcct gtcgccggat gcgaaaaacg aaggcaacac cgtttccagt ctccggcgga 60
aacggccttc atatatctcc atccgtaagc tccggccatt cccttacggg aacttcgagc 120
ggagtctcga aacagggtctc caattcctca aagaatccgg cccgggaata aaacggaata 180
tccccctcc tccgtttcgca tcacgattac ccgtatccgc ccgtttacat aaggcatcca 240
caaaagttag aatcgtacat aaaactcaga tctcccgtaa tcaaaagggt ggttcggaat 300
atacttcgga aaaccccatt gccgtggaag tggccccctc gatccgttgg ttccgcgatt 360
gctccattct cctcccgcat aatgcgcgtg ttgaataatt ggagataacg tacgggcgtg 420
gaattagccg catgcaaagc acatcatggg gaatatgcct taaaatcact tcgaaagcct 480
tgaggtcgct caccocgcct ccgccataaa ggtacgggtgc aggaggtccg ccttcggttt 540
atcttctgcc acgaaccggc ataggaaatt ccttcgggtg aaagggaccc ggtgccttgt 600
ctttcaaccg tccggcggaat tccttccaaa agcccgagct cccgtacata tatgatgggt 660
aagcgcacag aaagtgtccg gagccgaaac ctctcgtcta tcccccaatg ctccgcaggt 720
ttcgccctcc gtagaaagtt ttcaacatac gggaaatcaa cgagcctccg aaagaaataa 780
ggagtccgga taaagcgatt cgtcttctcc ggctgcagcc aataccgggt ctgcgtacat 840
atccccgtat ccgtacggat attggagaga ctctcggcaa acaaaccgta tggggaaatt 900
tgcatatata ctgcaatgcg gcggacacgt ctcgtcggga ggataaaaaa cggcgacgat 960
catcactctg ggagcttcca aaaccgcttt acgagcatat cccatacctc ttccggcaat 1020
tcttgccgtc cctcacgaac gttatcgccc gctcttttcc ggaatatccg gaggaagtcc 1080
gtatagcggg tcgcaaaacg acatattgat gtgtacgggt cctcgccggg catcagggca 1140
tggttcaaca cctcattcaa acggcgattg gcatacatgc cgaggcggaa gtatcgaatt 1200
ccgctctcaa gctgcaatac gacttacgaa accggccata gctccctcct gtccaatcgt 1260
ctgtccctcg tccgttcgat ccattcggcc ggacgggtcgg ccgttacccg gaccaaagga 1320
atccccgtga aaaagcctcg gcaacggcag gacataatt caacatggcc gtccggaagt 1380
acaaaccaat cctacggcct cacccgaggc caaagccaat cgagagcgaa aaaaaccggc 1440
gaacgctcat ccgcaatcac gtatttctcg aagcgggatt ccgggagaaa gaaaacagaa 1500
gaggagcatt tcgcgaaccg gcgacataac gagtttacgt atgcccttca tctcgaataa 1560
atccatcata cgcttacgcc tttcttatcc gaataatccg aatccatcat cttgcatatc 1620
atztatagtc cgccttatct ccgacggaat gtattccaag cacattaaaa gtagtagccg 1680
cttatccgag gtctcttccc attcgtcttc gaatacgaat ctccgtttat acctcctccc 1740
acataaaaggc ggaatgcccc gggaacaatt ccatcgagcg gatgttcaca tacaatctcg 1800
cagcatcctt accacaggcc ccaaataatc tccgtaaaat ttgcgttcac gcacctcgac 1860
ctccggatac acgcaaaagc ttccttacgg gggaatccgc cgagagccgg gtaggatgaa 1920
gcgccttgag caagctttct aagccgtctc cggtaaaagc gtaaaatccg tacacaaatg 1980
gcaaatattc ccggccataa aggtacgggc tccgacatct ccacgctgcg acagtgggtc 2040
tcaagcactt ccctgataag tccttgacca ctctctgctc tcttatctct ttttgtgtcc 2100
acgccttagc aactgcctt cgaaagatac ggtcttggtt ccggccaaag ccatcgcttt 2160
acacgtcctt tcgtataatc caacaggagt tccggactcg ctccccccat actccctttc 2220
ccggaataaa ataaaggaaa acgaaagcat ggggtaagcc ctccggagca actcccaata 2280
agaaaaaacg tcggagaatc cggatcgccc ctcttaaggg tcaagggtgcg ggataaaaacc 2340
accttttcca atccccggaa tctatccggc gcatgatttc ctcaaaagcc gtacgggtaag 2400
ctccttatcc atatctccg attccgggca aggcattgcg ataccggaga tacggcatcc 2460
ttcaaattcc gcaccgcctt atccgtcaaa tctccctcga ttcgaattcc cccggaatga 2520
agtaagcctc ttcttccgaa tcgaaagggc cgcaacaaaa cagggaacgg aaaaatccgc 2580
cgtcttacgc tctattctcc gctcagcgaa ac 2612

```

(2) INFORMATION FOR SEQ ID NO:101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

ctgaatgtgt	ataaaggaat	atatcattga	gccatttata	tctttcattt	ggagtagtaa	60
tggtcctatc	attacatgac	ggagcataaa	ttctttttgt	cttgtcttaa	tgtatcatta	120
gctacaaagc	gataccgtag	acttgaaaac	tatcagcgaa	ctgccaatat	tgtttgaacc	180
aagagtgggt	attatagtta	tagcctcatt	tagtaaaaac	cacatcattt	gatgaatttg	240
caggcaattc	ttgactttga	caactgggta	tataagactg	atactatatc	attattcgat	300
gtaacagatg	atgtccatca	tcctctctga	tgaacccttt	tattttctaa	gtattgcaac	360
aacattctca	tcataataca	ctggcggtaa	aactcattat	cattctgggt	cttataatca	420
tcaccctgtt	gtacagttat	gatgaaaaca	cacttgacat	ggcatcaata	taaagttgat	480
gattgntttt	gaatctgcat	agattgccaa	gtcaaaaata	tccataatgt	tggatttgta	540
attt						544

(2) INFORMATION FOR SEQ ID NO:102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

agaaaggctg	tccgacatat	gcctatcggc	agctctttcg	ctgtagttcg	aggcaagact	60
cgaacttcga	cctttgggtt	atgagcccaa	cgaagctaca	ttgctccact	cgcgatcaa	120
ttgtggcaca	aaggtaatcc	tttttgctaa	aaaccaaacc	gaaaaagcaa	tatagctcca	180
atttctaata	gtaaatcaac	acaaagagaa	aaacaaagac	cgattaagaa	gtacctctaa	240
ccggtaactc	aaaagtttat	ttctgtgttg	caatgaaata	caaacaattg	agtcgaggag	300
taaagataca	tgattgatcg	gctcttgaaa	cagggtaccc	cccttctttc	atcgctcaaa	360
ccattgaggt	tgaagagtac	cgtctccggc	agcgtatcgc	atttgaaagt	ttatactgta	420
tccttgacct	ctttcttctg	tatttgggac	tctcgacat	taattcgtag	ttgtttgata	480
accgagtgtg	caatcgtttg	gtttataagt	gtgttaacag	ttcaaatgta	attgtcctga	540
gccaaagtga	aggaa					555

(2) INFORMATION FOR SEQ ID NO:103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

ccccggaaac	caattggcat	gaacattgaa	aatcgacata	aaaatcgacc	ctgaatacag	60
cgttcatgga	gtatttcatt	ttcggatact	tcttcgatgc	tacgatcttg	ccatcggcag	120
gtgctacaac	ggcacggtcg	tcattggaaa	ggggctgtgt	ctcttaggac	aacgaaaaaa	180
gttgatcgta	agcagaagag	gaaaatggca	atgatcatta	ccaaatagga	tacaatagaa	240
gccccagaaa	ataaaacagg	cttaagcata	tccccgtgaa	gagggttgcc	atggtactaa	300
aagtcgggtg	ctctctttat	gaaccttcac	gtcgtttctca	tcaagttgaa	atgaatcctg	360
tgggattgca	cggaggaaga	gtatgccctt	ccccgtgttc	actaatacaa	aagtagcggt	420
ttttctcatc	ttcccagacc	gttgattatg	ctccgggccg	tgagaatgct	gaaaattctt	480
ttaagattac	gcatagcgcg	acagattggg	aaatggaaga	ttcgagatgc	aaaattcgat	540
ccccatgggt	ggaggttttt	gctatatattg	cgggccca	aagcaccccc	aagaggatgt	600
agttcttgaa	ggaagagttt	atctgcttga	tatagaaaat	atgacaaata	gtttacgact	660
aaatgacaac	gaatatgcac	acagcttcat	acatcattcc	ctttttcatc	aggccgattt	720
taccccatcc	gtgtcgatcat	accactgcac	tattcggact	aagcaagaat	atctctatga	780
cgaaaaagaa	gaataaggct	tccatagtct	cctcaaacat	ataaggcacc	cacgggatcc	840
tctag						845

(2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

cggacagctt	gcgatattgg	aaatgcgagt	catgatgaaa	ggggtgatcc	agaatcctat	60
agggtcgaat	tgggagaagt	agaaccgggt	cttttcctcc	gatcggactt	tctgtcgta	120
tcgaccgcaa	tcgtctttgg	gcttcgccc	taatggctat	tctgcttcaa	tctcatatcc	180
aggagagcag	ctcgatagac	cgtgctcccc	gtctatacgc	ctacggatag	cagtcgctac	240
cgcttcgga	cgaattgccg	gtcgtctcctg	tttgggctgt	tcgcagcagc	tttggaggga	300
ggatagctcg	acgtattgga	aaaatgtggt	tgtcgggtcga	gatataccct	gcatacagcat	360
gtaccttggc	atcgcgcat	ggcttgggga	caaagtatcg	gatcgggtgag	ccgttggcga	420
ttaggcaatg	agggattggt	ggggcttttg	tctattataa	ttatgcccga	tcatcttttg	480
ctggggcagt	tctgacggct	atttacgata	tggcttcggg	aatccggttg	gaagataaac	540
ccgncattat	atggtaccca	acgacgcaaa	agccggttga	cttcttgaag	caaactggac	600
tattcttctc	cgcaa					615

(2) INFORMATION FOR SEQ ID NO:105

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 614 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

ggatccccg	ccaaatgagc	tgtcgcaggc	agtacggagg	agtaagtcag	atattgaagt	60
ccgagatccc	ggcgtcgaac	aaagccatgt	gatacgaacg	gcatgcagtt	ccagatcaga	120
ctcgccacta	cccttggtta	tgaagaagt	ttggggatga	gattccctac	aagtttgctc	180
atthttgta	tgtcctgata	tgttgtagt	acttacactg	tttctgtctc	caaagatagg	240
attatccgtc	tatatccgat	gaaggtttat	agcacttttc	cccttgcgaa	tctgggaggg	300
aagtcctggt	tttctttatt	cgacatagtg	atgagccggt	ttgtcgatcc	ggcttttaggt	360
gagagggtt	ggatatgtat	tgaaagcact	gtctcccat	ggaagaatgt	catccgcatt	420
tcattaaaaa	tacgtgccaa	aaaagttttc	aacaacgaag	acgagtttgg	aatgattcta	480
aataagcgct	aaaaagaacc	ggattttgag	gtgaaaaaga	agagaaaaca	ggctccttgg	540
atctgaatct	gcttttccgg	agtttgatc	acgatttata	tataaatctt	tttgattgta	600
tataaaacga	tttc					614

(2) INFORMATION FOR SEQ ID NO:106

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3025 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

ctttatattc	ggagaaaagg	gaaggaaaaa	gcaacatccc	gccactgagc	agcggacggg	60
atgtgtattg	gaatgggtga	tggttagctt	tctgttttct	tgcaatagtt	atgcagcagt	120
tgtcaaggct	tcggatgata	gcgagcgctc	cactcttata	cctctttcct	gtagagcctc	180
tctcccgttc	tgaaagcttt	ctctatgata	aagccataac	cgacgatctt	agcacttgcc	240
tgttcgcaa	gtcgatgatt	ccttgggcag	cattgccata	agcgaggaag	tcgtgataaa	300
caaaatacga	tcgtcatccg	tcagaaagtc	gtggctgata	caacggtata	gtctcggctt	360
ttggtaaagg	aatgcactgt	cgtagtcagc	atthtatccat	cgtcttgggc	tgthttttct	420
tgacgaagac	aacgggcaga	tcatgatgta	acccaccatg	atggcggggg	ctatgccact	480
ggcttcgata	tgacgatctt	attgactccg	ctgtcggcaa	agagacgagc	aaattcttcg	540
ccacatggta	catcagcttc	gaatccatct	ggtgattgat	gaagctatga	ctttcaatat	600
accgccggga	tagcacttgc	catcttgcaa	gatcctcggt	tgagcaattc	cataagacaa	660
agattgggtt	ttctacttgt	ccgccgttct	atthtgccacg	gataagcata	ttagaaatta	720
tggcagcaag	accgcggtcg	taattcccga	agagaagata	cctctcagggt	caagagatat	780
gttggaaga	tgthccggcat	caactcgaca	cccaagccca	gtgacagact	gatgccaaaa	840
tcactgtagc	cctccggtct	atctcctgag	ctgcaatgat	gctataccgg	ctgcggctac	900
agthccgaac	atcagcagcg	tagctcctcc	tatacgggat	cgggcatcag	agaaaagatg	960
aggccgatac	ccgggaacaa	ccaagcacaa	tgagcatagc	cgcaatatag	tagccctctc	1020
gacgactggc	acacccgtga	gctggatcaa	cccgttgtht	tgggcgaaga	tagaattggg	1080
aacgaattga	acacgccggc	gaggagcgaa	ttgaagccat	cggccaaact	ccgcccgcata	1140

cacgcttcat	gtatttatca	ccctccaccg	gttcgccgaa	atcatcgaat	tggccgtaat	1200
atcccccggt	gcttcgatgg	ctgtataaga	tagatcaacc	ctatggcgat	aaaggaagac	1260
agattcaggc	taagccgtat	ttgaatggaa	cagggatatt	cagcagtgcg	atcttcgctg	1320
tctcataccg	gagagatcca	ctcgaccgag	gatgtaagcc	aaaacataac	cgcgagcaga	1380
ccgagtacga	tggagctcat	acgaatgtat	ttgtttttgc	tttattgaag	aagaggacgc	1440
ttaccaagac	gagagcagca	atgctgagat	ctgccagttg	ccgaaagtcc	cgctcgctcat	1500
cgccgcattg	cctcctccga	tgagataatc	cccactttga	tcagactcag	accgatcagc	1560
aagaccacat	tcccgaaacg	agaggcgtaa	tgatctgctt	gagataacgg	aaggtagcgt	1620
gacgatcatc	tctaccggag	ctgccgctat	cgtacaaccg	aatatagtgg	caggccgccc	1680
gccaggcccc	cgctgataat	cggggcgata	aaagaaaact	tgtgccctgc	acacatagca	1740
gcccggcacc	caaaggccct	actctctaca	ttggataaag	gtggataccc	ccgaagcgaa	1800
aagagccatg	gagcagggaa	agaagtagtc	tccagatcca	gatcgagtgc	tcttgcaatg	1860
atagtggggg	cgtaatgata	gccacaaaga	tggcaaggag	gtgttggaag	gagcaaagac	1920
agcatctttg	aaagaaggct	tgtcttcgat	ttttagatc	gatctacctg	tggggtagct	1980
tcattcgggtg	cgatggccat	aataaagtgc	tgtagtcggg	ataatcctta	ttcctcgttg	2040
ggagcaagaa	aggcacaaaa	taataatgaa	aatgcacctg	actacgctat	tgcaggaata	2100
attttcccg	tagcacagag	ctacatcatt	gggggggtac	cccaaaaaga	caacaactta	2160
aaggccgaag	agatagttga	gcttgacgcc	gagagtcagg	ttcgagatct	gccgtgaggg	2220
tcttgctgcc	ggttggttag	gagatcatgg	aagcatagta	tagccgtccc	tccaattcga	2280
aggtccccc	tctgccggca	tcgatccgaa	tccgggacct	ccgccaaccc	ccattcgaag	2340
cgctccgtgca	gacttgggca	tagcgctcgt	gctgcagttc	ggtgaagtcc	gagccttgct	2400
tacggttttc	tctgcaatga	tgaatccgaa	ccgaggcccc	aaattgagaa	agcatagaga	2460
cctctttgcc	ggattttaat	gtgtgtgagc	agaggtatct	cacacaatcg	aatgtgcgac	2520
gataggcatt	gtccggcttt	tcgtcaaatt	ctcctcccat	cctaagcgaa	tgtagctcgc	2580
ttcggcttga	aggcccattt	caaggtgccc	gtactctcct	catttacccg	tacaatgaga	2640
ccgctcaagg	agccaacaag	agcttttggt	ccacagcggg	attgaagagc	accttttggc	2700
cgaacgcct	ccggctaccc	cgacctgtac	acgtagcgac	tgctggacgt	ttgggctgtg	2760
gccgagttta	tcagacatag	gaaaacaaaa	agggtgatacc	tattctacga	atcatgttcc	2820
tctttggatg	agccggtatg	gaagggaag	tatggagcag	tgcatagcag	gagttatcga	2880
gatacgggca	ccgatccacc	cctccgctcg	agcgtagcgt	gacgaggaag	agattcagat	2940
gacaaaacca	ctatcgcccc	ttatctcgcg	gaattggaag	tccgtctgca	ccccgtagaa	3000
ggaagcatgg	agagttgttc	ctgag				3025

(2) INFORMATION FOR SEQ ID NO:107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

ctgggcaaaa	catgacgaaa	cgatgagcta	ccgtgccgta	ccaggtgtgt	gtacaccaat	60
cccaggtcgc	ccggtgtggg	agagacggaa	gaatcgctcg	caaagcagga	cgtgcctaca	120
ctgttcgctg	ccttcctatg	gccttctcgg	tcgatttgta	gcagaaaacg	aacaaggcaa	180
tggagagtgc	aaactatact	tgatgaagag	aaccgcttga	tcggagcaca	cctcattggc	240
aatccgcccc	cgaactcatc	gtaaccgctg	ccatggccat	cgagaccggc	atgaggatcg	300
acaaatcgaa	cgaatcatat	tccctcatcc	gactgtaggc	gaatcctaaa	agaaaactctc	360
gccggagggt	gatactcttt	ctgccctttt	ctaggaaatc	aaatctaaaa	agtcgctgca	420
gtcaacaaaa	actgcacgga	cttttctctc	cttaatatct	ttttctcaga	gtatttcggag	480
taccttcgaa	gacagcaccc	gaaaaacgag	acctttggaa	aataaggaga	tggaggaaaa	540
gacttaaa						548

(2) INFORMATION FOR SEQ ID NO:108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

gtaaaaaacac	agtatgacga	agcctgaacc	acagacatca	atatcttcaa	ataagaaatg	60
aaaaaagaca	gcgtaatttt	cgatctgac	gaaaaagaca	tcagcgccag	ctcaaaggca	120
tcgagctgat	cgcatcgga	aactttgaag	cgaacaagtt	atgcangcta	tgggtagctg	180
tatgaccaat	aagtatccga	aagttatccc	ggcaaacgct	attacgggtg	ttgtgaagtg	240
gtagacaaag	cgagcaaata	gccatcgacc	gtatcaaaca	actctacgga	gccgatgggc	300
caacgtacag	cctcactccg	gagcacaggc	caatatggcc	gttttctggc	ttgcctcgaa	360
gcaggcgata	cgttcatggg	actgaacctc	gacacggcgg	ccacctatcg	cacggctcac	420
tcgtcaatag	ctcgggtatc	cctaccgtcc	catcggtac	aattctgagcg	aagagacggg	480
aatgggtgat	acgaccacat	ggagaaaatg	gccatcgagc	acaaacccaa	gctgatcatg	540
gcggtggttc	ggcctattct	cgtgagtggt	actacaagcg	tatgcgtgga	tcgctgacaa	600
ggtgggtgcc	ttgttgatga	tcgatatggc	acacctcccg	gtctgatcgc	tgccggtctg	660
ctggagaacc	ccgtgaagta	tgctcaatcg	ttacttctac	gactcacaag	acactgcgtg	720
gcccccgtag	cggtacatcc	ttatgggcaa	ggacttcgac	aatccttggg	gcaagaaaac	780
cccgaaggcg	agatcaagaa	gatgagcgca	ctccttgact	ctgccgtatt	cccgtgtaca	840
ggtggtccgt	tcgacacgtt	atagct				866

(2) INFORMATION FOR SEQ ID NO:109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

ggcatatcca	tggtgatgaa	caaatatccc	cacgtacgtg	ccgccctttc	tggactgagg	60
agatcgctcg	tttggtctcg	cagcacaatg	atgccaaactc	ctctcgctgc	ctgcacgctt	120
catctcggac	gaacaggcca	aagctatttg	aaaatctatt	tggagacgcc	ttttgaaggg	180
ggacgccaca	aggcccaata	gacaaaattc	ccatccggaa	gtagtactta	acccaacaaa	240

aaaccagaaa taaagcaatg aatatcgata attcttccac aacgattcag ggaagaccat 300
cgtcgt 306

(2) INFORMATION FOR SEQ ID NO:110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

ctgaaatgga	ctatggcggt	tgggaaggac	ttcaaaggga	ggaggtaaag	tgcaattccc	60
tgaattatat	cggtaaatat	gaagaagacc	cctttcatat	tatccgaaaa	ggggagagaa	120
tccttttcgat	gtccaagaac	gagtcagaga	ttttgggaga	gagagattct	ttcactacca	180
agcagcggtca	atcaagtgtt	atagtgcac	ataaaacaac	aggtagaata	ttattgaata	240
atgttttagag	ggaaaggaat	cctcttttag	ggggagacag	atggataatg	cctcgttgca	300
aagatctctg	taaaactagg	aattgtagaa	gtcgagtatg	agataatcga	gtattttctct	360
cttaataaact	gatattttta	tggatattca	aagatagcga	agttcttcga	gcagttgcaa	420
aatcaagatt	ttgctcaatg	gaggattggt	tcggtaaata	tgacgttgaa	ttttctgatg	480
atacagctga	actttttctc	agtcagtgtg	tcagtgtgtg	ttgttcaata	acagactcac	540
aaagtcatgt	tgctcaaaac	atcagattcc	atactgtcaa	ttggtgggtt	caggctcata	600
atagggggaa	gattgaagc					619

(2) INFORMATION FOR SEQ ID NO:111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

ccccggcatc	gaccatccga	tagcgatagc	cgggagcaat	cagaatctcg	tcggaaaaat	60
cagcgtttcg	actccttgct	cgtccatcca	atcgagtata	tgcggtgggt	ctcactacga	120
gacaggcca	catcttcatt	ctcatagctt	cccactgatt	gacttttaag	gattcttgcg	180
atgtatgcga	agcggagaga	ggcttcttcc	ccagccaata	gagactttcg	agcgtccgta	240
cggagtgcgc	ccaacggcaa	cgatgctgcc	ttgccaatca	cgcagggtt	ccaggatgag	300

cgctcaatga	ctatcagttc	acggtgcatc	cggtgttcac	cgaagtctcg	cttttgacgg	360
gacggaaagt	gccggctccg	acatgcaggg	tacatcgaca	accggagtac	cctgtgctct	420
cagccgttcg	aactcctcct	cgtgaaatgc	aaccggccg	taggtgctgc	caccgaaccc	480
agatttttgg	atagacgggt	tgggtaggtt	tccaagtctt	cctcttcggt	atcccgatta	540
gatagggggg	aattag					556

(2) INFORMATION FOR SEQ ID NO:112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

cgggcagaat	gttcatgacg	gccagcatga	tggagagaag	tgccgtcatg	cccagaattg	60
aggccagttc	caagaggccg	ggaaaaggct	gcccaatgcc	cgaagccacc	tatctgtcct	120
gccccttctt	tggatgaagac	gtacttctgt	cgcttacgta	gctgcgcgatg	gtgccatac	180
cttgtgctat	tccggcggtg	tggcttcgaa	tagcgaatat	cggatatgat	cgatgggtata	240
gatggatcca	acgggtcggag	gtcactccg	ataagtccgc	cggatatctac	cggcgcgtta	300
tagtcagctc	ttcgcttgc	cggtctatgg	acagggctat	ggttcgcttg	catggctgcg	360
aatggctccg	atcacatcgc	ttgcatcagg	cacaacttgc	catttacggc	agtgatactg	420
tcgcccgttt	tcagctgaca	gcataagccg	tcccttgggg	catgacgcta	tcgatgacga	480
acggcacctg	atggacataa	agccgctgtt	ggctttgagc	acacgcttca	tcatatcgtc	540
ggaacatgta	cgat					554

(2) INFORMATION FOR SEQ ID NO:113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3038 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

gacgtgtaac	gttcgccgat	cgagccgtca	ttttacttcc	aaaacgggca	tgaggctttc	60
ataaatatca	gccggtgtct	tggcatagag	aaagacggat	atctgttctc	agtctcgtaa	120
tgattgccct	cggtcagggc	tgtctgatga	gcagattgtc	atcctccgtt	tgaagaatgt	180

agaggtaatt	gaagtaccct	gtttcatcat	gagggtaga	gtgtacatct	gctccgaagc	240
atcatgaaaa	gctcgcgttc	gctcatcggg	agaaaatcga	aagcctctcc	ggacaaagga	300
ccggcccccgg	caactttttca	ctctcgaaaag	agaagataac	ctctaatagt	ctccttcggt	360
agcactatta	gcaccatcgg	tagtacgaat	gaacgtctac	cgaaattgtt	ttgttcgaac	420
tgatagggta	atccgggtct	gttttgcgg	gatacaactc	catcacatag	tgcccgttgc	480
gcgagtaaga	cggtagaccc	ccataccatt	gtaactatcg	ctgagcatct	ctgccttccg	540
taaacattgg	ttgccggaaa	taaagctccg	gcatgctgat	catatacatg	gtattacctg	600
caatactcga	aggtccggag	agcgaacgca	tctcggatcg	cgcccgtttt	gtcccacgac	660
aagggtaaag	tcctccgagg	gggacagatc	cgtaagccct	tcagatctac	ctcaacattg	720
acttgctgat	gacgacgtgt	atatcttcat	aagtaacgga	cgtttgcaaa	cccttgaggg	780
aagcaacgga	actaccacac	gaaaggcgat	cgtaagaagc	gtttcgtccg	gatataaacg	840
tcgaatacgg	tcattgagata	attccccgag	agcttggggg	tgaattcgca	ttgggcaaaag	900
acagttcgtg	atgaacatag	ttgaccaaag	tgctctgcta	acggcaggcg	gatcgaattc	960
gttctccaga	aagccggaaa	agcttcagcc	ggagaaaccg	gactcgcctg	ccaatcgtga	1020
ccacagtgcg	cagtctgtat	cccagcgtca	tactctcatc	gcccataaga	tcaaaactat	1080
ccggagtcct	tccccactat	ttatatggta	gtagggatat	agcctcactg	ttctgtgcct	1140
gtaggagtaa	caagaagcga	ctgcactcgc	gaatcaaagc	tcgggtctgg	ccgacagacg	1200
gcaccgacca	taagaaggaa	agaaaagaaa	aaaatgagac	agacgaaaaag	aaaactgctt	1260
catactttat	aatgtaagtc	aaacaaagat	aaggttttcc	ccccttggtt	gggaagctcg	1320
gagctcaata	gcagattgat	gacctcgact	cccttgctgt	atttgaagca	ccttccttat	1380
aatagaaaaga	taccctgtgat	tgtaatttcc	aatagtaaga	gaacagagac	tacagaaaat	1440
tccccgaaga	ggccggcctc	ttcggcaggg	gctatcgcat	ttgaaagggt	gtactccgcc	1500
ttgggtctct	ccttctacat	taggatctct	aacacattaa	ttcgtgctta	ttccggacgg	1560
agcatcatag	gcttatatgtg	tgtaataact	tcaaattcga	ttgccctgat	gagaaaagact	1620
gcctgcatgc	ggatcggcat	gcagccgtaa	catacaaccg	tagtacattg	cgctcttacg	1680
gagtcgggtc	gtgtaagaga	atcgatgccg	ctacggcttc	cccggctctc	ttagtacgaa	1740
gccgccggcc	atcgaaaatca	tactgaagat	aaggccaagg	ccttgcgctcg	tcagggactg	1800
gcgcagatat	tgaagagggt	gttatagtgg	ttgtaggctt	taatacgaat	ggagccggac	1860
ggttgatttt	atattcggca	tcaaatccgc	ccacataggt	attctgtaga	taggattgtc	1920
ccgatagccc	acattcccg	tgataaggag	acggttattc	gcaaacgact	actcaggagc	1980
agttctatat	cgggtgctctg	aaaagagggt	tggtcgtctt	gatgctcggt	cctatctgca	2040
ctttgtcact	aaggcttcga	gcatattggt	gagctgctgc	gacagagtgg	tggtggccac	2100
tgccgtcagt	tgtctgtacc	gcttcccga	ttatagacat	tctccggcgt	ataaaaatttc	2160
ctaagacaag	aagataaacg	atctgcttcg	tcacgaatc	ttcgcgtgga	tgagactgcg	2220
aaccgcagcg	tccaattcgc	tgtcggaggt	gggtgcttga	tgtcgaagct	gacagcaggc	2280
tgcaacatgg	caccattgat	ctgagcaggc	aattcacccg	aatggtagtc	cgtctgacgt	2340
cgctcacgag	agttcgtcca	agtcggttcag	attggctgtc	agattgtatt	cgcccggttac	2400
atcagagtgg	cgtgcatcgg	attgccggca	aaattcacac	tactgccttc	ttgatgctga	2460
aacgtttttg	gacaatctgc	cggagggtga	aattataagg	cccgaacaac	gttccagccc	2520
tccgaataca	ttcagatccc	ccaatgtagg	taatcgatac	gcaaactctc	accggctgat	2580
ccgcgtaagc	catcgcgtc	tgccgatcca	gtatcaaatc	cacctctgca	tccgggtgtca	2640
cgcctaattc	atgaccaagt	ggaaatccgt	ctccggtatc	cctcccgtag	cagggtgaagt	2700
agagaaggac	gatccggcga	agtttcttgt	ctcgcctcgt	cacgctgctt	ttcggatcta	2760
cgaatcgcaa	gaaacgatac	tcttccgctg	tcgaggctgc	gtaaaagtca	gcacgatatg	2820
ggttcccttt	tcggaaatca	gatgacgtcg	catctcatcc	ctccgggcac	atcgcgcaaa	2880
tatgcagcac	cgacacataa	acccggccat	gtatattgng	gttggtcccgc	tccggcacgt	2940
ataagcaagt	atattacgag	cttcaactgac	tttcagatcc	actttgatgc	atcgaaagcg	3000
cgatgcgaga	tatgtgcatt	gagtcggccc	gtagtccc			3038

(2) INFORMATION FOR SEQ ID NO:114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

gcgctatagc	cgtcttttctc	caaagtcttt	acttgcgtaa	ccacacaaga	ccaacttcga	60
taacagtgc	tggcagattc	ttgcccctcg	cactgaatcg	gatgtcattc	cgattttctt	120
tcctaataaa	cctggcattt	cagttttatt	aaacgtttct	caaactttga	tttccacttc	180
cacaccgctg	gggagttcaa	tttcatcaga	gcatccacag	tcttggcagt	agagttgtaa	240
atatcatcaa	tctcttgtat	gaagagagtt	cgaactgctc	acggctcttc	ttgttacgaa	300
cgtagagcgg	ttcactgtga	aaatccgctt	atgctggggc	agagtatagg	accgctaacc	360
atcgaccgg	ctgctttcac	cgtctttacg	atttctcggc	agacttgctc	accagcatat	420
aatcgtaaga	cttcagctta	atctaattct	ttggctcata	tctatgttgt	tcttttattt	480
gatcaaataca	cgcgaccctg	agcttcggta	agcactgctc	tagcatgggt	agagggcact	540
ctgaatatgtg	agagaaggtc	atcgtactcg	tagcacgacc	gctcgttacg	tacggagagc	600
cgtcacatag	ccgaacatct	cagccagagg	caccttacct	ttacgatacg	tgctccggta	660
cggtgctttt	ccataccttc	cacctgccgc	gacgcttggt	caagtgcgcg	atcacatcac	720
ccatactctc	ttcggagtc	ccacttccag	tttcataata	ggct		764

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...529

ggcgaaagaa	acaccgcagg	acgataagga	agctttcttc	ttcaacgtac	ggttcgcgc	60
gtactctctg	tcttgggaac	tgcgaacccc	agtggtagt	accgggtatc	aacaacatcc	120
tcgaaggcgg	ctatgtaaag	gccgatgcac	taccgctatt	ccggtggata	gtatgatgca	180
gcgcggacgc	agagcgtcat	ggctcttgac	cgactacagc	aaggccaaac	aagccggcga	240
catggagctg	ccctacagca	caaatccggt	atagacgaga	atttccccta	tttcgctata	300
gctatatcca	gcacaagaac	gacatagttc	ccccggttgg	gctacctact	acagcttccg	360
tatcatggtg	ggactcggta	tgctgttcat	ccgttatcc	tcatggcatg	gctcctgagc	420
ttcaaaccgg	aaaaattcag	caaatgcgat	ggtccacat	gatcgtatc	gtatgtatgc	480
ctcttgcattg	gtagccagtc	agagtggctg	gatcgtaccc	gaaagtgga		529

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

gacttggagt	cggggcgaaa	gagcgaagag	gaattccgaa	ccgagctatc	cgatacatag	60
gaaaagaatt	gacctatcag	caggtgtacg	atgctctctt	ggttttcttg	aggagatttc	120
ggccgaaaag	ttcgattata	tcgactocta	cgccccgatt	atcgactctt	cctcctctcc	180
aacaccaatc	cttatgcctc	gatttggcca	tgagtcgcg	ttttcttccc	tcaggaagga	240
cgctgatagt	ttctttgata	aagtctatgc	cagttgtcag	atggggaaat	acaacccaat	300
gaagatattt	tcctcgaaat	gatagccgac	agcggtatga	agcggaggaa	accctcttca	360
tcgacgacgg	accggctaatt	gtggcaacag	ccaacgactc	ggtttccaca	cctattgccc	420
cgacaatggg	gaaaactgga	tcctgccatt	actcgactcc	ttcgcgaaaca	gaaataaaga	480
agggctgtac	gcgaatcggt	tcgctccgta	caagccccct	tttcgtatcg	aaagaacggt	540
gcttatttcg	taggctcttg	catcgtaga	tccacgttca	gcttattcga	tccagtcctg	600
accagttgcc	tgtaatagca	tcgatagcca	cgggaataga	ccaccgagta	catccaatac	660
caccacattg	gcttccacac	ggttgtgatt	atacgtaga	tgggctgttt	acccggaata	720
cgaaattcca	cgggtaggat	ttgtcagcct	tgagcgagag	ttgcaagggc	gtttgtccca	780
tctttcacca	ttgatgtaaa	cttctgctcc	ctgtgggttg	gaaaccattt	ccaagcatgc	840
gtctgtttgc	cgaaaag					857

(2) INFORMATION FOR SEQ ID NO:117

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

gtcagatttt	tttctttata	aaatccctga	cagatgttta	cgtattttata	atgatatgga	60
gaccgtggta	gcaaagatta	tttttggagt	aggtaaagtg	gtttcgtcta	tgtgcgggtc	120
aattccggac	agtggaagtt	gcattattct	atcgcgatta	tcaaggcagc	gtgacggata	180
ttaccgatgc	ctccggacgg	tggtacaccg	catgcgatac	agcccatggg	gaaaattact	240
gcataggatg	gtacacctta	taccggaagc	gaagagttat	ccaccgacta	tgacggcttc	300
tcttccttgg	acgggggttat	acagggcagc	agtatcttcc	ctgtttggat	tgggtcaatat	360
gaatgccccg	ccgtcca					377

(2) INFORMATION FOR SEQ ID NO:118

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 879 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

tacacancag	caccacgaag	tggcgaaatt	tccgcatatg	cagaaatatt	tttcgtatat	60
actccgataa	attttcgtat	atacgggaaa	taaatttcct	atatacgcaa	atatatttct	120
ctatatacac	aataaagaga	ggctcggata	ttgctctgga	actctatagg	agaatgaatc	180
cagagcaaag	ggctaactcg	cttggtgtaa	cctaagggga	aataccgatc	gacagttgta	240
accccgcata	ggactaaccg	gtatgtctgt	aaacatatat	gaatcccgcg	cacccaactg	300
tcaacttttt	tcagtacaca	acagtttgcg	agaatatccc	tactttacac	gtaaagaaaa	360
tagaaagcaa	attttgatga	ctacgtccct	ttcaacaacg	atgacctgaa	ccaactggaa	420
tctaaaggca	tcacaccgga	aaagcaatgc	gccaggtaga	agctctcaga	tatggattcc	480
cgtatcccaa	atcattgcac	ctgcttcatt	agagaatgga	atcatgctgt	tggatgaagt	540
gacaaatccg	cttatctgtt	ggaatgggac	agatatattga	atagtccgac	tgcaacggtg	600
tcaagtttgt	accggcatcc	ggtgctgctt	cgcgcatctc	aaggatttgt	acaacttcct	660
tgatgccgat	tcaatgagcc	aactacgatg	cagagaaggc	gttctttgca	caccttactc	720
gatttgcatt	ctatgctccc	ttaacgagac	atgcctgcgc	aatgcttggc	gcacagtgcc	780
caaatcatag	ctttcaaaga	atacaagacc	gtggtggaga	atctgctcta	tccaaaggtc	840
ttaactatgg	caatcttccg	aaaggttgct	tctctttca			879

(2) INFORMATION FOR SEQ ID NO:119

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2464 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

ctatctgcat	tgtataggtg	nataccgcag	tatgattgca	tccagcatct	actctcgoga	60
ggctatcgta	atttcacgga	catcgaaggc	ggattcgcag	cattgcgcag	accggtgttc	120
ccaaaacgga	ctatgtatgt	caaagcaagt	gtcaaaaaaa	taatatcggt	ttccttaacc	180
atcattatcg	caattgcatg	ttaggattac	tgaaaaaatct	attctcgcag	tctgacgata	240
aggcttgagt	gaggctattc	gcaacggcgc	ctttctggtc	gatgtgcgta	cgccgggtgaa	300
tttgcatacg	gcagtgtagc	cggagccgtg	aatatccgcg	tgccgggata	gcatactcgc	360
tgaatgaact	caagaataag	aagaccatca	tctcttctgt	cgcagcggca	acagaagcag	420
ccaggccaag	agcattctcg	acgcaacggc	ttctccaacg	tactcgatgg	aggcacctgg	480
gggcatgtag	ctctctgaaa	ggcgatcagt	gataacgaag	tctgagaaag	acttcgacct	540
tacaactctt	tctctattaa	gaaggattgg	tttttgaatt	tttgtcttcc	gaagacaaga	600
atatcatcat	aaaaccaatc	cttttttaca	tcatataatg	aatcctattc	tcttttactc	660
tgctgtctat	agcatgcaaa	aggtctaaaa	tccgatatta	ccgctttcta	taccctataa	720
atcacatcca	aagcaggcaa	ttgcatttga	aatataggtc	tgatgatggt	ccgtccggaa	780
taaaacgaat	taatgtgtta	gagatcctaa	ttgtagaagg	aagagaccaa	ggaacggagt	840
acaacctttc	aaatacgata	gccccctgcc	gaagggggccg	gttcttcggg	gaattttctg	900

tagtctgtgt	tgctcttact	attggaaatt	aaatcatggg	tgcctttcta	ttataagaaa	960
tgagtcctga	tcttcccaaa	aagggggaaa	aatgaatttt	gaagacgcaa	aacagggaaa	1020
acttccaagt	tattttcatt	tcaccttaat	tggccataat	gtactggtaa	ttagcatgtg	1080
taacgagcac	cgtacgccta	cgccgggtctc	ctgcaccgtg	caggagacat	cgtacgccta	1140
cgatcgtaa	tggtttcgtac	cggtttttca	acacttttcg	tattcctctg	cataatcttc	1200
aatctcgtac	cagaggtatc	acctggagcg	tagagaggaa	aacgatcagg	aataaaaaagt	1260
caagaggata	aactctttgc	tctctatccg	tgggtccgag	accatgaaga	gattttccga	1320
taggactgaa	tacatgactg	acggctcatt	caacgactat	aaaatttata	gacgctgttt	1380
tgaatgcctc	tgccctgaca	tccaaagtga	tgtccttttc	ggatcagcct	tttcctaatt	1440
tcttttcgat	ttttttctc	cgggatgtaa	agacatggat	tgcatcaatg	ggcacgaaca	1500
tgtcgagtag	atcgaatggg	ccgaattctc	tcgtttttcc	gatatgtatt	tggatttgct	1560
ttgctattga	cagtctaaga	cccttttttag	gcttttttgc	cgaaaaaatt	acggagaaat	1620
atgctacttt	tgtggcattg	tacaaacaaa	agattaccaa	ataatgatat	gatcaacaga	1680
cgcatacgcg	tacgtttcgc	tccgagtcct	accggccgtt	gcatatagga	ggggtagcgt	1740
cggtctctata	caactatctt	ttcgccgtca	gcatggaggt	gatatgatcc	tgcgcatcga	1800
ggatacggac	agcacagatt	tgtgccgggt	gccgaagcgt	atataataga	ggcattggaa	1860
tgctcggcat	caaattcgat	gaaggtgtag	gctatggtag	ccgatttggc	cttacaggca	1920
gagcgaaaag	cgcgatattt	atcgcacata	tgttcgccaa	tactggattc	gggacgggca	1980
tatatcgccct	tcgatacgcc	ggaggaactg	aagctcggcg	agccgaggtg	cccaacttcc	2040
aatacgaatg	cactactctg	ggcaaatgcg	caactctctg	acactgcctg	ccgaagaagt	2100
ggagcggttc	ttgccgaggg	gacgcagtat	gtgggttcgtt	tcctcgtgga	gccgaattgg	2160
acgtagaagt	gaacgacctg	attcgcgagc	gagtggtgat	caactttcca	tcctcgatga	2220
caaggtgctg	tataaaaagt	ccgacgactt	gccccctacc	atctgggtca	atattcgtgg	2280
acgaccattc	tgatggaaa	tgaccatgtg	atacgtgggtg	aaggagtggg	tgcccaagtg	2340
caccactttc	atgtactgct	ctaactcgtg	ttttcgggtg	ggaagatacg	aatgccgaga	2400
ttgcccat	ggcactggct	gcttgaagcc	cgaaggaaac	cggttaagctg	agccaaacgc	2460
gatg						2464

(2) INFORMATION FOR SEQ ID NO:120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs:
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

ggcgacagaag	gctctgccgc	atgtgtccac	cggagcggat	gcccttgtag	gcggaagtg	60
ctggtgacgg	aaaccataga	tccgacgacg	gacaaaggcg	cgtggctgtg	gatggagatg	120
tttgacggc	tcgctctctg	acaggggggt	gatagaaaag	ggtatgcgtg	tggaaatcgt	180
atcttacgaa	agcatttcct	gaatgtagt	gttcttggtg	acgacaaaca	ataataatcc	240
aacaaaaaac	ttatttcatt	atgacagcaa	caggatttat	tccttgcggct	ctgacattct	300
tgtgatagcc	attattgcca	atggcttgaa	gatcgtgcag	cagccgagac	catgatcatc	360
gaacgacttg	gcaagtatta	tcgtacgctc	agtcgggagt	caagtatcat	catccccctt	420
atcgacaaac	cccgtcccat	agcaagcgca	tcgcttatac	actacccttc	ggaca	475

(2) INFORMATION FOR SEQ ID NO:121

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

tatgaccaat	gctataagat	actgtcttct	attcataatg	ttgctgatag	attcaatcaa	60
tggttacatg	ctcagcctcc	acttcctcct	taaggaaaagg	gatgcccaatt	ctccaaatth	120
gtccggactc	tccgtggtgt	agtaggagtt	ttgccaccct	tctcaatgcg	tctgtccatt	180
tgggggtggc	gactgaatag	tctttcaaag	aatgcgccac	aagttcaccc	tgtgctatga	240
gcttgtagta	ggcgtaaagca	aacgcttcat	cttaggacgc	aatagaggat	aatgggtgcac	300
gccaatataa	tcgtatcgat	ggtatcatcc	ttggcaatga	tacgtccaga	tgcttgcgaa	360
tgaatatgtc	agcccccggg	ctgtcaactt	cgccgtttcc	acgagtggta	cccacatcgg	420
acacgcctct	tcggtgactg	aatttcgggg	aacaattttg	cgatttcgag	ctggtagcta	480
tgcgaaactaa	tgtacctgtg	gtggccaaaa	cacctacgtg	cttagtcctt	gtgatctcac	540
tacggcttca	accgtagggc	ggatgatacc	gaggacacga	cgggtgggtc	ctccatattg	600
ggcagatcgc	gttgctgaat	ggttcgcaag	gcttttgca	tgccgtatta	caagcgagaa	660
tgactagcgg	acaaccgagt	tcaaaggctt	tctcacagcc	tgtagcgtga	atttgtaaac	720
tacttcataa	gagcgttgcc	atagggagag	cgggcattat	cgcccaagta	aacaaagttg	780
tactcggcat	gagtttgccg	atctcactca	agatggtaag	tcctccataa	ccgagtcgaa	840
tatgccgatg	gatgggttca	tggttgatgct	tttatcggag	gtaagggtacc	aataattggg	900
ccgccagtat	attccgcctc	attatttttt	acagaaacga	ccagcataac	gatgccccca	960
taggggtgtt	ggtgctcgaa	caagtctcaa	gctcatataa	gcccgcataa	acctgagcac	1020
aaagaatagt	cccccatgcg	tgaagatagc	tatatgcccg	aacggcatcg	cagtcaccct	1080
tccagaaaaa	tgcttacgcg	ttccagctgc	atgacgaaac	tctcgcccc	gttgccaggtg	1140
ttcgtagata	atccgcgtaa	taatcttgca	agcgagatcg	tctatatggg	catatcgctg	1200
catctccac	aaaccgaaat	taatcccatc	agtcgtccgt	cttgtagtgg	atcaggataa	1260
ccgcaaaaaa	gagcaaacgg	gcacaacggc	tgagcggact	cgtatagaca	gcacggaagt	1320
ccaccccgat	agccggcggc	gtacgacctc	ggcctcttct	tcaaagggaag	ccgtaggggt	1380
acatcggatt	gcccgtagca	tattccggca	gggacatccg	ggtcgtgtgg	cggatgagag	1440
taatctgcat	cttacaattc	tatgatccta	tcataataag	cattcctacc	caaaaagaca	1500
gctcacagag	aagaaaagtg	ctccgcagca	atcgccgtga	taaccgccta	tcttcgctt	1560
cataagacgc	gcagcaagag	gaaagccaaa	atggggatca	agactgccgg	ccaataagga	1620
gtggaaggaa	gagggccaag	ggtaaagctc	cggcagagaa	tgagaccaa	aagtcaagac	1680
acccatcgga	ctgtatatgg	cttgacactt	actctatcct	cggaaacggg	gtaggggaag	1740
gtattgatga	gctgggaggc	caccatttgc	acagaggatc	gcccacacct	aatgcgacaa	1800
gcgtcaggat	cgggggagag	aagacagaga	atagatccct	atcatgaagt	aaaagatgaa	1860
ggcagaatac	cataagtacc	cgtatgcgaa	tctttcatga	tagccaagat	ggctccttgg	1920
ttcgccctgc	accgaatcca	tcgaagaagt	caccatcc	tcctcatgga	aagccccctgt	1980
aaagagaacg	cgagagagga	gtgcaaggga	acgacctag	tgacaggaag	gtcgatcagt	2040
agtcccaagt	ggcagattga	accatcagtc	ctcccgtgaa	ccaacccacc	agactccaat	2100
aatcgggtgc	cgcttgaaag	cagcatcagg	gacactcacc	aaacgccaca	gcggtagcgt	2160
gtgagcagca	taaatgctgc	caatatctgc	tgatatggtt	ttgccgcttt	tccttcattga	2220
acttttagaa	atacttagtc	acagccgctt	gagcaaaagta	tgcatctcgt	tgatcatgct	2280
gacggccgat	actatgatgg	gggttgagca	acgcgtccgg	aaccttctcc	caagcgaagc	2340
cccagattca	gagagggttg	gccttcatat	actccagcag	gcgtgcatgc	cccgatctgt	2400
cccgcagtga	ccgaatacgg	catagtcgca	gacttcggga	tagaactgcg	tgacgcaagg	2460
aggcaattgg	tcatgatgaa	tccatccacg	atgatcagct	ccccaaactct	gccgcctgaa	2520
gcattccccc	aacggccatt	agcatctcaa	tcctccaaaa	taagtgatga	cgtcctcggt	2580
cgatccggtg	cctttatggt	ttctttggcc	tggttgagaa	tggtataact	atgtctgact	2640
ccctccaat						2649

(2) INFORMATION FOR SEQ ID NO:122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

ggagtagtaa	ttcctgaaat	ccttgagctt	ttgcagaaag	tcgaacaggt	gctcttcaga	60
ttgtccaagg	agagcgcgtt	ggcttgcaat	tcttcctttc	tttttttggt	agttctttct	120
tcttgaggga	tttgtttccg	gaagattgct	ttcgaagagt	ttcttgccgt	atgcggctcc	180
ttccaaaaag	gagaaagctt	caggatcaaa	cttctcagcc	gagctttcct	ctccagatcg	240
ttgtcaggtt	tttccattgg	cccttgaaga	agagtatatc	ctcatcggtt	gttaatcggc	300
cttgctgtag	gagagctgcc	tgtcgatgtg	ggcgagggtg	ataaggcggt	gtgacgtgcc	360
agattgaaga	aagctgccca	gaaatgtttg	tctccagcgt	gtagtaggta	ccgttgtagc	420
gtttctcggt	ttgttctgtc	aattctaaaa	taagtgggtg	ggatcgataa	gcaggcctat	480
cgggtttcgt	atgcgcccca	atgcctgccc	gtt			513

(2) INFORMATION FOR SEQ ID NO:123

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

gagatcgttc	agattgcctg	tccccaagta	tttacgggtg	tactggacgt	gcctccttcc	60
acttgatcaa	cggatccgaa	ctggtaccgg	gatgcggata	aggaagcact	cccgcactca	120
tagcaatgga	tttggaata	ggaaaaacat	ggcgaaatac	tcaatgtttc	ccattttcct	180
attgtccttt	ttcccgcttc	ggcataccac	gtaattccgg	tagatgcacc	gaaatcgaag	240
ataaagtcac	cgaatccaca	gccgagtatg	aagcaggatt	gacggcattg	acgttggtgc	300
ctgacgcaga	ccgacgccga	gtcctcccat	ggaatgccca	ctatagtcgt	ccgttctccg	360
agacggccaa	ggccgaagcg	agtgtaaagg	gatcggtaaa	gttgttggtc	tgagcctgta	420
taccgtctgc	tgcaaatagc	acccaatgat	cagggcatac	caccgaagcg	acgcatacaa	480
acccttatag	ctttatacat	tatatcttaa	aattctattt	angccca		527

(2) INFORMATION FOR SEQ ID NO:124

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

tcgttcatct	tctcagaaga	aggaatatgg	atatgccaat	atcttatata	tggttacttt	60
gctaatagat	aatcagttgg	gggcgattat	tcgtaagtcc	agaattttga	agaactttct	120
gatttgatta	gtaaacaagg	attaattctc	gaaaattagc	atctttcgga	ccatatttca	180
taaatgctat	ggtaatctca	agcaaagtaa	ggttatcgct	atatcaggcg	atgttggtgca	240
attaatgatt	attcttttcc	tgatgagaat	ttgcgttcta	agcgattgga	gagattatca	300
atgataccaa	tgttttattg	gatatgtgta	gtaacttatc	ttcaaagaaa	tttataacaa	360
attgaatgta	caattatgaa	tctatatatt	gcagcataaa	agttgtgggt	caagggggtt	420
aaagaaaata	cagaaagatt	cataacctac	tcgttcgaac	caaataaaat	taat	474

(2) INFORMATION FOR SEQ ID NO:125

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1023 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

gggtttaccg	tggtctacgt	gggcaatgat	ggcaatgttc	ctnatgtcng	cattttcttc	60
ttctgagtaa	ttggggacaa	aggtagtaaa	acgggctggt	ttcggaatgg	atatccaagt	120
gttcggattc	tgcacattcc	atctgcagag	cgttgcattt	gcaggcaaaa	aaagacgccg	180
acgaaagtgc	tctcatggcg	tcaataggat	tccaagatat	ctcttgatag	agtttttcag	240
ctgacataac	cgtcttacag	gatgatgttc	ttagatgtct	gtgtattatc	agcaacaaaa	300
cagtgcagag	aatatggcct	ttcgtcttta	agtcgataca	aaatctctgc	cctgtgtctg	360
actcgtggca	aaaagcatcc	gtcctgccat	atataaatat	agaccgattt	gatcagtttt	420
tctgccttga	tgccgatggg	cttccttgga	tgtagacggt	tatatcgttc	gacgaaggta	480
caactgtttg	ctatctgtcg	tatggcatga	tttggcaacc	gtgctataga	agataatgga	540
tacttcagct	gataatcctg	cacaatgtct	ccctctaccc	tgacgcgctt	tggaggggat	600
aggagtcttc	ggctatcatt	acttctccgt	tttcaactctg	ataaagttgc	cttcgtctac	660
tttgattgcg	atctcgaagc	cgctgtgtct	tttacgcaaa	caatagtcgc	tgctacttcc	720
ggatacgtaa	attgcgcata	gggatctcgg	taaccactcc	ctcgaaagtt	cgattgggga	780
gagtatgcgt	gtgcacatca	gttcatagta	ggcatcgaat	tcattggaaac	gacttctgta	840
attagcatat	cgcccaactt	ggcgtatgga	cagaactccc	ttacccccca	taataagctg	900
taggataata	ataacctttt	ccctgataac	taatggtgct	ctaaaggcta	tcggttgtca	960

aaggcattca gttgtgcatc cagaccatcc ccagccgagt gataatcgac cgggactgtg 1020
tcg 1023

(2) INFORMATION FOR SEQ ID NO:126

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

```

ggcgcatcttc ctccttcacg gtttcatcaa tatccaatgc ttcgataaac ttgcaatgga      60
ttcggctgtc accgtctcat tcgtacgcgt cagagcctca acgtttcgta tggattggga      120
tacccttctc tacgaagaat agtttggttag cctcagccac cacagcatag ttgttctgca      180
aatcccgatc gagagcgctt cgttgagaag cagtttgcca agccctttgg ctatgctcgt      240
gactgtatga gagaatgcgc caaaggagtt ccacgttacg aagtacagtg gaatcgtcag      300
atctcgctgc aagcgggaaa taggcaattt gcgcgacaaa tgccaaatat ggcattcgca      360
atacccgatc tgccttcgga attttcatag gtgatcggat tcactttatg tggcatggca      420
gaagaaccga cctcgccgcc tgat                                     444

```

(2) INFORMATION FOR SEQ ID NO:127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

```

ggctgctgtt ctgccagcac ttcgctcagt gtctgatata gcctttggta aagagcagcg      60
caaagtcttg caaggcattc agagcgaatc cgatttgcac aagcctctaa aagaaatttc      120
gcccgtacgc tcgaatctgc gataggtggc aacttcattc ctgcccgtaa agcgattccc      180
tcttgtgtca gattcactcc aaccgtcggg cctttactcg ggaagcaacc tgcatagcta      240
cggacgcgga ttgcagtcta taagtgtcaa aatattatcc atacatatca aaaaatctct      300
ttatttatatt atgttatcac tttcgaagat aataaaaaccg ttcaaaaaca caatcaaattg      360
gactgaacca ccaaacgact agaattctgt ttttaatttat cgttaagagat tgtccagtgc      420
tttttcaagg gtgacatact taaacgatag cccgaagaga tgattttttc ggccgatacc      480

```

ctacttcctt cagtagaatg gaagcccgt cgccgaatac gcgacaaata acccatttgg
tatggaggga aag

540
553

(2) INFORMATION FOR SEQ ID NO:128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

gcacatttcc	gctgaagcta	agattgttag	ttgcataata	ggaaagcgat	ggcttacacc	60
ctgattttcc	tgtgcacgaa	aagttttcct	atacgtttct	ccaagaccgg	ttcgccggat	120
ccttttttct	tttttatttc	gaacggatat	tctgccagcc	atccgtatgg	tagaagaaat	180
agttggtatt	gctactaact	taccgatgtt	tatatcgagc	gaagtattgg	tttgccgatc	240
gttgctctcg	atatgcgatg	tgacgtatat	gcactcagtc	gattcgtatt	ctttttgtga	300
tcacattgat	taccccgggc	atggcatcgg	atccgtagag	cgactcgaag	cacctttcac	360
cagttcgatc	cgttcgatct	gatcaggaga	aaacgactca	aatcggcctg	accgcctaca	420
tcgccgtaca	cacgcttacc	acgataagga	tgaggatata	cttactgcta	aggccgttca	480
gctgcatgaa	gagccccatca	gattggggcc	gaagtcaaaa	gacggactca	gcccctgcat	540
aaggccctcg	aagtaggagc	cgagaaagag	gctatgtcct	tagcggtagg	acttccgttg	600
ccacaggagc	atcgaccaag	cggtaacgtg	taccggtccg	gtaacgacga	cttcctccaa	660
gttggttcgtt	cgcagtcgca	atgcaaagag	atcgtttttg	tctgtccggc	ttcgatggca	720
accacctcct	ctttcgtcca	taccccccca	acgaacatat	aatagtatgc	tgccctgccg	780
gcagttcttg	atctcgaaat	gtccgcccgc	atcggcaccg	gctactatgt	tgggtgtttg	840
acttcgattc	gagcaccggc	aagaggctct	ccggtttcgg	caccgacaca	ctaccggtta	900
aaacggcctt	gctctgagcc	gacagagaag	agacaataga	gcaataaaaag	agataatcgc	960
aaaaaagata	gtttttgtcc	cataatcggt	actaaaaaat	gtcacataag	agcgggacaa	1020
ggatgctgca	agaaagagat	catcggaacg	aaccgatgga	tcttgaaaac	cgccgaaaat	1080
gatacattga	cctgtttgcc	taatcaaata	tgcaaagccc	aatgacgatc	ggcagaatac	1140
gcctttttct	aacactcctc	aatccctgga	gttctataga	acaaatctac	taaagcaggt	1200
cttctggcct	agcttcttat	cggttttcgt	cgcccttccc	ataggggact	acgcccttct	1260
acagtgaaca	tcgcatggac	tatccacccc	atcacctctt	gttcggagaa	gtgacatcga	1320
agcttacagc	tgaggggtca	gctccggaat	tgacccggat	tcctttgcac	cgcttcatga	1380
aagaaacggg	tacttcagtc	ttttcaaagg	caaaagtata	gttttatatg	aacgtaagc	1440
acagtacagg	gctatcgcat	ttgaatagtt	tactgtatcc	ttggtctctt	tcttctctct	1500
aacacattta	ttcgtgcttt	tttgacggga	gcactatcag	gcttatatgt	gtgtt	1555

(2) INFORMATION FOR SEQ ID NO:129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

```

cgcctttcag tttcggcagg aatgattccc agtcgtcctg caagtcgcca atccccatgt    60
ggaagagccg agaagcagta catcgtattt cgctgcaggg cagcgtcggc atttgccacg    120
tccattacat tagcggagtc aacgcctatg cagaagcaat tttttgagcc agatcgctcg    180
tcgttccggt agaagaccgt agaagattcc gattgatttc atgtttttga atagtattata    240
ttggttgacc tgcgcaaaag tagaggagat caacgacttg taatatcacc acaatagcta    300
aaaagaatag gtccatacct atatgtgggg ggattcccat cgaaaaaagc agcccgacta    360
aggccgtgcg gaggcgaaaag catagagacg gctacctgct cggccgtgcg ccggagggtg    420
tcccgtgcat aagccggatt ctgcctcttc taaggctgac gggagaagga gtaatcgga    480
agaggccgag aaaccggcgc ggttaagagc tacagcatcc tcgatactgg ccggccagca    540
taccacgggt atcttctgct tcatagcctn agccaacaca cc                    582

```

(2) INFORMATION FOR SEQ ID NO:130

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

```

gaggatactg gatagtatcc attgacatac ttatctcctc gccattccac aatctccaaa    60
aaggagaagt acccccccggt acccggcata ccattcttct gatattggaa tgcattacaa    120
cccattcttc gaatcggtct ccgtagtttt atacttcggt ctttgtttga agtactgcaa    180
tgcttctttg agttcggaat aagccgggtt aatatctcca tagtatattc aagaaaatgc    240
gatgtataga atgtgttgca tatttattcg ttgcctctgt ctgaataact tctgctctta    300
gctgatttct atcggaattt gaaatgcaat taagcaattc tttttttgtg taagttttta    360
attttatgtg tgctgttatt atggttctga ttggctattc taatacattc ttctcgtgat    420
tcttctatta tttgaatttt accggattgt ttganaggtt aagtaggggt agatgt        476

```

(2) INFORMATION FOR SEQ ID NO:131

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 522 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

ttagcttctt	tggcctctgc	atactacgga	catccatctc	gccatctgat	ctggtcgggtg	60
taaccgggtac	gaacggcaag	accaccgtag	ccactctata	tatcgactat	tccgaaaaat	120
gggatataaaa	gccgggtctgg	tgagtacgtt	tgcaactatg	tgatgaccg	gtccgaaccg	180
accactcaca	ccacacggat	ccattggcat	tgaatgctct	tttccgtcga	atggcagatg	240
cagggtgcgaa	tatgctttta	tggaagttag	ctctcatgca	gcggcacaaa	agagatcggt	300
gctcttgact	tcgacggcgg	aatctttacg	aatcttactc	gtgccatctt	gactatcacg	360
gctccgtacc	ggagtatttg	cgagctaaaa	agggtttttc	gatggcctcg	gtgcttcagc	420
tttcgcattg	gtcaatgccc	agataagaac	ggcctcgtaa	tggtacaaaa	cacccgagca	480
cgtgtatgta	ctatgcactg	agagcatggc	aaactatcga	gc		522

(2) INFORMATION FOR SEQ ID NO:132

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

gcctcagcat	cggagtgcac	ctgctcaatc	tcctttgcat	ccctgccatg	ctttgggtgta	60
ttactatcgc	cgtgctgtta	aacccacagg	caggggagtt	tgttggcact	tttggttcc	120
ttcgccctta	tcgggggtgat	gatgttcgtg	tgatacaggg	tatccctaag	gttgccggcg	180
tattcgatgt	cttcgcgtca	acacccttgg	tttgagcttc	aataacggtt	tgtatttcta	240
tttctcctgc	tggtgccat	attgatttgg	tctgtgaggg	agacttattc	cgtaagaccg	300
acggtgataa	gaagggtaca	accaaataca	tgcgcattcg	cttgccgcgc	tgctgagtgt	360
ggtctgatgg	gtattccttt	tatcggcaat	ggatccttct	cgcatagcc		409

(2) INFORMATION FOR SEQ ID NO:133

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 776 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

```

gtcaaggata tgcattggcaa gtatcctttc cccgaggcca cggcaacgag gaagtactgg      60
tcacggggaga gaacgcaggc aaacaaatga agctgctgtg gccagcggac tcgtgggagg      120
tctgtacgac ttcattcgtg gcaccttggc tgggtggacgg agaactgttc caccgggctg      180
gccgaatggg gagccgactg gccgagaagt acaagctggg ctttaaggtc aataccggag      240
cggcctcctc ggccctgggct atatcatcgg tctgccttat gccacgatca tctggccggg      300
tcgtttctcg tctgggttcgt tatcatgccc cttatcgggt actcgccccg ggtatgactc      360
aggccatcgg cgacgggtgtg tcgctgacta tcgctgtatg agccctgagg atattttcgc      420
cgtctatcgg cgctcctctcg gatcggaggt atcgccatgg cgggtatcat cgggatcctg      480
cgctcgtccg aattatcggc cgggcccgtc agctggccgg taccgaattg accggcaagg      540
gacgagtacc atcgatgagc ctgcacaca gcgtgatctc tcgatgaatt cattacgctg      600
ggcgatcctg tcgctttggg ggtgacgatg cttttctcca gttcaacgtg ctattcaact      660
ggggacatac gctgatatac ctgctgtcgt attcattatt accttctttt ttaccactgt      720
ggctgccaat gccatgccat cgtgggcagc aaccgcgttt cgggatgac cctgat      776

```

(2) INFORMATION FOR SEQ ID NO:134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...2691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

```

atggtattct tccgctgtac aaccgttggg ggggcttctt atcaatagcg atccggatcg      60
gagatcgcgc ggccacgatt ggcattgctg gcgtagcgaa attgatcatt gctgcattccc      120
aaataccatt gtcgctgtta gaatatcacc agctttccac ttgtcttgaa tgcgaaaga      180
ggtacgcca ctgcccacg caccgtatgc cccaagacca gggcatcaat tcacccatt      240
cgcatcggag aagaacggag gacgtcccgt tgccgcaagt gcgcgcccc tggcccatc      300
cgttgctgcg caacgatgga tataggcggg gaacagcagt agtgattttg ataaaatcca      360
caccccactc ggagaatgtg gcggcatcta tccctctttc taaaaactac cactcaagcc      420
atgaacgtta agaggagatg cttggaggaa aggccgagcc gcataccgcy acgatgcagt      480
tcacggccca atgtttgatc ccattgggga aacgtaaagg atccgcctta attctccgc      540
gctatcacgt acggacgttt gccagtggct ttctatgatg atatggttta tccggctgca      600
accagtcctt tactttgcat cgcattcgcc acatccaaat agtctgctcg tttatttctt      660
tctccttcag ccaacgtgta ctccaacat aacgggagcc aatccattat accgactcac      720
ttccacctgc caaatcaact gtcggcaccg gattcgttgg ctgctgatat ttcaaattcg      780
aatagatgcy agaagaagcc ttaccgcgaa taattccttc gtgggaatcg aattaaatcc      840
ttcgggcaaa tgcttgatag cccaatgcgt ggggcgtgat ccagataagg tatcttgaag      900
gtccattcac gatccatggg ccaaatagat ctccgggcaa agaatacgc ggactaccct      960
ctgtcggact cagtgcatag gagcagaaa tgcgagaagg agaatacaga gaaagcctgt      1020
cggctctcca acagagagaa agcgacctt ttcattcgca gtgtactatg gccaatcccc      1080
ctgtagagggt tctttatata gactcggcaa atccttgcgc gtctgacct cacttccacg      1140
acctgatcga acgaaatgcy gtgtctgcca tcgctgaatt ggcataagta ttggcatcca      1200
aagctcgtgc tgccgcaaa gcatctgttc gatacaagg acctgacca atccgcatac      1260
agggtcgcag gtcattccgag gtgatgctcc aaagccatct ctgcagcata ttcgatttgg      1320

```


gacgggtacc	cccgaatagc	tggtgtgtgg	ctgccgctcc	catggcacaa	gcactcccac	1380
ttcgccctga	cagccgactt	ctgcacccga	aatagaagca	tggtgcgtac	cacattagca	1440
aaaaggccgg	ccgtagccag	tgcacgcaat	tgcgcttatc	gctgaagtca	cgagtctgtt	1500
ggaggtggtg	gagtaccgcg	gtacaacgcc	gcacgaccca	catgtcggcg	ccgttacgat	1560
cttgccaccg	atgcattctg	ttcgctcaca	gccaaagcat	aggcatatac	attgcctggc	1620
ttcgtacacc	cggcgaatac	ccctgcgcac	gaatcagata	gctggcgcct	tccggcgaac	1680
gcccagtcca	ccggcgagca	ccccctcagc	atcgacccct	cctgaatggc	gctccgcatt	1740
accgaccaga	cctcagccaa	atagcccata	tatcgggatc	ttcgttttct	tccacatact	1800
cccaatagct	tagccgcgcc	tgttcagttc	gtcgagaata	tctgccatct	tgctgagcgg	1860
attacctcgc	gacctcgctg	ttcgttgaag	tggtcgttgg	ccaagactcc	gcgccgatgc	1920
tatagatgag	ccagtcgtcg	agctgcttgc	cctctttgtc	aagctctcga	agagcatgcc	1980
gttggggtga	aaatttttga	agatctccgt	ttccaaacga	tttcgggtcg	agcctttgct	2040
tccaagacgg	caaggatact	gcatacgtga	ggtgtccttt	gcccgtggca	gcaaggctgc	2100
cgtataggtg	acacggaaag	aggtcgccc	ggggttccga	tcgagaaaca	tctcagagcc	2160
cgacgtgggc	caatcgtgtg	gctactgctc	ggaccgtagc	cgatggatat	atttgggtta	2220
tcgattccat	tgtatttgtg	ttgtactatg	cttcagggtg	tgaaagagtg	atagtttttg	2280
aaagagccaa	cgaagaccgg	acagcgatcc	gtgtgtagtg	gctcagtaat	tgagtctgta	2340
ggaaaatccg	atcgtgcgaa	gacgttatac	atccggtaag	gaatagcctt	gaagtgtgta	2400
cggtcagagg	gatcaggccg	aatgtgacat	cggcaaacgc	acctatctgt	gcgcgaaata	2460
atagtcggct	cctattatga	caccgaaatc	cgctccctta	tcttgtccga	gaagttcagt	2520
tcgcgcagat	ccatctgcgc	tgttcccact	tgggatcgtc	atagaccatc	gtaccgtcga	2580
tgatcacgcg	gaaggaatct	ccagcagcag	ggacgtatag	agacctccgc	gcagcttcag	2640
cctgtcttga	gcatattgta	ttccgcctgt	acgggtatcg	tcaggtagcc	c	2691

(2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

cagcaacacc	caaactggca	ccggagctga	tgccgagaac	ggacggaccg	ccaaaggatt	60
gcgaaagacg	gtctgcatct	gcaagccact	aacggataac	ctgcgccggc	aaaagcagcc	120
gtgagggctt	cgggcaggcg	ggatttcata	ggatattgta	gtgcacgagt	gcttctcttc	180
cttcggggacg	atctgaaaaa	gatgtcggaa	gatctcgctc	atcggaatag	ccaccgagcc	240
gaggagagat	taaccccga	gagaatgagt	acagccccctc	ccagcgcagc	caggtacctg	300
cgacagaaat	tgtacgtaag	tggtgacg	atgtcatttg	agcaataata	gaaatgcggg	360
tggtgggtcgg	gaagtgttcc	ggggtgcaag	atgcgataag	atcgccagc	acccaatcgg	420
gatgcatggg	catgagttcg	tgaaggctgt	ttccctcagg	ttgcagtata	tcacgccttt	480
ttccttgaat	ccctgaaatc	ggcatatcgg	ctgtcttcgg	ctttcaaagc	ttcgtaacca	540
actccccggg	atagctgttg	aggattcgcc	agtagcgagc	cgaatcggtc	ggctgtagac	600
cgtctcgaag	tcgaggga	caccaccgga	tcgttgac			638

(2) INFORMATION FOR SEQ ID NO:136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

ttttccca	cgcccttg	cggcgtaa	gctgtcac	gatcagatt	cctttttt	60
ttttcttc	tcgatacag	ttagcggc	tttgnccg	atcgctcc	tggttcta	120
tggtcgac	gcaagtcg	tgactctc	tctgttcg	tctttgcg	tcgatgtc	180
gtgcaatc	aatgtcgat	tcattctat	ttattttt	agtttggg	tccttttt	240
gtgatttt	attcgctgt	tatataaca	aaaaaga	aatcggtt	acggcgat	300
aaaagctt	ctttcgaac	atttttcag	aagattcaa	tcaaaaaa	cactgttat	360
gctgctaa	ggaaaaaaa	gaatttcgt	ttgacacta	tgtaatgct	cacgactat	420
aatgcatag	gaaatttg	gaaacgac	ctatatcc	atcgtttc	tcgaagaat	480
ggataagtt	aaaaaggaa	cgaacaaat	aacttcaac	cacgagctt	tgtccgcgc	540
tggtatgat	atccgatca	gatctgttc	cgaaaggag	ttctctgg	aaggcttag	600
gcgaatctt	gtcaagatc	atggccaat	ccacacca	taaaaga	gttcggcg	660
aacaaggcc	accatcgat	cctctcat	ctatgacg	ggctgatg	cagccta	720
tcaagact	cctcgcac	aagacgtga	cctgcggat	aaagcccgt	ccctcgga	780
gctctagag	attacatca	tgacaagg	actcgatg	accttttc	gaagccgag	840
cggaatacg	aggtgttg	ggcgatct	tcgatcgt	tttgcata	aagacggc	900
cgatatag	gagtggga	tggtttcg	gtcgatcc	acgactgt	tgtgatga	960
agcgaacgc	acagtgtat	gcacgtta	atcctttc	cggaagata	gttagggt	1020
agaaaggac	tatttcggg	tccaaccac	caatgcag	cagaccttc	ccatgcact	1080
cttacagat	cgaatgtaa	gtcatttga	ctgacgggg	aagccggag	ggcaaaac	1140
tgctggctc	ggcagcag	ctcagtcag	aacagtct	aaacaaat	tgcttgca	1200
gcccacgtc	tcatttggc	ataagact	ggatttcct	cgggcgat	gaaagccaa	1260
gtggcacc	acatcaacc	cttttcgac	atctgaat	gatcaaag	cagttggct	1320
aaatagcag	gaactccgc	ggctggac	aatgcagaa	accgaaaag	tcttatcg	1380
gctttggc	acatcagag	acgtagcgt	tcggaaac	ttttatcgt	gatgaagc	1440
aaaacctga	tcctcagca	atcaaaac	tatcaccgt	gcaggaga	gtagcaag	1500
gatttttca	ggcgacatc	acagatcg	tctccata	tcgatgccc	gagcaacg	1560
ttggccta	gatcgaaag	atgaagggg	aaccgctct	cgcccatgt	aatctgaca	1620
gggcgaac	agcgagctg	gcgaattgg	cagtgtatt	ctctgatct	cggttcggt	1680
tttcaagg	aacaaagag	ccgacacaa	cgtcacgt	cttatccgg	ttccggttg	1740
cgaagtctt	ccaattctt	actgcgat	gcccgaac	gccataggt	ccgacgtct	1800
aaagaagt	gagcggcag	cgccagtc	tcogtggc	ccatttcag	taacatct	1860
tctcaggt	tcgtaaatg	cgttggag	tcggcgct	ctgctcttt	ccgcattgg	1920
attacctgt	atcgcttgt	tgatgcgc	cgagcata	ccgtaatag	aatgtcgcg	1980
gccaaagcc	ctgccatag	gacaccct	cccgcctaa	cttgagcata	ctctgtac	2040
tcttcccaa	gaaaggtgt	cgatagcc	ttcatccgg	aggaattcat	cgatcagac	2100
tgtaatctg	cgaatatgc	tttcagac	atatagtga	tgtcgaatt	ctccagcgt	2160
ttaccccat	agccatgag	cggggagta	tccccacga	gtgaacat	cgtagccat	2220
cagtaattg	cggggtcta	ctcccatgat	aatggttc	tcggactcat	tctttgctt	2280
caattctatt	cttctctat	tgggaaaa	cagatcag	accgagat	tgaggattg	2340
cttacaatt	tatcttctc	tcgtggtgg	aaaacccat	accctgttg	cgaacttcc	2400
gtgagggtc	ctatatgtt	tgccccaga	ccgcacca	attcatct	tcagtcgat	2460
ggtctgcga	gaaatggag	gccagcgat	cgccttctt	tgtgctcc	tttcgatgc	2520
gtgtaggca	ggggaatgc	tagatccgc	gcaatgacc	atgggatga	agtcgaac	2580
agatagtcg	tcaatgttc	tctacggcg	cctccgttac	ccacgttata	ttgtacaaa	2640
tcattcgtg	attcctttc	gagataac	aaagtatt	aaaaccgca	tgagccttt	2700
cccttcaaat	atgtggaac	ttagaagct	taatgcaat	aaaaaagaa	ttgagata	2760
ttgactttt	atttgaaaa	aagaagta	ttgaggcag	gcagcaaat	tagtggtat	2820
cggtatctac	cgtaattgt	tatcataaa	aatcatgg	tgaacattt	caattttat	2880
tcgttgttt	cgctctgg	ttattcttt	gtgtgaaa	acccttgc	aacaaaaac	2940
gaggagtgt	cacctgtgt	ggatttac	gcagaagc	acggctct	gttttcttc	3000
actggactc	gocgatgac	aatccgat	ttcctctag	gagagtttt	aatcaggt	3060
tccagctata	tggaagacca	ttgacgcg	ggcgatgg	ataattgg	gcatttgac	3120

aatttcacgg	gacagatggt	ctctgtgtct	cttcggcttc	atacataggc	ggcgtcggag	3180
ctttgtccg	gacaattatc	tgataacacc	cgaattaaaa	ctaccacacag	acgcttggtg	3240
gaaataatct	attgggtatg	tactcaagat	ctcactgctc	catggagcac	tatgccgttt	3300
attcctcttc	tacaggcaat	aatgctgctg	acttgtaa	ctcttatatg	aagagacttt	3360
gactgccaaa	cggatacaat	ccccgagttg	atccgcgga			3399

(2) INFORMATION FOR SEQ ID NO:137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...4696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

aacctattct	tctatcagcg	gaagaaatcc	ttcttcactc	atcagccgga	caccgagctt	60
ctcagctttc	tctctctaac	ttcgggcccc	aatatccgtc	ccggcaagaa	tgaaagaagt	120
tcttggaaga	aacccgatcc	gggccatcgt	ccgccattgt	cctctaccat	agcttttgta	180
ctcatcacga	ctacgctttc	aaatgtacca	ctgataacaa	ccgtttttcc	ggctaaacga	240
ttggaaccgc	cacggaaaact	gtctcagctt	ccaacgatac	accggccaaa	cgaatcgctt	300
gatcaactcc	ctgtttctgcc	gaaggctgaa	aaaatgaagt	acacagcagc	tattctttcc	360
ccgatctcgt	ctatctgtac	taattcctcg	ctgtcgcagc	agccagggca	tcgatagaag	420
gatagaccgc	agcaagtttc	tggctacggt	ttctccgaca	aagcgaatac	ctaattccga	480
caaaatggcc	gatacggacg	ggctttggag	gcttcgatac	tgtccaaaag	tttggcagcg	540
cccgcttttt	gaagccgggc	agagtgaagta	gctgctcttc	cgtaagggat	aaaagtcagc	600
aacgttacga	atcatattgc	ggctataaag	caattcgtcg	tctccggggc	gatattgatg	660
tctgccgtct	tgcgtccgca	atagtgtcga	gccgtccctt	ctgctgctgt	gggcagccct	720
cggcattcgg	gcaatatagg	cagcttcttc	ctgttcgcgt	accaatgggtg	tagcacagtc	780
tggaagagca	ctgtaaaaaac	tataggctcg	ccatcgatac	tgcgtgcac	cgttccacac	840
ccactatctt	gggaatgatc	tctccaccct	tttccacata	gaaaagtctc	cctcgtgaag	900
gtctttctcc	gcaataaaat	cagcattatg	cagctggcgc	gtctcacgac	cgtaccggat	960
atcagtactg	ggtcgagatt	gccacagggtg	tgaccgcccc	cgtacgccct	acttgatagc	1020
ttacatgctc	agacgagtac	gtactcgctc	ggcctgatac	ttataggcaa	tagcccaagt	1080
gggcttttgg	ccgtaaagcc	aagcaaatcc	tgtcgagccg	gagcattacc	ttgaggacaa	1140
taccatcagt	agctacgggc	aatgtcagag	gctcggatcg	aaacgatcga	taaaggcata	1200
tacctcctcc	ttactacagc	atagttgacg	gcatcagaga	ctttgaaacc	ccactgacgc	1260
gcctgcatca	gtcgtcgtaa	tgattctctg	ccaaagggtc	atcgctatat	agatagtaga	1320
aatagcatcc	aagtttcgtc	cggctacgat	atgggggtcg	agctgcttaa	tgtaccggaa	1380
gcggcattgc	gcggattggc	aaatagaggc	tccccttcgg	ctcccgttgg	gcattgatcc	1440
gatcgaattc	cttgaaaggg	agcaatatct	tcttcgaact	tccaacatac	ggggataatc	1500
atcgctctct	agtcgcaaag	gacagatcgg	atgggtacgga	cattagccgt	tacatcatct	1560
cccattatcc	atcgctctcg	gtaacggcac	gcaccagcat	accatcttcg	tagataacga	1620
aatggaaagt	ccgtcgaatt	tcagctctgc	aacgatttcg	aaaggtcgcc	ttgaagtcct	1680
tcggacacgc	gacgataaaa	atctccaatc	tcattctaatt	atatgtattg	ctgagggaaa	1740
gcacgcgtct	gtcgtggcga	acggagcgaa	tccttcctgt	ttgtcgcttc	cgacacgatg	1800
cgtaggcgag	tcagactatc	ccattcgggg	tattcccgtt	ccagctcctc	aagctgcttc	1860
atatggcgtc	atactcgaag	tcactcgatg	tcggagatga	gagaacgtaa	tcctgtattc	1920
gtgctcacgc	agaatgcggc	gcagctcttc	tattcggaca	cagggggaac	tatcttttcc	1980
ataactgata	aagcaaaaaca	tcagaataac	gccggcatgc	cacatccatt	ggcggagggt	2040
ggctgtatgc	tcgaagccgc	agcttcgaac	agcatccggc	tcggcttggt	atcttccagc	2100
acataaggat	gatctgatgc	aagcgtaa	agtctaaaac	ataatgggat	atcttgggag	2160
agactcgacg	gctattccca	gccgacggta	ttcgggaata	acgaaaaccc	tacggctaca	2220
cgtcgatgaa	aggcatcgta	ctcatacaga	tctacgcacc	gacaggctta	tcgtcatccg	2280

acaagcagat	gacaagacgc	atctgcccaa	ctccatcaaa	ccttcagaac	tcttttcgat	2340
atattctttc	agcgattgcg	tccgatagg	accagcatat	tgccactctc	acgcaattcg	2400
gatcattttc	ccataggtag	agaaagtcca	aatcttccgg	ttcaagggct	ggagccgtac	2460
ttgctctgaa	gagaaaagg	cggtcatgga	atatcagaat	tgactgagtc	ggagaaatcg	2520
gtacgattga	gaatagaacg	accgagggaa	tctcatcggc	atattcgatc	tcacgccta	2580
tagcaatgcc	tcgagcatta	cactgaccgc	aacgcgggta	ggctccaact	tcgaaaagag	2640
gaaaaattgg	tagtatcgcc	ctccatcgtc	gtactcaaag	ccaatataac	ctcataatct	2700
gctcagaagc	tactcgatgc	accaaagaat	ctatttgcaa	atcgccgggc	cgatcccatc	2760
catgggagat	atgactccac	cgagtacatg	ataaagcctc	gatactgtga	ggtattctcg	2820
atagccataa	cgtcacggat	atctctacta	cgcagagtgt	actctgatcc	cgagtggggt	2880
ctgcacagat	atacaaacat	cggaatcact	gatattatga	cagtgcctgc	aataggaaat	2940
tgttcccga	gatctacaag	ggctgctgca	aattgacggg	tattttccaa	ggttggcgca	3000
ataagtacaa	agccaggcgc	agggtgtct	tgccgacctc	cccggcaatg	tggcaaattg	3060
gtctatcgcc	ttctcaagca	gacgcgagaa	tatttctgta	tcattcatcc	aaaatatcca	3120
gctcgttgcc	gtcgtatcgt	aaaatgtgta	gtccaggaat	cccagactct	catcggggat	3180
aagttgatcc	ccttggcata	cttgagtttc	catttcttca	agatagaaga	aaggaaacct	3240
tcttgaggta	tgctgccacg	tatggatgta	cgtgaagaac	gaatgtttga	cttgggtgctc	3300
cgtgaccatt	ttggccactt	tttcttccaa	ctatccgtga	agagtatgga	ggattctacc	3360
ttgccggtag	ccaaacatgt	ggacaacact	cttcggtagt	gatgaccatc	gccggacgaa	3420
cacgctgacg	gtaatctgca	taacgcggaa	tttgctcaat	ggcaagatat	tgtgtcgcgt	3480
ctgtcagccg	acatcaattt	gaccatgtgt	tcgtacaact	gctgacgggc	tgggcttcgc	3540
tcatatcgat	gaagtccact	acgatgatac	caccttctcg	cgcgaagcgca	attgtctggc	3600
cagttctctc	gctgcagcca	tattgaatcg	acggccgttg	cttctctgctc	ggtactgcca	3660
cgcgagcggg	taccgtatta	acatccacca	cgtgcatggc	ctcggctctgc	tcaataatca	3720
gatagcacca	ctcttatacg	taacagtacg	tccgaagaga	gctttaatct	gctcgtaatg	3780
gcaaaatggt	cgaaaatggg	tagttcgccc	tgataatact	gacgatttcc	tcccgtcccg	3840
gagctatcaa	ctcgacatag	tcgtcctaaa	ttcccgaata	gccttgctcat	tgacaataat	3900
actctggtta	gagggattga	gttgctccctc	aagagtccca	gagtacggct	ggcttctctca	3960
taaacaatga	cggagccttg	gcacgcataa	gcttcttgat	gttgctgctcc	caacgacgag	4020
taggctctgc	aactctttgt	ccaattcgga	tgcccgttta	ccttcagaga	agtgcgtatg	4080
ataacgctaa	aattcttggg	cttgatgctg	ataatcactg	ccgcaagcgt	gctcgtctct	4140
cggcagaacg	aatcttctga	gacacgacac	tttgcttgca	aagggtagca	aaaccaatga	4200
acggccggga	aaagaagctc	ggcagtcagg	cgtgggcctt	tggtagagat	cggctctttg	4260
gcttctgcac	caagatctgc	tgccggcct	tgagcacatc	tgcatcttcc	cctctttagg	4320
gaggtcgtcg	ccgaggggca	ctttggacaa	ggatgggaatc	gtttgctttt	tgatcatcatc	4380
tccatcatct	tctgctgagc	atcgaaagtc	agcccaaatc	aagataatga	agaaatgcgt	4440
ccttcttgta	tcctacatca	cgaaagcagc	gttcagaccg	ggcatcacct	tcttcacttt	4500
accgaggtaa	tatccccac	tgcaaaagaa	agattgcgcg	gttcgcgttg	aagctcccga	4560
gtttgccatc	ctccaggacg	gccatagata	cctctttggg	cttaactcaa	ttactaattc	4620
gctgttcact	tatatggtag	gattgtcttg	atgatataaa	tacaagtaag	cgaatacggc	4680
ctgtgggcgg	ggatcc					4696

(2) INFORMATION FOR SEQ ID NO:138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

tccccgcgga	agatttgcca	gcctattttg	gtgtaaagca	tgtaatccct	gcgccaatgg	60
tacagacgca	ttgcaaatca	gtctgatggc	tttgggatga	aagtcggaga	tgagatcatt	120

gtgcccgaatt	tcacttatgc	agcaagtccg	aagctatagg	tttgtttagga	ttaacacctg	180
ttttcgctga	tgtagacctt	ttacatttaa	tcttacatct	aagggtctgcg	aaaaagttct	240
gtccgcaaga	cgaaagcaat	cataccagta	cacctctttg	ggcagtcctg	cgattggagc	300
cgcttttggc	ctttgccaag	cgaaacgatt	tgtttggtat	cgagacaatg	ctcaggcaat	360
gggaggggga	tatactatct	ccgatggatc	taccgaaaaa	caggaacaat	ggggcatata	420
ggctgtgctt	ccttctttcc	acgaagaatt	tgggttggtt	tggagacggt	ggtgctgtca	480
caacaaatga	gacgaattgg	caaagcgagt	gcgaatgata	gcgaaccatg	gccaaaagac	540
aaatacaaac	atgacattat	cggatgcaat	tcccgaactcg	atactattaa	gcggccatcc	600
tcagagtaaa	attgcaatat	ttggaccgct	tcaatgcctt	cggaatgagg	tcgcctcaca	660
ctatacctct	ctgctcgaag	gtattgatgg	ctacaaacac	cgacctcctt	gcagcagtct	720
tcgcatgttt	atcataatat	actcttaagc	tcttggatca	gaacactcgc	gatggactgc	780
gagacatctg	acgaatcata	agatcgcttc	gatgatatac	tacccgatac	caccacaggg	840
caaccggcat	tcgtcgggat	tgctcattgg	ggtgaatctt	tgatgtgtcc	cgactctttg	900
tcgcgaactg	ttctctccat	ccccatctat	cggaaatgga	gatagagcaa	atccatgctg	960
tggtatcagc	aatcaaaaac	tcgaaccgtc	tttacaatga	caaaagagga	gggaggctcg	1020
tctatgaaga	aggacgaagt	tccatgatgg	caaacagcat	gaaactgatc	agcgccggac	1080
ct						1082

(2) INFORMATION FOR SEQ ID NO:139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

tcaaccggct	atcggttaagt	aggaatcaga	ttcagcatcc	gataaagagc	gagcgtaact	60
cccagaggaa	agtcgataat	cttgtaaccg	atggaaagag	gatgcccaca	caaagggcga	120
tcagggcctg	tccgcggaag	tagctgtcat	attcttgtcc	acttctttga	gtatgtcctt	180
aacgcgaata	cggtgtcgac	cgggaaaaga	ttgacaaatc	ctttgcccag	tttttcgaaa	240
tcgaaaaggat	gaaaatgaag	tataaaacac	ctatgaagaa	gatcgctcgt	tagcgaacaa	300
gctgatcgta	ccggagacga	gcttattgag	ctgtccgaat	atcccttgct	attctccatc	360
attttctcgt	aagagatacc	tttgaacaga	tcttcatgct	gccactctct	gacagaaact	420
cgcgatcgg	agccggcagc	actgtagcaa	attctcatcg	atgcggtact	gctggagcag	480
ggttattggt	tgtttacctc	ttcttctaca	gcaggaacca	aagagagaat	ggcaaaaaaa	540
tcaatgccga	tatgaaaacc	agcaccgtga	tcaccgacag	aaagcgaagc	gaaaatggag	600
ccgatactgg	acaaaacgaa	ccagaggcat	cagcacaagg	caagaatcca	agagagacaa	660
aaaggtataa	ggatgcctct	caagccatga	ctatggccat	aatgcctcca	accaacagga	720
tgatgaaaaa	caggctgcag	tacggctcga	cgtaaattcc	ctgtcaaaaa	aactttgcat	780
aagcgtgtcg	attagaatgt	gagtgagttc	ggataccgaa	gatagtcgtt	tttctgtttt	840
cttttgcaat	tttcacaatc	atccatgtag	atcgtttttt	acgaggcttg	tcctccctgc	900
atgttcgggc	cggtaggcga	gtgtcagctg	actgctttct	cgaaaatacg	aacgggaaat	960
gctcggattg	cggtctgaga	tcctgaaaaa	caggcgcgag	aatttttttcg	ttgtggcgcg	1020
agaatttttg	cttcccgaac	caaaacgaaa	attttct			1057

(2) INFORMATION FOR SEQ ID NO:140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

```

cggcacacat cgctccggtt acgaatatgc ccagatcctg agtggagaca gggacatcat      60
tccatccgcc atcgcaatgg taatgaatgg atccggtaga cggctgcgtc gatctgtccg      120
ctgcgaagca tttccaagcg caaagggttt tattgacttc ggtcttggtt atctcgcttt      180
cgctccagtc tgccggtttga taattcggtc ggtggtgtac tcaatgaccg tattgcgcga      240
tataccagat tctttccttt gaggggtttcc aagctctcac ctgtataatc tttgacatta      300
ccagccggaa gtatccggtc agacgcacac ccagttgcag atcatacctc ctgcttgctg      360
catggctgct cccgtataat cgatgaccgt acctccacat tggccgaatg gaaagccgca      420
tcacgttcat tgggcgaata gacttgacaa tctccagttt cagtctgagt gaatcgtaaa      480
tgccgggttt tgtgctacaa cgaaaggcag atagtcacat gaaggcatgg ctccgagagg      540
agggataaag gctctttttg tttgtctgca gagcttttct tgttaccaat gaagagaggg      600
tgatgctcaa aaccgccaga acaaggaggg taaaaaagaa aaattttt      648

```

(2) INFORMATION FOR SEQ ID NO:141

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2149 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

```

cgccggtgaa agctgtgata agcgaagcag ccaagccgaa tggagcgata tcttgatgtt      60
tttgagagca aagtccttgt gtttgtcatc ctttcgcaca ggtagatgcc acatacgccc      120
aaagcaataa cggatccgag agtcagagg aagagatcgt gtgccagaac ttattgatcg      180
cagtggaaag gaatacaaaag cccagaaatc cgtcatttcg tttgcgcacg gtatcggggg      240
tgaagtcatc cctaccggct cctgcaccca tgcattggcg ataagaatcc atacgctgac      300
aagctggctc cgatgatggt cagccatgtg gcacttaagt gaaacctttg ctcaccttgt      360
tccagccaaa gaacataacg gcaataaaaag tacctccatg aagaaagcca aaataccttc      420
gatggccaat ggcgctccga aatatcgccc acaaagagac tgtaattaga ccagttggta      480
ccgaactcga ttcgagaatg gattcctgtg gccacaccga tcgcaaagtt gataccgaaa      540
gcttctgcca gaactgagca taacgcttcc actccggttt gccattgcat aatagatggt      600
ctccacgata gccatgatga cacccaatcc cagtgtcgcg gaacaaacag ccagtgtatc      660
atggctgtaa gagcaaaactg tgcacggacc agcttactaa ggcattctaaa ttcataatca      720
tacgcttata tcttatgttt taggggttta ttccacgttt gataagttcc tgctgcacat      780
attcgatttg gcagtgtgtg cgctaccgac ctgttgcttc agaaggttcg ggagaagaat      840
actttcagga tggcgaacat gatgaatagt ttgatgagga tatagcccat agcgtctttc      900

```

ccaatttcat	attcctgaag	ccatctatat	aaagcgagct	atacgcatga	acaagttctc	960
gcgctttgct	ttgattggtg	catagttttt	tcgattcaaa	aatgaaaaac	cgtgcaggtc	1020
tcgatttttt	gctgtggtga	ttcagctttc	ttacaaatat	aggatgggaa	ttgttttttg	1080
gacgcgtttc	ctctctaaaa	tatcacattc	ggctcaatgg	agtcgttttt	tgtttgtttt	1140
tgaagatca	tcaagtacca	aatcaatacc	agcaattccc	tcgcgagagg	tcatgaaaag	1200
ctccacatgc	gcaccggatc	gaatcgattc	catgtgatat	atgacctgtg	ataggggttg	1260
ccatccactt	ttacgactcg	atataccggt	tcttctcact	tagattgtga	gccgtcagtc	1320
gaagatacga	ccattgggct	gagggatagt	cacatgttcg	aacaggggtg	atccagttcg	1380
taatggccgc	ttattggatc	caccggatag	aaccccaggg	cgagaatacg	taccaagccg	1440
aaagttggcc	gcagtcttcg	tttccgcata	gccgtcaggg	gtatttttgt	atagttctgt	1500
caggatgcgg	cgtattatcc	cgctcctttc	catggctgcg	ataccttggt	gtacaagtaa	1560
gccacgtgtg	gctcggctca	ttgccgtggg	catattgtcc	gatcattccc	gtactgaaat	1620
cggcaatgct	atatgagagg	gagtaggagt	gccgaaaaag	aggccagacg	gcgagccatc	1680
gaatctgcac	cgcccatcag	ttccatgaga	ccttcgtatc	atgctggact	ccgaagagat	1740
attgccatgc	attactctct	gtgagtcctc	agtgtattcg	aaaggatcga	aaggaagttt	1800
ccattccccc	gatctaattt	gggtctgaag	aaaccgcttg	cgggatcata	tacctcttgg	1860
tagccttggc	gtggtgcgca	tatgccatcg	accgcttggc	tgccgctgcg	tttcccttgc	1920
aaagagtgcg	atgcaggcat	tgtcgtaggc	gtattccatc	tcttgctcaa	gtccagttc	1980
gtacagtcgg	cgggcacata	gcccaaatgc	gataattgtc	cgtatcggtt	ctgccggttt	2040
tttccatggt	cgaaaccaca	ggcgcgatgat	gcgctgcgga	ttctctttgt	aattgccttt	2100
ccgatagctt	ctacgatgac	cggtatggaa	tggtagccga	tcatcatac		2149

(2) INFORMATION FOR SEQ ID NO:142

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...508
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142

cgccgcttgg	atctcttcat	ggtcagctct	ctggacaagg	gcggattggt	tcgggtggta	60
ttttctctat	tgttttcgat	atggtagccg	tggtggaata	ccctccagat	ccctgctcag	120
cgtctcttct	cccttgatgg	cgcagcgcag	aaacggaaac	atctgggtcaa	agccgacgaa	180
ctcttcaagc	gcgtctgctg	catcagcttc	tttccggtgg	ccttatcttc	ttgcttattt	240
gggtcaatat	cgacagcatc	ttctccatcc	tcccgaacgg	tcacctctat	gccgcggcaa	300
atatgtcgtt	ttctatttgg	gaatcgctaa	gatgatcgaa	atccgctgaa	ctacggcaat	360
ccgatcgtga	gctgttccaa	gtattatcac	tgaatcttta	ctatactttt	cctcgtcacc	420
cattctggcc	cgtgctcacc	atctggtggc	tgatcctggt	tttggaatc	aacggaccgg	480
ccatggcacg	tcttgaccac	gctgcttg				508

(2) INFORMATION FOR SEQ ID NO:143

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

cgttttctcc	cgctccgctg	ccaatggtgt	gatcgctatc	gacctgcgaa	caacgatggc	60
ttggtaagtg	tccgattgac	caatggtaaa	tgcgacatgt	tattgccaat	tgcggtggac	120
gtgccattcg	tttccatgaa	tccgtgggtcg	tccttcgggt	cgtacagcca	tgggagtaaa	180
gggaatgacg	ctcgacatga	tggtcaggac	gaagtantag	gaatgatctc	tatcaaagca	240
tccgnagaag	agaccattct	ggtagtaagt	gaaaagggat	acggcaagcg	ttctatatcg	300
accgactatc	gtattaccaa	tcgcggtggt	aaaggggtga	agaactgaat	atcaccgaga	360
agaccggaaa	gctggtcgat	attcgagccg	ttccgatgcc	aacgacctta	tgatcatcaa	420
taagagcggt	gtcgccatcc	ggtaaaagtg	gctgatctga	gcattatcgg	tcgagctaca	480
caaggtgtta	gctcattgat	ttgtcc				506

(2) INFORMATION FOR SEQ ID NO:144

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1022 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ctcaccaatt	tttattttcac	ctatattata	gtggctcgtc	atgttaccca	agcaaaaatc	60
gtatataagc	cgtcttttctc	caaagggatc	agccattctt	tgcagctgac	aactggacat	120
cctcaaacac	attggcactg	cgaagggaac	atccttatcg	aaagcataaa	cgttcaatcg	180
ggcaacttcc	gcaggaaaga	aggattttcg	gcacactcag	tctgagaata	gaagttgaca	240
tataccctcg	aggacaatca	tcgtaattgt	cataaatcat	cttatcgcac	gaagcaagcc	300
acccacacag	gccattattg	ccggcaaaga	aataataagt	ctggaatata	catatgcttc	360
cgtttgttca	ttgtttttaa	aaatatagag	gggggagaac	ggtgggaacc	gaaatcccac	420
cctcaaaaag	aaaattttac	atagctaatt	agagatcaac	ctcataggaa	tgaactttcc	480
aaggcaaaac	gtaacctcaa	ccgacatgaa	cgtatcctga	tcaggtaagg	ggtttctcga	540
tctgtaggaa	caggagtacc	cggctcatcc	ggattcgggt	cagggttatc	ggattttccg	600
gattgttagg	atccggatcc	ggcaccaaag	gattccattg	aagcccaact	tcttgatgct	660
cttgatgtgg	atatggtaga	tattgtgcgc	acaacgggag	aattccacca	tgaatcggga	720
gaagtagtac	tgggatcaac	caagcatagt	acagtacttt	gcctttcaca	tatttgtgtg	780
ccttatacca	gctacaccac	ctacccttgg	gtctgtaacg	gatttcatag	acaatagaac	840
tggccattct	caccaacgaa	gaaatcttca	cctgctacat	atcaggaact	gcagtattat	900
ctgaataagt	ttacctctat	gcataaaggc	tctttcttgg	gagtaaactt	cgcacgaacc	960
aatacatagg	cagtattacc	ctcttatagt	ctgacgaagc	agcattagca	cctgacttat	1020
gg						1022

(2) INFORMATION FOR SEQ ID NO:145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

```

cggtttttct tttttgcaga aatgcaatgt caccaagttt aaaggggtcag tcgctgcaca      60
tcatatacag ctatattaat tccatggcca gtgccggata aaaatcattc agctcttggt      120
ttaaatactc ggcataggcc aaatttttatt attagttgtg tgccttagca actttgattt      180
actccctttt tggaagggtc tatctgtccg aaagagagtc cgttataata attctatctt      240
tttcttttaa tcatcgagaa gaatggtatt aatattatct tcaagctcca aatatcccca      300
aaagatatatt gggattgctt cttaataaca ctatccaata atgaataatt gtttgctttt      360
tttgctcggg gaagttttct atgatgaaag gatggtgaat aattcttgat gtttaacaac      420
atctctctca ataccccatg agaagttgtc ataaaagcat aatattgagc aaatgatgaa      480
tttaaaaaat gcaagttagt ttcaaaatat ttcatcaga tttttcggaa ataatacctc      540
gattccctta aaataagaac aatcgtaatc caaaaaagaa gccgtgagtt atttttctgg      600
actccctcat tcaataatag gtgaggagcc ctatatgatc aacatatcct aatcttctga      660
aaaaggaatt tgttattcta gtaccaagtt aatagggtgta taaaaacggt tgattgtttt      720
tgatgtgtga tgaggattaa tttgatattt tcatctgttt ttttgcaagg aacacttggt      780
tctatccaac accatagaca actttatctt taaaactcct ttgtaaagaa ggaagggtgt      840
ggataggcgt tttattagat tataatctgc aatattgccc caatggctat ttccatatt      900
ttactgtttg gaatttgcca ctccgttcgt ggagaaattt gatatctgta gaatcaacta      960
ataccccatc aattaagttg atttaa                                     986

```

(2) INFORMATION FOR SEQ ID NO:146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

```

ggtttcggcc gacatcggac gggggaaagt ggatttcagc ttgtttctca ggaatccggt      60
agtacggatg ttgtatctca gatattcgat acagaaaaat gtcctcttat ttcttccaac      120
tcaaggaatt cggcgaagaa atgggaggga agtaccgcga ggaggatggt tcgaacagct      180
acttcggatc cccgatcat tcagatagat gaagataaag aagaagaaat tccagaagat      240
gaatggctgt cgtaattgaa acttgctcga gagcccttga tcagctaata ggatccgcga      300

```

gcaggagggt gctatgctgg agcagggtgtt caccgagaaa atactaatat ctcttctttg	360
cttctgcaaa tcgaacagta tgaacccgat agatccaacg aatcaaagag cggatagaag	420
agaacctaac caaaatatca ggaaagactt ccaccagaac ngattcgaac caagagatga	480
tttattatat gaaagggt	497

(2) INFORMATION FOR SEQ ID NO:147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

ttccctcagc gtaactggttc actacggggtc tctcggggagt atttagccta cgggatgggc	60
cccgccaatt cacacaggat gtctcgtgtc ccgcgctatc aggtgctccg tcgtctattg	120
ttcgatatgt cggatacgca gctttcagct cttcggccat actttccagt aggttctcct	180
atatctatca ttaaaactttg tcgaagtcct attaccccgga ctttgccgaa acaaagccgg	240
tttggttaat ccccggttcgc tcgccactac tgagggaatc acttttgttt tctttcctac	300
gggtaatgag atgttttcagt tccccgcgtt cgctcatgaa atcattcatg tgtcaggcct	360
tggcctgacg ggttgcccca ttccggatata tgggatcaat tcgtatgtgc cgattcccgc	420
agcttttcgc agcttatcac gcctttcttcg cctccgagag cctaggcatc caccgtctgc	480
ccttacttac tttgttcgcc cggcaatcaa ttgccgcccg cggatatactt aagcttgttt	540
gctctactta aattctttat ttgattttct tccaatatgt caatgatccc tgttttcttt	600
cgtggagaat atcggattcg aaccgatgac cccctgctgc aaagcagggtg ctctagccag	660
ctgagctaatt cccccgtagt cccaggagag ttgaactgcc gacctctaca ttatcagtgt	720
agcgtcttaa ccaacgagct ataggactgc ttctctctta ttcgaaactct tccgtctgcc	780
tgtgcagctc cttgggctgc atgaccgttg ccccttatct ctctttatct tttctttttg	840
ccctttttgc ctgcgttcaa aaaaagaagc aaagttcgaa gcgggaaagc tcgaaagata	900
aacgaaccaa ggcctcgggg gagggaaaga cccttatctt cctgtatctc tccatcttcg	960
attcaagaga gagagaacac ctcccggaca tcccgttga ttgcatcgga atatcccgag	1020
gttatattct ttatttcata cgtcgaacaa atatggcttt tcgccgtgca gtaaagtgtt	1080
cggataaaaa aaaagccgag agccgaaacc gaaggcgata tatggtcttt cttcttcccc	1140
cgatcggata aatctccgac accggttcgg ttgcaaaaaa cctaccttca accaattctc	1200
cttaattttt cgggcaaccg tttattcaat cgggtccgaa tccagaaagg aggtgttcca	1260
gccgcacctt ccggacggct accttgttac gacttagccc cagtcaccgg tattacccta	1320
gtggccccctt gcggttacgc ctttcaggta cccccgactc ccatggcttg acggcggtgt	1380
gtacaaggcc cgggaacgta ttcaccgcgc catggctgat ggcgattact agcgaatcca	1440
gcttcacgga atcgagttgc agactccgat cgaactgggg aagggtttag agattcgcat	1500
ccggtcgcgc ggtagctgcc tttgtccctc ccattgtaac acgtgtgtcg ccccggtgt	1560
aagggccggc tgatttgacg tcatccacac ctctctcag ccttacgacg gcagtcgtgt	1620
agagtcctca gcgaaaactg ttagtaacta ccgatgtggg ttgcgcgctt atggcactta	1680
agccgacacc tcacggcagc agctgacgac aaccagcagc acctacatag aagccccgaa	1740
gggaagacgg ttttcaccat ccgtatctac atttcaaacc cgggtaaggt tctcgcgta	1800
tcacgaattt aaacacatgt tctccgctt gtgcggggccc cgtcaattc ctttgagttt	1860
cacgttgccc gcgtactccc caggtggatt acttaacgct ttccgtgtgg agcttgacgg	1920
tatatcgcaa actcctagta atcatcgttt actgcgtgga taccagggtta tctaactctg	1980
tttgataccc acgccttcgt gcttcagtg agtcgcagta tggcaagctg ctttcgcaat	2040
cggagttcct cgtgatatta tgcatttcac cgctacacca cgaattccgc ctgccgccac	2100
tgaactcagc ccggcagttt caacggcagc ctgaacgttg agcgctcagg tttcacgctg	2160
acttaccgaa caacctacgc accctttaaa cccaataaat ccggaacgc tcgcatcctc	2220
cgtattaccg cggctgctgg cacggagtta gccgtgtcta ttcgttacgg acattcaatg	2280
caatactcgt atcgcccggt attccgtata aaagaagttt acaatcctta ggactgtctt	2340

ccttcacgcg	actggctggt	tcaggctctc	gccatttgac	caatattcct	cactgctgcc	2400
tccgtaggag	tctgggtccgt	gtctcagtac	cagtgtgggg	gataaacctc	cagttcccct	2460
acccatcgtc	gccttgggtga	gccgttacct	caccaacaac	taatgggacg	catgcctatc	2520
ttacagctat	aaatatttcc	ttgtaataca	tgcaataata	caagtgtatg	cggtttttagt	2580
ccgtctttca	acgggtttcc	ccctctgtaa	ggcaagttgc	atacgcggtta	cgcaccccggtg	2640
cgcggcgccc	atcaacctta	gcaagctaag	atcatgctgc	ccctcgactt	gcatggttaa	2700
gcctatcgct	agcgttcctc	ctgagccagg	atcaaaactct	ccacgtcata	tttgtgtttg	2760
tttgcttctg	tttttctcgc	tcagacgccc	attttaccct	ttggataatt	cgatttatca	2820
ggtagtagac	ctcggtttct	tttctctctc	ggtcttttctg	tttttctctt	tgacagagta	2880
tatgtcctcg	tgagagacgg	tttcgtcaat	aacagccggt	aaatcggccc	tcctctctgc	2940
agagggcaga	aatcctgcaa	gaaatggcga	agcccttctc	tctccttctg	tactacactt	3000
ttgttcttctg	tatgaacaat	gtcaatgata	gctgtctttt	atcccctatc	ctcccacctc	3060
acggcacaga	gccgatcaag	cagcgggaag	gggtgcaaaa	gtaaaacctt	tttccgaatc	3120
ggcaaaatca	atcggccttt	tttcagggct	gacgctcaag	aaaaagctcg	tcgcctgata	3180
ctcccctaaa	aaaagaatcc	cgacgcgctc	ggcgggaaca	ttcctctatc	aatcggcagc	3240
aatcgctttt	gcggtcacaa	aagtacgcct	tttttcttta	cagcaaatct	ttcaaaatct	3300
tttttcaacc	ggttcgacna	aaaaaaacag	ccccgaagaa	aaggactccc	tcccaagaaa	3360
gaagacaaaa	gggagcggat	aataatatgt	tcgcgcgcgt	aagaacaatt	aaaaagaccg	3420
caaacgaaaa	aaatgagaag	atgttttttc	cctcgacaaa	aaaagatttt	ttgaccgaat	3480
gttgccgggtt	ggtccggaat	aaaggggtaca	agggaaagag	aagggtgtga	aaaaaacaga	3540
ggcaccaatc	gcacaagccg	aaactcgaac	cgaaaatgcc	caaattctcaa	acccaaatcc	3600
caaaa						3605

(2) INFORMATION FOR SEQ ID NO:148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic).

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

tggttcggac	gacctttttg	gttttcctca	cttattccgt	cgtacagctt	cgttctcgct	60
gatgcaggac	ggtcgggtag	agatgggaga	cgggctgaca	ttctctattt	cgggtgtgaat	120
ctgatcttcc	tcatgttcag	ctacctgtcg	tctatctgat	ggagcgtgct	ttcggctacg	180
tttccaatat	cagtttggtg	agctgagcga	cgtcaatacg	ccgctgctca	gtcagctctt	240
cggaagtggg	cgccgggcac	ctttcagcat	tcgatccaag	tgtccatcct	cgctcggagg	300
cagccaccaa	gatcggagca	gatgtacagc	ttgtacgcac	cgggctctct	atcatgatata	360
aggaaaaatt	aagaacccat	cttatttcac	aggaatcagg	gagcagagaa	tccgcactcc	420
aaattgcctt	ttgacgagag	tctcgcatata	tcattcgtca	tgtgaccgat	ggtattgcct	480
tggcgcagaa	caccgtttgc	cggactccgt	tatcgatttt	atccggacgc	atcacggacg	540
ggtaagacca	aatacttcta	taattcctat	tgcaatcagt	atcccagaaa	gaagtggatc	600
ccgagttgtc	acttatcccc	ggcccgaatc	cattcaacaa	ggagac		646

(2) INFORMATION FOR SEQ ID NO:149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

acgctgtcgt	ttttatttca	attgcacccat	acaggaatta	aaaccgcctt	atgctcgacg	60
acgcagacga	atcggatcat	ttcaattgca	ccatacagaa	ttaaaacgct	ttggctgcga	120
attcccttac	gggccaatcg	aagatttaaat	tgcaccatac	aggaattaaa	atgtatccat	180
tatactactc	ccaaaactga	caactagttt	cggggttatt	tggcttgttt	tttaggtat	239

(2) INFORMATION FOR SEQ ID NO:150

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 697 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ctgacatccg	ctcgaacccat	ggacacctcg	tctatgataa	tcagatcgaa	cttcggatca	60
gtttcttgtg	ttcggtcggtg	tagcgaaaca	catcgaaccc	cgtctgtcac	gagtactcaa	120
atcgggatcg	ttcggcgga	tccggcgaga	ggcagtttga	aaaacgagtg	gagcgtctgc	180
cctccgacat	tcagtgcgca	aggnccggta	ggcgcaagca	cgacaaactt	cttatgcgtc	240
gtagccagat	atgccgaagc	agtgtggact	taccggttcc	ggccttgccg	gtcagaagag	300
gctttgggtc	gtgcgttcga	tcaggctgag	cacatagccc	atccctcatt	ggcaaggctc	360
attgcgga	ggccctcctc	tctctttttt	gtttgcgacg	aggcatgcgc	tcaggggctg	420
ttgtatcg	ctttgacttt	cgcttgccg	gtttgctctc	gttggtggaag	cgatctacgg	480
ccgtcaccca	taagtataat	cggctgaagc	atgggaagtc	gggaaggcga	atgctgtttc	540
gggagtaatc	acccaaatgt	tttcagcttt	gntggatcgt	ttcttcaccc	atgacggaag	600
gcatagacca	cgaagtagga	agctttgaca	gggtcggatc	atcctttcag	cagccnaatc	660
aggtgaaaac	tgatggcaac	caagcggatg	cagcctt			697

(2) INFORMATION FOR SEQ ID NO:151

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

aggtaaggga	tttaggccca	acgcttagta	actttgcagt	aaacgataat	cggtattttca	60
aggctttgaa	aacatacatt	tcgagagaat	aacatatctt	cttcggaacg	aattttatttg	120
cgtcagtgca	aatagcaagg	tatgtctgcg	ttaccgcgaa	ttatttcggt	aactcaaaac	180
ccttgctcct	gcagaggcag	aacacctccg	aagtccggtgt	tcttgatag	aagttttcgt	240
tgtctgattg	gctattttat	cgtgaacgct	ctctaattga	tttcaattat	gtttgcacgt	300
tctattttcca	gaagagagaa	ttacaaacca	ttaaaatcca	aagaatgaca	aagagaaatg	360
tggggcgacc	tcccaagaat	gaacgagccg	acattgttgt	atggttcgat	ttacggacac	420
agaatttgct	cgtttcctaa	cctattcgag	caatcggggc	ttcaaaatag	agccgctttc	480
atcaaggcaa	ggtcctttaat	gagacctttc	gagtataaaa	agtggatcgt	tcgttgctca	540
ttactaccaa	aaactgacaa	ctttgtacgg	acaatttcgc	agtgtcgggt	gaattataac	600
caaactgtag	tcgctttgaa	aagcaatttt	acggagagaa	agcctttgcg	atgctcacta	660
agttggagaa	actgacactc	gaattgctat	tattggaggg	gaaatcgtag	aactcactcg	720
taaattttcaa	gagaatggca	acatcggcaa	tagacatatt	atatcatatt	gctccttgca	780
tggagtaaaa	atcagaacttc	cctttttatt	gaggaagcct	gattaaccaa	tgcatattcg	840
ctttttgaac	ttgcgcgcct	tcagatcgct	ttccaccata	cgttattaag	tttctcacgg	900
agttcatcaa	gaaaataggt	gcggtctatca	ttttgcgacg	tttcatgttc	atatagacgt	960
tgtagctggt	ctttatcgcc	ctccgaagat	cttcgagag	agcgtctgcc	agttcctcta	1020
cacctatttt	ccgttggtga	tactgttgca	agtgtcgaga	gcataaagga	gttcaactat	1080
ctgttgcttt	gcctgtccaa	cagagtttct	tagcaggtct	gactggcatg	caggaagaag	1140
tccctgcatt	cgcattttca	gtaattcaag	ctcggttcaa	tgacaaagag	cagttctgat	1200
acattttttc	ccctctccgt	ccattaatct	cccttttgca	aaggttgtag	gcaaaagcgt	1260
gtataacgga	gggtcgaaac	aatgagacta	aatctctttc	tgcatcacat	agggaataaa	1320
tctcagaata	aagtgtctg	acgctttttg	tatctgtcct	ttttagagac	ataagagatt	1380
attgtcttaa	agtcttcagt	ttgagtaagt	cttagcataa	tatatctttt	atgttcaaca	1440
ttgtagattc	tctgttgtag	gatgtgattt	tgacgaattt	ccctatgaat	ttgaatggca	1500
aagaacagtg	tcatacaagt	gcaaagacgt	cggctaccgg	ttgtgcataa	agcactccgt	1560
tcaatcccaa	tatgatggga	gcagcaatat	tacaggaata	aagaagagtc	cctgtcgcca	1620
atattgagca	aaaggctctg	tcttgctctt	ccgatttgcca	tatatatgtg	gaatacacia	1680
actggaagcc	gaaagtgaac	aacattagcg	tattgtctta	agggaatttc	gtgcaatttc	1740
ttgcattggt	tcgtctttgc	cgaacaactg	ataacaggag	aagcaaaaac	gagtatgaaa	1800
gtgctccaaa	gtaacaaaat	gaggttggtc	gtatcaagga	acaacgtact	gcctctttta	1860
acttttgaaa	ttttctgccc	cgtagtata	gccagccatc	ggttgagatc	cttgacaaat	1920
ccgaaaacca	cgttcgttcc	caatgtttac	attttcagaa	gatgcctact	gctgctacag	1980
cctctgcccc	atattttacg	gcagctctcg	caataaacta	atcgaaagtg	tttgaggag	2040
ttgcaaacag	agcattgaat	acctatcttt	atgatgtcca	agtacattct	tatcgttggg	2100
acgaacaggc	aaacgaaact	ttcacctctg	ctttcataaa	gaagcagggt	taaatgttgt	2160
tgtaatgatt	cttgaaagaa	tggttgccca	cgcagcacct	ttcaccceca	gccgaaagca	2220
tagataaata	gaggatccaa	tgcgacattt	ataaagaacc	tattatcatt	gccgatgcag	2280
acgttttgaa	gccccctgag	aaatataata	ttggacatcg	acacattcaa	cgttcctatg	2340
acacaactaa	cgtgaacagt	ctgccatag	cttcgcgtaa	gctcatcatc	tcctcgtttg	2400
ccccatgaaa	agcagaattt	ctggtagaaa	cgcattgcat	acaagggcaa	gagagcagct	2460
aaaatcacag	aggatgacac	tgagacggaa	gctacctgac	agccttgaca	atttgcttcg	2520
cacccaataa	gcgagatata	tacactcccc	cccaacacca	aacatcagcc	ctatcccaag	2580
aaacaccaac	gataaaggaa	aacaactgat	acggcagcga	caggaagagt	tcccaaacgt	2640
gcaaccagaa	agtatctacc	acattgtata	ttgccataat	cagcattgag	atgacatagg	2700
tatccccaac	tttgtcaggg	atttcatcat	acttcttctt	tgcaaatatt	cacagcgttg	2760
ttcatcctta	taactctgat	cttcttaagt	aaaaaattct	gctgcaaagg	tacaggggga	2820
tacaggtcgt	cacaatagac	aacaacgggt	ataatagcac	tattcgtggg	aattctttct	2880
gaaaagcggt	gagaaactcc	tgcaaccttg	gtaaatagtc	gtgtgaagta	ggagtaatcg	2940
caaatcccaa	accttgttgt	atctctttta	cagaggttgt	tgtatagaca	attgtcgctt	3000
agcttgcaag	atgatttcat	cctgaatatt	ccgacttaac	tcgttcccca	aacagcattt	3060
atcgcttcat	tcaggtaggc	aactgtttat	tcaaacgttc	ggcaagaa		3108

(2) INFORMATION FOR SEQ ID NO:152

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 575 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...575
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

ctcagaaata	tcggtctacc	atcggtccagt	atatcagctc	tcaggtagtc	cgagtgtctca	60
agacatggca	aatgcagaag	tggagatgca	gaaggtagca	ccgagatgca	acagcaaagc	120
gatgtggaag	ctcttgcccg	caactatcgg	acaagttcgt	atctccttct	ttcctgactt	180
cggcggaact	cgatcgatga	acctcggcgt	aagcattacc	gaatttatca	agactgcgac	240
accggcgaag	tcaatatccc	gatgttgagg	aataaccact	attccttggt	aaagtgggtg	300
ctaaaaagtc	cggattcgaa	tcgctcaatg	tggcaatcat	tgcttggaat	ccgccaatct	360
gtctaaggcc	gacagccttt	gcaacgcctt	gatgaggggg	gcgacttcgc	tgctgcagct	420
cgcacgttca	gcgcagatcc	tcctctcggt	agacaggcgg	tgtactcacg	ttccccaacc	480
agttttacaca	atgcccggat	tagcaattat	taccagaagg	ctatgggctc	agcagcttga	540
nccttcgaca	cctctttttt	agcgggtcca	tcgaa			575

(2) INFORMATION FOR SEQ ID NO:153

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 522 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

ggattcgctg	cgggtgcgcg	acaaagcctt	gctgctcatg	ttctattcga	tgacttgctg	60
gttcgggata	tagcggaagt	gaccggtatg	tcggagttca	cgtgaaggtc	aagctccacc	120
gacttcgcac	caaactctat	aaaatgagag	aaaatgaaac	agaatataga	agacaaaaag	180
ctcaaagagc	tgttccacag	ttacccaaac	agccgggtcg	gactcaaaca	acgcttcgac	240
gtgatcgctg	cgtacgagag	gaagctgctc	ggcgcgaaac	gcgtgcccac	cgctcggtcg	300
catcgccatg	gtgggagtat	gtgtccttgc	ggtggttgct	ttctagtatt	agactccaag	360
ggattgttta	gcgggtctcg	tttcgatagc	ttgttcaaga	ccgatctttc	cgcaatccct	420
tcgtcggttt	gggcagcgat	aagccggagc	acctctgatc	ttcctgtccg	tggtcatcct	480
cttcgggcta	tcctctacga	actatatcgc	aacacgaagc	at		522

(2) INFORMATION FOR SEQ ID NO:154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

tccccgggaa	atccctcttt	tcagtatgca	acactccgga	aataatcgcg	cgatatagtt	60
gctcttgccc	gttccctcac	cacccgtaat	gcagaacaat	tgtcgtagg	tcccaaagga	120
acgtcggtca	cggaaataac	cgttttgaac	gatcgggcgg	attgttataa	ttgatttcac	180
acgaacttaa	aagcatatgg	tttgtgtata	taattgttcc	aaatggtcgg	atatcagctt	240
cctgaatctt	ctgtgctgtt	tcccagcttg	aagtaatcgg	agatatcttt	ctctgtttgt	300
tccccgataa	aggcaattcg	atccgctgta	atztatggtg	agaaaacgtt	cgcaccagcg	360
tgtagaggct	tttatgccc	tttcgtccat	atgtacaaaa	agaaaatatg	cctgaacctt	420
cgtgcaagca	tttcgatgac	gattcttcga	tattgcctgt	ctcactgttg	aaacagatgg	480
catggaatcc	tgagaggcaa	gggataatac	atctttctct	cctcccgtga	tgaaaagtaa	540
tctcctcttt	gcggaagtgt	ctccatccc	aacacatagg	tttccggcat	attccccctg	600
aaacgaaccg	gcattgactg	aaaggacgat	atatcttaca	tagtctttgc	gcaggaagcc	660
gaagatcggc	tctt					674

(2) INFORMATION FOR SEQ ID NO:155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

ggccgtctcg	gacagctttc	ctgttcctgg	caacggactt	tgccacgctt	gcgcccagta	60
gtccgctccg	catacttttc	ctttcgctct	tgtcagaagt	tggcgatgtt	ttgcccgcgg	120
ccgcaaccga	tgtcgagaat	atcctcccac	cggacggtcg	gatacattcg	tcgatgcacc	180
agagagccat	tttatttggc	cgtagtctcat	ccccgcaagc	atcatttttc	cccagaaatt	240
gttttaggtc	tgcggaatt	gcttatgaac	ttcttgaaca	gtctcatctt	ctatcagcag	300
ctaaaagaac	aagaaataac	gaggagtctt	ggccttgat	tcgggtattc	ctctccgtag	360
gtctcctcac	aatagcgttc	ttctcccagt	ataggaaatg	tgtggcaatg	atgaagggta	420
tcatgacgag	tagcatccac	acgaggcgga	agcgatacaa	acg		463

(2) INFORMATION FOR SEQ ID NO:156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ttggggattc	acattacccc	tgctgcggtc	gaagtccgta	gcgtgtacag	aaccacgagc	60
ggcttccctg	taaccgtttt	ggcatgtatg	ccggccggta	ggtgagccag	tcgtgggagt	120
ggatcacgtc	gcacggtatg	gtacgcgtat	cacgcctgct	acgatggagt	aattattgat	180
ctcttccagc	agattgccgg	atagcgtccg	gaaaattcga	tacagccgag	ggcatccgnc	240
ttcttttagc	aaaatcggca	taaatgttgc	tgccgagatc	ctcgtatgtc	cggaatccat	300
tcggttgccc	aagagttggg	tcacccgttt	nggtggggac	attttgata	ctatgggagt	360
gcaagttggg	gcctatgagt	cggaggaaac	tctgtcctcg	tctccccacg	gtttgggaat	420
ggacgaaagt	aatatccatg	tgggctgcat	g			451

(2) INFORMATION FOR SEQ ID NO:157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

gccaacgctc	ggaaaacatg	ggcgatccca	gtaccactac	agccaaggcg	catctgccag	60
aaaacgggag	ccatgctgct	tcacagggct	tagcacttca	gcttatcacg	gtcttccacc	120
agtatatacc	gggtctgttg	cctgttctgc	cggacgggagc	gcgcagtgcc	gctgtcatca	180
gagcctgcac	gtcctcggga	aaagctgctc	ttcggagaat	tgtcggatag	agcggcgatt	240
ttctataact	ctgcaaatga	tttcatatag	acaaagatac	acaaatagcc	ctctggctat	300
cttttcatct	acacgagaaa	tagcagcaag	gcagtatgcc	ggtttcctcc	tgcagtacgc	360
ccgatcaaac	ccgatggact	ccactcataa	aagactcgat	cacaaacaag	aaaaagtcca	420
tttatgatcc	ccaaaaaatg	tgcgcgagaa	aatttcactt	ttggagtcct	ttgaaaaaaa	480
ttattgacaa	ccctcatttt	ttcagaggnn	tctatatcgg	ttttactcgt	cgccgttcgt	540
tgttttcttt	ccggccggga	aaagtttccc	cgacagccga	caaaaatatt	tttccggccc	600

gaaaagctct	atccaaagcc	ttcggatatg	tatccaagcc	tttgtacaca	tatacgaaaag	660
ctttgtttat	atatccgaaa	cctttgataa	agaattggat	tatggctttt	tcaacttttc	720
cgtactgcag	aaaaactttt	tccggccggg	aacgattatt	tnntttttatt	gctgtgacct	780
gtgtgtggat	actacctccc	acaaacgagt	gttcgggtaa	agtatccgcc	tcccaaaggc	840
atcagtgcag	caccgaatcc	tttcgcatct	gtgcataaac	ctccgggcaa	acaccctttc	900
gagtatgcat	acagaggtgc	aggaatatgg	ttgtcgttgc	ggtgggttag	atztatcttt	960
gccgcaaaag	aaatccttat	aatatggngt	acaaagtttt	tttgtcgcctc	tgcataggtt	1020
tagccctgat	gcaagcgca					1039

(2) INFORMATION FOR SEQ ID NO:158

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...643
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

agccatttca	ctgtgtccga	tcgcttcgag	acagcgtgcg	gcttcgcaag	atgactgcgt	60
tcatacagct	cgtgtggata	gtacggggct	gagacagtga	cagccaaaga	aaacgatgct	120
gaagagcagc	caaccaaacc	ggcgacttcc	ccacatatcc	aagggtataat	cattcaaggg	180
aagggcagtg	tcgggggtttg	cagcagccgg	gctttcaggt	ttgagcggat	gcgtgtcggg	240
gataggaggg	ttttttcagg	acagaataca	aagtcctgtt	cgctctttgt	cagcaggccg	300
gcaggagacc	caaatcgccg	atcatgcttc	gtactacggg	tggggtacgt	agggcttctt	360
ccctatgatc	tccgggtacca	tctcgtgacc	gggttgaaga	gcaagaggcg	cggatgcttt	420
atttcgcgtc	gaagtcggcc	gtatctccat	ccagtcgaca	gtattccatt	tatatatagg	480
ggttggtaat	cgatgagtag	agagccaatg	ctctgcacgc	tctatgaggt	agaagatcgt	540
gcgtttttat	ctgtacgagc	ganaagggtt	ttgcattttt	tcttttcgacc	cagctgatag	600
ccgtcatgct	atccgaatag	ggtggggggg	ggtttttttt	ttt		643

(2) INFORMATION FOR SEQ ID NO:159

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1144
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

gcgaaacat	tcccgacttt	catatatgga	gttcaggctc	ggccaattaa	cgatgcctta	60
aagactgac	cgggtgggacg	cgctgaggaa	gttcgttata	catcgatgaa	atagaaaagc	120
gagcagagga	aatgtgcaag	gcggaactct	gcacgtgag	ggaaaactgc	ccaaacgggt	180
atgccactgc	gacacgaggt	aaacaacatg	cttttcgacg	aagacggaca	tgtactttgc	240
gtcatgacct	cgacaccgtg	atgccgaact	ttattttctc	cgactatggc	gacttctccg	300
taccggagcc	aacaccggcg	aagaggacga	caaagacctt	gacatgtaaa	cttcgacatg	360
gaaatcttca	aggcctttac	cgaaggatac	ctaagggggc	aagctctttc	ctcaccgacg	420
tcgaaataga	gaatctcccg	tcgccgcagc	actattttcc	tatatgcagt	gtgtgcgctt	480
cctgacggac	acatcaatgg	cgatacgat	tataagatca	agtaccccga	acacaatctg	540
tacgcactcg	tcgacaattc	aggctgctac	agagtgtaga	ggactgcagc	tgcagatgca	600
agctttttatc	gaccaatgtc	ttaggtatta	agctctttacg	tgtaccaatg	tcagctacag	660
acacactttt	ctaaagacaa	gaagaccac	cgacttttagt	ggctcttcgc	acaatccttg	720
cggatacgat	gaagcggact	taaagtcgct	taacgttcaa	gtttttgata	taaaagttaa	780
tcataaagat	tatgaactca	ctacttgcca	tccacaaact	ttattaaaga	gaacgagaga	840
aatgcaatcg	gcattttctc	cgttttgcaa	agacgacgta	ctctccggtt	aggacgacct	900
tcgcgtccgtt	taggtcgacc	taatcgctct	gaaggacgac	ctatttgctc	cgcaaggctg	960
acctaaccgc	tcggttaggt	gacctgactt	cttgtcaggg	tcgacgtatg	cggttttatc	1020
ccttgtagtt	gcggacgaga	aggggggtac	gaactggaaa	acaacccttt	ataaatcacc	1080
gtttttcaaa	ggtctcatgc	tgtggagaag	agactgggtga	taagtattcc	tctccgatgg	1140
atgg						1144

(2) INFORMATION FOR SEQ ID NO:160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

cttctttgca	gctctcaact	ctgccgtatt	tagcgacggc	tcctttgtga	tatcccaaaa	60
ggcgctcagat	gtccgatgga	gctttctact	tatttccgat	caatgcagcc	aatacaggac	120
agttcgaacg	aacgctgac	gttgccgtga	ggattcttat	gtgagctatc	ttgaaggctg	180
tacggctccc	cagcggatga	aaatcaactt	catgctgcaa	tcgtggagat	cattgccgag	240
accaagcgga	agtcaagtat	tctacggtac	agaattggta	tcccggagac	aaaggggtaa	300
aggcgggtatc	tacaacttcg	tgaccaagcg	agggtgtctgc	aaagcgacaa	ttcaaaaata	360
tcttgacgc	aggctcgagac	aggttctgcc	atacatggaa	atatcccagc	tgtgtcctgc	420
gtggcgacaa	ttcgatagcg	ggttttactc	cgttgcgtgt	accaataatt	tccagcaggc	480
agatacgggt	cgaagatgat	ccatctcggc	aaaaataacc	gtagccgtat	cgtatcgaag	540
gtatatcggc	cggttcaagt	cagaacagct	accgaggatt	ggtcaagact	ccaagaatgc	600
ggtcaatgct	cgtaaccatt	cgcaatgcga	cagtctatgc	gtagcgatca	ctgcggtgct	660
catacatacc	cttatgcgga	tgtccaaacg	atacggctat	catcgagcat	gaagctacga	720
catccaagat	cagtgaagac	agatattcta	ctgcaactaa	agaggaatcg	gtacggaaga	780
ggcctagggc	tgatcgtcaa	cggttatgcc	aaagaagtga	tgaataaact	gctatggaat	840
ttgccgtaga	ggcacagaaa	ctacttagta	tctctctcga	agatcgggtg	gataaagatc	900
tctgcaatca	tttcaaaaata	aaaaacactc	agtatgctta	agataaagaa	cctccacgcc	960
acagtacagg	gcaaagagat	ttgaaaggaa	tcaatctgga	gatcaatgcc	ggagagattc	1020
atgctatcag	gggcccgaacg	gatcggggaa	aagtacgctc	tcttccggtt	tggtgggaat	1080
ccctcctttg	aagtcacgga	aggagagggtg	acattcaatg	gaatcgactg	ctcgaactcg	1140
aaccggaaga	acgtgcacac	ctcggactct	ttctcatttc	caatatccgg	tcgagatccc	1200
gggcgtcagc	atggtgaatt	tcatggggca	gctgtcaatg	aacataggaa	agcgatcggg	1260
gcgaaccgcg	tatcgcaagc	gacttcctca	agatgatgcg	agagaagcgt	gccattgtgg	1320

agcggacaac aaattggccc agccgttctt gtgaacgaag gcttctccgg tgagaaa

1377

(2) INFORMATION FOR SEQ ID NO:161

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 989 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

gttcgaggta	gcagaggtag	tgtcccggca	cgcagtgcat	caggaagaag	taaggccgaa	60
gatacagcacc	atcagttttc	cactcatagg	caccaccaa	gcataatagcc	tacaagtatg	120
ccgaatatgg	agctgtat	gagcaactta	ccttggtgca	gaatccgggtg	atggccgttg	180
cgattcctat	gagaatagta	caaggggaag	aatagccaac	gggaaacgat	aagccagtat	240
gctcatgccg	taacattcag	tccgatgggt	atccatgtcg	tgtctataaa	tccggtatct	300
gtgtacgtgc	atgtgcttct	ttctgtctct	tcctattaca	aatatgggtca	ggccccctcc	360
tactatcggg	atcagcatcc	acagataaatt	ggtcgataac	cgatatgggg	gtaaacgaaa	420
aggatcagca	gactcgtggc	aaagtgcgct	atccccatat	caggctgggg	atgcctgctc	480
cgcggtacag	cgtttacgtg	tctgttcgag	catcttctcg	atcatctgta	cgctctcttg	540
gggtgaagct	gtttttcttc	catttttttg	ctatccgtta	gtgggttcgat	tccatttgaa	600
aatgtctccg	caaggcattt	cttaccgctt	ccgatgcaat	ataaattagt	ttacagtata	660
aaccaaatat	aaatgaaaga	attttttcgag	agagggagaa	gattaaggaa	ggcgagagaa	720
tattttacgc	cggcgatata	aaattggaag	acgatggaat	aaggcttcac	cggtgcaggg	780
gataaagccg	aggagaagat	tctcggaacg	ggaagcggag	aagtccggtc	gcaacgacgg	840
aagtcgcgac	gtgcacgaac	aacagcctgc	atatggcgga	attgccgggtg	agcaagaaaa	900
ccatggcgga	gaggaaatcc	agtagagcgc	gatgcgcgatg	gtgggcttga	gggctgtttc	960
cggcaaattc	ttgtacagca	cagcagatt				989

(2) INFORMATION FOR SEQ ID NO:162

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1093 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1093
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

aacaggggagc	caagcgtttg	cgggcccctct	tcttctctga	ccacgaggaa	tgccacgggc	60
tggttaattat	gtgccgaagg	agctatgctg	ccggcttcag	gatggccatc	aacttctctt	120
cctccacagg	acgatcgata	aacttgctac	agatctgcgc	gtgcggaaga	aatcttctat	180
caaacgaaaa	tcttgagaat	ctgttttcatt	atatctcttt	ctctatttta	tagttgtttc	240
tgtccaagcc	tgacggctga	tcattctcacc	gacaaatccg	gttaggaaca	gttgggtgccg	300
ataatcatcg	ccgtcagcgc	gatgaagaaa	taaggccgat	ccgcacaaa	ggtgcctgcg	360
tatgcatgat	tatagcggac	aacttattga	caggacaacg	gccaaagcta	tgaagccgat	420
taggaacatg	cctgaaccga	gagcccgaag	aagtgcacgc	gcttgcgctc	gaacttgctg	480
ataaaccaaa	cgtaagcaaa	tcgagatagc	cattgaaaaa	acggctgata	ccgaacttgt	540
cgagccgtat	ttacgcgcct	gatgctgtac	taccttctcc	ccgatgcgcc	gaaaccggcg	600
gatttggcca	aatatggaat	gtaacgggtg	atatcgtgta	caactcgata	ttctccacta	660
cctcgtgtcg	gtatgctttc	aaaccaaatt	aaaatcgtgt	agcttgatgc	cggacagctt	720
tcgggctgta	gcattaaaaa	ctttgagggc	agattcttgc	tgaacagagg	atcgtaaccg	780
ttaccttcca	accgcttacc	aagtcataat	ccccctctgt	caccatccgg	tacgctccgg	840
gatctcatcc	ggactatcct	gcaaatccgc	atccatcggt	atactacctg	ccccctgtgtg	900
cgggcaaaac	cacattggag	accggccgac	tgccgtagtt	gcggcggaat	ttgatccctt	960
tgacctcggg	atgctctgct	gcaaacgttc	gatcacactt	caggagccgt	cggtacttcc	1020
atcatctaca	agatgacctc	ataggaatag	ccatgctcat	tcattacacg	cctgatccag	1080
caaaaagttc	ggg					1093

(2) INFORMATION FOR SEQ ID NO:163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

ggctacgatac	ggtagcgtgg	gcaactctga	ccatgctctg	gaaaaatcgg	aaaggccggg	60
cgttctcgct	ggttggtgctg	cagacctcac	aaccgagggt	ggtgatgaac	cctgtggatc	120
accccatggg	tggtggtgaa	ggtcgccgct	aggaggtcat	ccccgttcac	gcaagggtct	180
gtatgctaag	ggcttgagac	aagagctccg	aagaagcatt	cttctaagta	catcattgag	240
agaagaaaaa	gtaatctgat	ttaatcaaa	aaaattatga	gtcgttcact	taagaaggtc	300
catatattaa	tctcaagctg	gaaaagaagg	tcttgccgat	gaagagagcg	gcaagaaagc	360
tgctattaag	acgtgggctc	gtgcttcaat	gattctcccg	acttcgtggg	acataccatt	420
gcagtgcata	acggaaataa	atattattcct	ggttttggtg	cccgaaaaca	tggtggggca	480
taagttaggg	aagttctttt	ctacacgtac	ttttc			515

(2) INFORMATION FOR SEQ ID NO:164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

```

gggccaaaagg ttgcgaattt gccgtactcg tctctctgct ggagccggaa acgagttgta      60
caacggcggt attgtggata tgtcctacag atacgataga tgtatgtgat tcgtccgcag      120
tttttcattc cgatgataac cctcctgtgc agacgtccaa aaaggggtctg gagtacagac      180
agcagcttgc catcgccaga aacaatccat cgatgtttcg aatttcgaga gtcagctcga      240
agatttcggg aaagattcgg taaaaactat cgccttgcca gcgaacgatt caaacggcta      300
tcgacgagat agacaagtcc atacagcact tgaataaaa caagaagcct tggtcggcag      360
cgagtacaac ctccgccttg cgaacgacaa ggtgaagccc tcaccatcaa gaaactgaca      420
cgaggcaatc ccacgatgaa acaaagtctg aagaagccc cctcgccgaa gaatgacgca      480
ctccgggata aatgccaacc gtacatctcc atgtgtatta taacaatttt gcgcaaagca      540
tctgaggtgt actaataaaa tgtcagtcaa agaatagata ttgacagagc gaaacggatg      600
ccggcggaagc gacagagaaa aaagtaatgc cggatggaag ctgccttcgt atcgaagata      660
cggcggtgct gtcagagaaa cagatcgacg ggtaaaactac cctctccaga tagagggcat      720
gagccggagc cgaaggcccg caccgctgcg atcctgcatg tcgatgatgt cccgaaagtc      780
tgtgtggata gcttgcccgt cccacatgg aagagcgtgc cgactatggc acgaccatat      840
tgcgcaggaa tctgtccgcc gtgatggaaa agacccattg acggtctgtg caagtggcat      900
ccatcgggct tccgttatac ggcagttggt cttttgacgt cggatgacg tttgctgaag      960
ctcgtgaagt cgatatatcg ggaagaagag ccgccgcttc attcatgctg ccgaagtcca      1020
gcttacgatg gtcttcagca tcaagccttc cataaaagga tctttctgct cggtcagaag      1080
tagtggttaag ttcgggagat ggcacgaa cgcgcggtgg catcggttg acaggagcca      1140
ttcgggtatat gacgatgtcg cgtgggagga gtttatgagc ctttctgtca ggggtggcagc      1200
ttccgccggc gtatcgcagg gaagacggca tgtgtacca tctcgtgggc atgaactcct      1260
gcacggttc ttcgcgtccg acgaccccg caggttggcg cagatggta gatatggctt      1320
ccttacggtc tgctgcacac cgggggcatt aggtgcgtt tgccagccgc tgagcgagtg      1380
csgttgtatg ccagatagat gaagaagcgc gccatttatt attctt      1426

```

(2) INFORMATION FOR SEQ ID NO:165

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

```

cggcgatttc ctaaataatac gataaattat agagtttttc tacatagttt catttaatat      60
ccagtgccta aaattctggt aagttttttt tgtgttgga gcacttttgt attaaaaatt      120
aaagcaattt ctccatcagg acaaaaacca tggatttatg tagaaatggt aaaaccatct      180
ctttgccaaa attatatga cacaatagtc cattatcgat ttgacaatt tcttagtccc      240
aaaagtgggt tcccaataac caaattcacc ttttcaaaat catcaggatt cactccccaa      300
tagtatcccg acaccacaga ttttttcctt ttttttcttt aatgaaatat cgttaggatt      360
atctatcaaa taagggaatt tattggtttt gttatccaga gtttcttggg gtttaagatgc      420
tcaactaatg ccaaatatag gtgaaagctg ttactttaat agctaattga tctatttcga      480
ttccaaagat ttttttacc agtatatcat taagttcttt gaaggttatg accttctctg      540

```

```

atattatattt tccatntcct aataagtctt ttataacttt cgactaagaa attccagaac 600
cacaagccgg atctaaaatt taccatggga atttgggtcat t 641

```

(2) INFORMATION FOR SEQ ID NO:166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

```

cgcttttact cgcacatga aatataaatt ctttatattt gcgttggttg aaaatgctaa 60
ggtacgatat tttgattggt attttaatgg gatcgtaaca gggtaaatcta aatagcaaaa 120
tgatttggtca agataagagc aactaaagac taataatata gggcaagaaa taatgcccg 180
ggataagtct gacagaggaa atcagtagct aagggtcatta ttcctctcgc cataggcggt 240
ctgctcttct ggggtgggtgt accgcaaaat ggattttctcc gccattggca agatgtccgc 300
gacgggtgtca attactacat catagctttc tctctcttgt tcgattggcc gccactgta 360
tacgcggcct gcgctggcaa ctctcatag aactttgggt tctctcctc cgcgaaaat 420
caatgccatt ctgactactt tggcaattac acgggtcaata tggctctgcc ccgtgccgga 480
gaattttggc atgcgcggaa gaaagccgct acgagaaaat acctttccc caactnctcg 540
tacgcttttt atggacagga tcatggactt ggtgatggtc ggacttatac attgagtatc 600
atgatgggct ttcaagggtt tttctcgcgt tttttcgtcg caatccacaa ctgacacaag 660
gctttttcac cattttcagt tccatcggtt atacgttggt gttgtaggta tcgggctact 720
tttcttcttg ctctaaaata cctctcacac gtaggcccc ttcgcaaagt agcagcactc 780
atcgtaggat actggagggg cttcgggtcta tctggcatat ggagcacaag tggctctcat 840
cttatattcc atctcttctt gggtaggata tttcttttac ttacaccac attctttgct 900
ttcgacttta cagcatcggt ggggatggga gggggttgat cagcttcgcc atgagcagca 960
tagccgtagc cgtaccgcta agggggggcgt agggccgtgg cacttcatgg ttattgctac 1020
tcttggtggt tcggcgtgac gaaagaagat gccggagcgt ttgccttggt ggtacacaga 1080
ctcaaaccgt ttggactacg gccgcgggt tctgggtat cggcttggtc cttttgtcaa 1140
taagaaatac gatcgcataa aacagtcaaa caattacaac aatcatccaa aacacttttc 1200
acagttatgt caacagagat caaaacctca aaccacaagc tgtctgggag tacttctacg 1260
acctgacaca aataccgac ctaccggaca gatggacgag gtgaccaagt acgtattcga 1320
cttggttaaga ggcttgggtt tggagaccga gcaggacgag gtgggcaatg tctcattcgc 1380
aaagcc 1386

```

(2) INFORMATION FOR SEQ ID NO:167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

ttgcttcaat gcttcatatt gagacatctc ttgattatag ctcatTTtga cacaatgttg	60
tatttgatcat ctgcatcaac acttgacatc accatagggc gtgagacgta atgataaact	120
ggagcctggg gaatgcctta cgaagtcctt gagaattgat gcttgcaggc gaggggtgtag	180
atgaaggtct atttcacgat gactactgtc cctcggact tgagagctga atcagattga	240
tataagtctg attgagcaag gcgcatctga aagccaaatc tacgactatg ctgacactcg	300
gcgtt	305

(2) INFORMATION FOR SEQ ID NO:168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

cagactgatac agtaccatc cccaaaaaga atgccggaag aagaaataaa acattgaaag	60
gatttgacac taccatatt gcctcgaaaa tcgagtctta ccacatacga tcgtaaaaat	120
ccgattggag cattctgatt ttctcctttc ttccgattgg caaaactcct cctccgatag	180
atagatcttt cccaaccca tcgttctgct tgccgattga gcgtatcgtt catgatcgga	240
tgcaagcttt catcttctga tacaaatccg ccacatgccg gtacaaaccg aatacctcgg	300
aaatagcttc acaagcgaaa aactcaggac atacaatact gctcgcatat aagagcataa	360
acgattgtag actccagacc taagggaata tcacaggcag cgagagatgt aaagaggaga	420
agatgattct aaagaccacg agaaggcaat gccgggcaaa ataatggcaa ggaagtcata	480
aagagaaaaa tttccataaa gtatcatccg tatttaataca aagaataaga tagaagtaag	540
attccccctc tcttttagtg tcgtagtctt attcaggaag cgcaaattag tcatattcgt	600
ccgcttttca atggaataac ccgcatctt tttccgtttc caagcattac cgag	654

(2) INFORMATION FOR SEQ ID NO:169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...4512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ttcgaaaggt	ctgaccctaa	tgaatgcaaa	gaacgcogtt	gggtatgtgt	gtgaagctga	60
ctcgtgcagc	tctgtggtgca	gccgtgaaga	aacagtaaaa	aaacgtacaa	gaagcaagcc	120
ggagcttcga	tcgaaagtcc	ggctttccat	aacgaaggag	agccgcccct	gatacccctg	180
aagtggggca	acggagcggc	tcttccatat	tcgagagtc	tatttttagtc	gtagcgtatg	240
aaatactgat	cgtcggcctt	ggcaatatcg	gcgagagta	caacggcact	cgcctaattgt	300
gggtttccgg	atggtgaatg	ctctggccga	agacggtgga	gtgagttcgt	ggaagctcgt	360
tacggagcga	tagcgcgtat	gcgtgtgaag	aagcggagct	gatcctgctg	aaaccaaata	420
catatatgaa	tctgagtggc	atgccgttcg	ctactggatg	caacaggaga	atatcccctcg	480
cgaacagggtg	ttgtccttgt	ggacgatttg	gctttgcctt	tcggcacttt	gcggctgaac	540
ccaaggggaag	cgatgcgggg	cataacgggc	tgaagaacat	tgccgagggg	tgggatcgat	600
cgattatgcc	cgtctgcgtt	tcggccttggg	cgacgagttt	ccaaagggaag	gcagggtggac	660
ttcgtcctcg	gccgttttac	ccccgagaag	aggagaagct	gccggagctg	accaagcatg	720
cogtggagat	catcagagtt	tttgccctggc	cggtatccaa	aggacgatga	accggtacaa	780
ctaaggagat	ggaagaggta	aggatagacc	gttggatgtg	ggctacgcgt	atctcaagac	840
acgaacgata	gccacggatg	cctgcaagaa	aagccgagta	acgtgaacgg	gctgcaagcc	900
aagccttcgc	gtatggtagc	tgtgggcgac	gcatttcaggt	aagggaagcca	ccggtgacct	960
attccttttcg	tattctggct	tggctcagaa	tcggatgggt	gccaagctgg	tgaaggactt	1020
tctggaaaaa	tactccgcc	cgaagagtat	gagatactcg	aaatgcaacg	catttcggct	1080
ttgtggacag	agccaagggc	accggtcgtc	cgacaaaaaa	ggacagggag	agctggagca	1140
gttttagcgaa	gagatgcccg	atctgccgta	ctcgttgatt	cgttcgcactg	ggatgaagaa	1200
gactttgccc	aagactgaag	ctcccccttc	gtaggtaacg	gttcggacag	tccgatcgaa	1260
ttcgatgcc	tcataggcaa	gtacccgata	tggatgcgcg	atacgtagag	attccatttg	1320
acgcaagacg	gtatacggca	aagggcgagt	gaggggtgaac	gccactttcg	acgttatccc	1380
tatacgggat	atatcgttcg	tatgggcttg	ccctgtcata	tctcggtttg	cgacaggata	1440
ttcgtcgagc	cataggcaag	cagcccggcg	tagcgtctac	gttacccctgc	tgccccctctg	1500
aaatatcccc	tccttcgggtg	gggcggtttg	ccctctgcga	gtcggaaagg	agtgaagaat	1560
agaccttggc	aacgtagaa	tacacttcct	tcgtcggcag	caaggcggaa	ataaatgtta	1620
agtttggctt	gtctccgctg	tgttgagatg	ctattcccgcg	gagatagggt	acattaagtt	1680
cagcttatta	ttatggcaaa	gagtgcacta	catctgcgcg	gatgtcctac	cagcctaaaa	1740
tgctgcac	tctgcaggga	gcaggaagat	aatagaagga	aaagctacgg	aggcggtttc	1800
ggacaaagaa	gagttgctgc	tatttttccc	cgcacatacg	gcttgccgct	tatttctttc	1860
gccctggagg	agagcggacg	gagtatcctc	ctacgaatgt	gggggttatc	cttcggggcgg	1920
acaggctccg	ggtggacaca	atgtgatagc	cggctgtgtc	atgagatgaa	gctgctcaac	1980
cccgatagcc	ggctcttcgg	atttcttatg	gacccgtagg	cctgatcgag	cataagtatc	2040
gcgaactgac	tgctgaggaa	tagatgaata	ccgcaatacg	gggggcttcg	acatgatcgg	2100
atccggagta	ccaagctgga	caagcccga	cagttcgaag	ccggactgga	gatattcgag	2160
agttggacat	caaggcattg	gtcatcatcg	gtggcgacga	ctccacacca	acgcctgcac	2220
cctggccgag	tactatgcct	cgatcgatgc	cggatacaag	tgatcggctg	tccgaagacg	2280
atcgacggcg	acttgaaaaa	caacagatag	aaacctcctt	cggcttcgac	acggccgcca	2340
aagtctatag	cgactgatcg	gtaatatcca	gcgcgattgc	aattcggccc	ggaagtactg	2400
gacttcatca	agctgatggg	gcgttcggca	tctcatatta	cactggagtg	gccctccaga	2460
cccaccccaa	tatctgtatc	gtatccgaag	agggtgaggc	aacaattact	atctggacga	2520
tgtggtgacc	tatatcgccg	agaccgtgtg	cgtcggctcg	aggcagggaat	gaacttcggg	2580
acggtactga	ttccggaggg	ttgatcgaat	tcctgccggc	catgaagagg	ttgatcaagg	2640
agctgacgag	tttctctccc	aaaatgatgc	cgaattcaag	ctcatcaaac	gttcgcacag	2700
agacagtata	tcaagaacaa	actcagtcct	gagaattcgc	gccttacgac	agcttgccgg	2760
tggatgtggc	tcgacagttg	attgccgatc	gcgccctcac	ggcaatgtgc	aggtttcgct	2820
cattgccacc	gagaagctct	tgacagacatg	acggctcaga	agctggccga	atgggcggaa	2880
gaaggacgat	tcagggggcg	ttcagtagcg	ttacccactt	cttcggctac	gaaggacgct	2940
tgccatgccc	tccaacttcg	atgccaaacta	ctgctactgt	ctcggacgtc	agcttctatc	3000
ctgatcgcag	cgggaagagc	gggctaacatg	gctgcgataa	gaatacggca	gacccgtgat	3060
ccgaatggga	agccggcgcc	gtgccagacg	gatgatgtatg	aatatggagc	gtcggagcgg	3120
aaaaatgaag	cccgtgttcg	aaaagcattg	gtggatatgg	atggtgaacc	gtaccgagca	3180
ttgcggagat	gcgtcgcgaa	tgggcgttga	gcaccgagta	cgtttacccc	ggccgatata	3240
gttcttcggc	cccgaacatg	tatgcgatag	ccccacgatg	acatccgctt	ggaaaagaac	3300
gatcgtctgac	tcttcgcgtg	cattagtcgg	gtgataagca	gttgcttctg	tttgttttgt	3360
cgaaaaaaaa	tgttttttctt	tcaataagtc	tcatttaaaa	gaatcgcccta	tcgacgcata	3420
tctaccttctt	aaacataaatt	aaagaggatt	ctcctatgag	cagtttccac	aagctgacta	3480
tgatgaattg	gtcagccttt	atacagaagg	atgcgatgag	gcttttcgag	catactgtcc	3540
cggatgatg	ctgtagttca	tacttacatc	cgtttttcgt	gagfgatgcc	gatttggcgg	3600
aggatatattt	tcaggacact	tttatcaggt	gatccatacg	cttcgtcgcg	gacaatacat	3660

ccccaccggc	aagttaaagc	ttggetgcta	cgccttgccg	acaacctcgt	gatggatcac	3720
taccccggt	cagaggggaa	ggagccagat	tgcagtcttt	cgatgatgac	gacccgctcc	3780
tgtcgaaaag	gtggcgggaca	gcaatctgac	ggcggaaagaa	cactgatcga	actggctact	3840
atcgaagagc	tggaacagta	cctgagcgtc	cgcccgaagt	gcagcaggaa	gtagtggaaa	3900
tgcgctactg	ggaggacatg	gcttccgaga	gattgcagat	gctaccggag	taagcatcaa	3960
tacggcactg	gccgaatgcg	atatgcgctg	atcaatctgc	gcaaaatgat	gggcatgtgg	4020
cttagtcgat	attccatata	ataataaagc	agtcgtaagc	gttctctaaa	gaatggaaaa	4080
aaggagaatg	actcctttca	tccttaaccc	ttttgggaat	atgcttatga	cagacatcta	4140
ccgtattctt	gatcacaaaa	agctgaaatc	gttttcgatg	cagcagaaga	gcgatgcagc	4200
ctcaaacaca	aacaatcctt	gacaagctca	aacttatggc	ccgttcacgt	tgctcgtgat	4260
agcgctgttt	ctttttttgc	acaagcaata	aggaatagca	tttcggagta	tcctaatga	4320
aaagatatag	cagccgaaac	tgtgcagaga	tatgaaaacc	ttacagtttc	ggctgatccc	4380
tttgtggata	atcgtaactt	tgcagcatta	atataaaaaa	gagtttttag	aaaccgatga	4440
aaccacact	ttttgttttg	ctgcgggtat	gggcagccgc	tatggtagtc	tcaagcaatt	4500
ggacggcaag	gc					4512

(2) INFORMATION FOR SEQ ID NO:170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

cattacagca	agcatttcac	gttcataacc	tttgagccac	cctctgagat	gtccgggtata	60
cgggccgcat	cgaagtgcc	cttgaaagca	tatccgatac	ctccgggaac	cgatcatccg	120
ctgcgacgag	gagaaatccg	tctttcttcc	tgcattgaaa	acgaagaata	gtgcctcctc	180
tctttctgca	gctttgaaac	gaaatccatc	cggagactcg	ctgtcgatga	agacagcgtg	240
ggttgcgttt	ggcaaaaaag	ttcttagccg	tctgttcggc	tttggatcgt	gtcacgggtcc	300
tgcttgagc	atagggagac	acagtaataa	tagccctaag	gtgagaagat	acgtttcatt	360
attgcatttt	gttttgttgt	tccaagcagg	agggcagaag	aagcgataat	cccgatcatcc	420
tctttaagcc	gcactaagat	aaaaagagca	ttattaagag	tttgcagaaa	gaaaaaaagg	480
gatacttgcg	atc					493

(2) INFORMATION FOR SEQ ID NO:171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

```

ggatatcttc cgtggtacgc tggacggtct gacggaagaa aaccgcctgg attcaacagg      60
cggatgtgcg gaggcaaata gctgaaacac ctgttagagc actggcagcg cgggaaaccg      120
acgaaattaa agcagagttg ggacgcgcta cgaggaagag gagaagaggc tgaaaagcga      180
tgatcctcac cctgtcctcc gcttagctgg gataaagctc tgataggagc aaaggatcgg      240
atcatccggc taagaatcaa caggcttttt ggcatgctg aggctgtcgg aacaagagac      300
cgtagcggaa ggcatcact atttgtttaa ccgtttcacc gaagggagca gctttggagt      360
tgagagaggt agacagcgaa ctggtcatca aaggtttact tcggctttgc cctactacga      420
gaagtatgcc gtggcgagc acgtataggg gagcggtcgg ccgatcttct aacggctacg      480
gggcgtcacc ttctgaacat gtgctggaat acggctgcgg ctgcggtgtc tatacgcgca      540
actggctcaa accgttacgg taaagcagtg gacgctcaat gatttatgcc ggtctgcgag      600
gagtataata gcgtaagctc tgtttctttc tatgcagcga agccgagaca atgccccaca      660
cggatactta cgatctgata acctcgc

```

(2) INFORMATION FOR SEQ ID NO:172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

```

cgagcgtcgc tatccggcct tcggcaacct ggtgcctcgt gatgtggccg ccgtgctgcc      60
aaagaacggt gcatgcccgg ttatggtgtg aacaatacgg ccttgccgta ttcctcgact      120
tcggcgatgc catcaaagct ttgggaccga cgtggtggag cagaagtacg gcaacctctt      180
ccagatgtat gagaagtcgc agatgagaat ccgtacgaaa cgccgatgat gatctatccg      240
gctatcacta tacgatgggt ggtctctggg tggattacga gctgatgact accacccggg      300
cctgtttgcc atcggagaag ccaacttctc tgatcacgga gccaccgtct cggtgcttct      360
gctctcatgc aggtctctgc tgacggttac ttgttattcc ttatacgatg cagaactatc      420
tggccgatca gattcaggtg cgcgcttcag cacggatcgt cccgaattcg aagctgccga      480
gaaagagttg aagaccgcat aaccggtatc atgaatgtca aaggcaataa gtccgtggag      540
accttcacaa ggagctgggc cacatcatgt gggacaatgt gggaatggac gagacaaagc      600
cggtttgga aagccattg tgaagctgga cgagctgaga aagagttctg gagcaatgtc      660
tatgtgccgg gtgaagcaa tgacctaac tagagctgga gaaagccctt cgattggcgg      720
acttcacga gatagtacgc tgatggcgca cgatgccatg gaccgc

```

(2) INFORMATION FOR SEQ ID NO:173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

```

cggcaagacc tataacaacag cttctatcgc tgtgcatatg tgcaacaaga ctttacagat      60
tataccgacc acagcaaagt catagaagag tacgaacgct gagagatact ggtcaaatag      120
cattctgtac cttccaccag tcaatgggta tgaggatttt gtggaaggat tgaagccaga      180
agtgaaaagt aacaattgga atacaatgtg gaaaatggga atcttcaa atcatctgtga      240
acaggaaaga caaaggaaga agcagatatc attacttgta ttgacaagta tctgagtcta      300
tcaagggtta tgaaaacaag aagaaaattc caacgatttc cggaggtcag atctgtgggt      360
atggtggata gagggtaatg acacaataag catcgcagtg ccatttctaa aagtgaaaaa      420
ggggagcagt attcactatc acacttaaca ttgagaaagt caagctgcag gcaattgggtg      480
aagctataga aataactggc gacagtatgc acaagcattt atcaatgccg taaagaaagg      540
taccaacttg acaaacaaat ttcagacaaa ctttatgttc tcattattac gagataaacc      600
agagggtaat gtgtccaaaa tattcggaga acttatccct tacttgaagc tggataagcg      660
t

```

(2) INFORMATION FOR SEQ ID NO:174

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

```

ttgtgacaga ttaccatcgg cacaccgaga tgtttggcat agctattgga cgcttcgtac      60
ctccgacatc aggcgtagct actacgaggt tctctaaggc atattcttgc ggatgtattc      120
catgaaaacc gtagagccgt agagatgtcc accggcacat cgaagaaacc ttgaatctga      180
tccgcatgta ggtccacgtg atcagacggg taataacctgc cttgcttagc aggtcggcga      240
tcagctggcg ccgatagata cacggggcct gtctttcttg tctgtcttgc cccaccgaag      300
taggggatga cagctgtaat gtagtgtcgc gaagctcggt tgggtgcatc atcatcagga      360
gcagcttcat caggtgggtc gaagatggga attggactgt acgaggaaga catcccggcc      420
gcgaatgctc tctcatagg aacggcaaat tcaccatcgg cgaagtgtc gatattcatt      480
cgccccagag gcaaccaga ctgttgacga tcttttctgc aagataacgg gaatttgtcc      540
ggagaagaca gaaaagtgtt tttcgttgtt catctttgat atggtgtaag ttatcgttcc      600
attgccggca aatcgaagcc gtcagaccac ctccgagcga ctgctgacgg acatgatgca      660
aaagtaatat atatacatta tgtatgaagc tcgaagaaga aaagaagatc gggatgaagc      720
aatggcagag gcgttctgtc acgctcgatt cggctctatc gcctctgtct cgtgectcgg      780
cgccgcgtcc gttcgaagcg gtttttccct gtcttttgtt cgtttcggat cgacagaacg
840

```

(2) INFORMATION FOR SEQ ID NO:175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

gatccccgtc	cggtcgggtgc	cagcagttca	caatctgtct	cctgctcgaa	atagtctgca	60
ccacagaagc	gataagctgt	gtcttaccgg	taccggcaat	ccgcgaagca	aaaaaaccga	120
ataaggttcc	ctgtcgaaca	gatacttgcc	aaagatcgaa	tagccgaatc	ttggctttgt	180
gtcggggtaa	acggcaattt	ttcaatat	gtcgggcaa	ataattgtcc	atctttatac	240
aaatctatat	ttgcggggac	taagttactt	cctttgaacg	atatcctcgg	attcgtgggg	300
caatacggat	taggaagcgt	ctttagaaga	gattttaata	caaacaaagt	aagataacga	360
tgaagacttt	aatcaagatt	ttgggtggctg	tacagtcgtg	gtggtggcat	atctcaccgt	420
gatgagcata	tatacccccg	tagtttcgac	aaagattcag	gccagtcctg	gaaacaagct	480
atccaaaaga	gctgaaaaat	atagctgact	atcaagctgc	attcgaaagc	atgtatggtg	540
ctatgccaca	gcagatgaat	tggttaagctt	cctcgctaac	ggcctgtgta	ctacgtgaat	600
gccgaaggcg	aatacaccca	cgacatgcgc	gacaaagaat	gaccgaagca	caggcagctc	660
gtgcaggctt	gctcaaacgc	gatacatgtg	ggttgcagcc	aaggactctc	tgctcaaagg	720
tattgacccc	aatacgtctt	ggacattccc	ggttttgccg	gcaaaaagat	tttggttgag	780
gtagctccat	ccaacaggag	ataggtcggg	acactataga	tgtatccgta	tttaggcac	840
ggtacctttc	gtcgactacc	tcagcgatca	ggatcagatt	cgctgaagat	gaaaataaac	900
gatgcagaag						910

(2) INFORMATION FOR SEQ ID NO:176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

tcctgggatac	aagcaaattc	aggtaggtga	gcctagcccc	taccagccct	ttccaacttg	60
acagctacaa	cgcagggtca	gaaagtaacg	ctcaagtggg	agcaccgagc	gcaaagaagg	120
cagaagggtc	ccgtgaagta	aaacggacgg	agacgggtct	ttcgttacga	tcgaacctgc	180
aaacgatgta	cgtgccacga	agccaagggt	gtgcttgccg	cagacaacgt	atggggagac	240
aatacgggta	ccagttcttg	ttggatgccg	atcacatac	attcggaagt	gtcatccggc	300

aaccgggtcct	ctctttaccg	gaacagcttc	ttccaatctt	tacgtgcgaa	cttcgagtat	360
ttgatcccg	ccaatgccga	tcctgttggt	acacacagaa	tattatcggt	acaggacagg	420
gtgaagttgt	aatccccgg	gtgtttacga	ctattgcatt	acgaaccgg	aacctgcac	480
cggaaagatg	ggatcgcagg	agatggaggc	aaccagcctg	cacgttatga	cgatttcact	540
tcgaagcagg	caagaagtac	acctttcacg	atgcgtcgcg	ccggaatgga	gatggaaactg	600
atatggaagt	cgaagacgat	tcacctgcaa	gctatactat	acagtctatc	gtgacggcac	660
gaagatcaag	gaaggtctga	ccgaaagacc	taccgcgatg	caggaatgag	tgcaaatct	720
catgagtatt	gcgtgaagtt	aagtaacacg	ccggcgctatc	tccgaagggt	tgtgtggatt	780
atatcctgac	ggagtggcag	acgtaacggc	tcagaagcct	tacacgctga	cagtgtagga	840
aagacgatca	cggtaacttg	ccaaggcgaa	gctatgatct	acacatgaac	ggtcgtcgtc	900
tggcagccgg	tcgcaacacg	gttgtttaca	cgctcagggc	ggctactatg	cagttatggt	960
tgtcgttgac	tgcaagtctt	cgtagagaaa	ctcgctatca	agtaaactctg	tcttggaactc	1020
ggagactttt	gcagacactt	ttaagatagg	tctgtaattg	tctcagagta	tgaatcggcg	1080
cccgaacctc	ttttaaggaa	gtcgggcgac	ttcgttttta	tgcttatatt	ccaatatact	1140
tctgaaacaa	tttgttccaa	aaagttg				1167

(2) INFORMATION FOR SEQ ID NO:177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...3217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

aacgattgtc	ggctgattct	tgcttcctgc	acgatgcagg	acgcgattgc	agttgattct	60
tgctccctgc	acgatgcagg	acgcgattgt	cggtctgtct	tgctccctgc	atgatgcagg	120
acgcgattgt	cagctgattc	ttgctcctgc	acgatgcagg	acgcgattgt	cagttgattc	180
ttgcttcctg	cacgatcagg	acgcgattgt	cagttgattc	ttgcttcctg	cacgatgcag	240
gacgcattgt	caactgattc	ttgcttcctg	cacgatgcag	gacgcattgt	tcagtgattc	300
ttgcttcctg	caccgatgca	ggacgcgatt	gtcagctgat	tctctcccat	caatgcgcta	360
actatcagct	gtttgcaact	attttatagg	acttcattga	agtcttttgc	cgcagagctg	420
attcttaagt	gtttttcaga	tacttgaggt	ttgcagagag	atcgcatgaa	gctctccttt	480
cttcgtcaaa	caatgcttgt	gtctgtcttg	atcaatatga	gaggggggta	ttgtgcaacg	540
tctcaagctg	taaaaccggc	agctgtgtat	agaaacagtc	tttcgggtga	tggcaatcga	600
acttcctaac	tgcccaaatt	ttaccggaca	gcaataatga	ttatatgggg	ttagtccatc	660
gggcggaact	tctcttcgac	aaaggcattt	cgctttcgtt	taagccgtat	ttgcggtaga	720
gttggcgatc	aatttcgccca	ccggctgtgt	ccaatcgatg	tccgattctg	ctgtgaagtc	780
ttgcggggga	ctaactcgcca	agtttctttg	gggttatctt	gcgttgccct	gagataccca	840
gcatcgtgcg	agcaaaacttc	gtcttcacat	agcgcagaca	agctctgcct	cgtttcgggt	900
gtcgaatgcc	ccaataactaa	tgaaggatc	atataaccca	taatcggcgt	gccaataatt	960
gggtgtgctga	gtacttcacc	attgcccccg	agccatttgt	cttggggata	atcaccttgt	1020
acttggaag	ttctctggat	gggtgatgta	actacgctta	caccacttat	agcatcttgc	1080
ttattggctc	gtccatagat	acatgccatc	ttctcttccc	ttccttgggg	tattcatcaa	1140
agaaaacctc	aggaaacaca	tcaaagatat	tggcacaaag	ctgtacttgt	gccctgcact	1200
ttgtcttccg	ttcaaactcg	gatgccttgg	tagagttcgt	ctgtaatacg	atagagctct	1260
cgagggtgca	caagtttgaa	aatggtagag	gattgggttg	ctctacttta	tacagaatat	1320
gataagctca	tcaaaggccg	aaaacatccc	aatcgggtcca	agaatcattt	tctgttccag	1380
tatgagggtg	cgattcctcc	ttttacatct	acagtaggga	aacctccgca	ctattaggcc	1440
aataatcgac	tactctataa	tgcttgtccg	aagcatcttt	tcattccatt	ctttggcggt	1500
tttacctgcg	ttgaaaagaa	acgagcagga	tgaataagtg	taccctgtgg	agcaagtacc	1560
attgcgagtc	aaagaatttg	tggtagatgg	ggctcgagcc	attacccttg	ccttgatcat	1620
cacttggtac	ggtgggttgc	ctataatagc	gtctatcttc	atatttcgtc	gttgttgatt	1680

ttccagaacc	ttttgcccga	acgtagcata	ttgacacgct	gtcgggctgg	ctggtaaatgt	1740
tttctatcag	atcgggataa	tgcttgtatg	agtcactaca	tcacggaaac	cccgtagcgt	1800
acgcatcgtg	ataagcgggc	catagggggt	ttgcagacca	cgaaaatggt	ttcttcgagc	1860
gtctgtccca	cagttgtaag	gcaaaggcac	gtgttacgtc	gccatacttc	ttcgagcttc	1920
ctctaccctt	gtacgataaa	tgttataggc	agcataaagg	gatagagacc	gctcttggag	1980
ttgatctcca	aaatgatgct	tttgggggtg	atacctcatt	cgttataccc	tgatgctcga	2040
tgtagcgagg	caatgcaagg	gagtagagaa	gtcttcgctc	ataaagcagt	agccacctat	2100
gctgtcccga	gatgcatggt	caccacacgc	caaggagtca	gtactgtttc	tttgtcgggt	2160
tgcggaaggt	agagaagata	gaagcaatac	gccctatacg	ctcctgatgg	tgaacttate	2220
cgccatacga	gccatctcac	ggatgcgctt	ccccctcac	gaaatatgtc	ggggtcgtag	2280
taacgcttga	agcgacgaaa	gacgccttgg	taacgccgcg	aggcataaat	tcctgccaag	2340
actgctcatc	gagagattgg	caaaattgtc	aatggtcagc	tccttatcct	catccttcac	2400
tcagccccc	agagcatcag	aggcatgcgg	atggatatgc	ctcggaggat	gaaatagcct	2460
ctcggcggtg	gtcgcctttg	gctttcagtt	cgtccagtct	tttttctctt	cgggtgttag	2520
gcctttcttt	ttcctcttct	ccagtgcgct	ttctcctcgt	attgctcatg	ggtgagacct	2580
tggtgattga	tatctattca	ccggactttg	ccatgcgctt	ggttttgcca	atgatacctt	2640
tgagttgtcg	aagtcgtgca	gctctacctc	ggtaagtttg	agtagctcgt	cattaagagt	2700
gccccattct	caaagccatc	ctgcaccact	ttttctattt	gtgccgcttg	agctgtccga	2760
gcatcgatt	gacatcgtaa	ggcttcatcc	ggcgcttctt	atagagatga	tgggacagaa	2820
gttgagaaaa	ttccccaaca	gctgcgatca	ctctcgtctt	gtttgcctgc	tttgtatgat	2880
accttggcag	ctcggcaagg	acacggaggg	tgcggtcggg	agcaaagtcg	aaggcataac	2940
ctctgtcttc	atgtaccat	tgtgggtata	aggcgtttgt	acgcggaagt	agtttgcata	3000
tagccggatg	cggaggtact	atatgaaccg	gccatcataa	gacgccggtc	caaggcttaa	3060
tgcttacacc	ggtagtcaat	cgtccgctga	gagggtgatt	gtataagtct	catccgggtc	3120
tttgccgatg	gcttgatgac	taactcaagg	gcatctctgc	tttctctctc	ctcatcatct	3180
ccgtccccgg	ccacattggc	caccttaaag	agaccga			3217

(2) INFORMATION FOR SEQ ID NO:178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

acgctgatca	acaagaaata	cacgaagcga	caaaatgcc	tcggcgcccg	gcttatgacg	60
tgattctctt	attcaacgcc	agttcgatct	aagcgaacta	ccataaaaaat	aacaagtagc	120
tgtaaatcat	actcttttgt	gattctcggc	tgcataatga	tcgggaagaa	ggggcggctt	180
ccaagtcatt	gggcttagat	gtagataaaa	agccatctga	aagcaatata	agtgtctgaa	240
aaacatgtgt	ggaaaataaa	acacactaat	aaccaatgtg	ttgtgccatt	ccttatatcg	300
aactcac						307

(2) INFORMATION FOR SEQ ID NO:179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

```

ggcccaaggt cgggagtttc gacggagggt tcggttcttc ttatcttgcc gttgtgtagg      60
tcagaagaag acgagggaga tctgggtttt atgccgtcgt ataccgctgc ggaggccgaa      120
gctatgggga tggtaaaca ggtgggtact ccgcgagggt ggaggacgaa acggtggact      180
ggtgcaagac gatattagcc ggagtccgat ggcgatccgg atgattaaac gggctttgaa      240
tgccgggctcg acggtcagag aggattgatg gagtttgcat gggatgccac cctttgtatt      300
atcttatgga agaagctcag gaggggaaaa atgccttttt ggaaagcgga ctccggattt      360
cgacaagttc cctaaatttc cgggttgatg ctaaggccga ttatatcccc tataccttga      420
aattcaagga gccggcaggg agtcgcgggg cgttttgcat accaagcaga cttatttcgt      480
gaggggtata acgatacttt cccctctcgg gcagggttac gcgaggcggc tttattccgg      540
gattgagtgc ggaagaggga ggcgattacg aagagcggct ggcgagggtt gcaacggcgt      600
ttgcgggttt actcccgacg cctggcaggg atatcctctt tgtgtttcgg gatggaaacg      660
gcgcttgccg acttcgaggg cgggggttgc tttttccctc ggctttcact tccggcgagg      720
cggggattcc cataacgggt tgatatggtt ggggagcttc gaagctatgc gaaggcgtgt      780
ggagagaaac tggaggagggt ctttccgctg tataaaaact tcggaaggat gccgttattc      840
gaatcggaac tcgctttggg acggatggtc cgcgagaaat tgcgaaggat gccgttattc      900
gtctcgatgc gaacggggct ttcgaagaag agaggcgatg tataaatttg aacgtttatc      960
cgccttcggg atccattcgg ggagcaaccc gtcaggggac ggaattacgc ggctatgcgc      1020
aggattgcgc gaatgcccc gttgccgttg ccttggatga ggaattgata ggcttataga      1080
tgaaacttcc aaacggggaga tgttggttta tatcgctccg gcctgtacgt actcaagcct      1140
tcacttgctg gaggttttta cggcacggag caatggtaag gattgccgaa tccatgggga      1200
tagcgtgggt gatcacttcc gctttgagtc gaatataggg ctgaatgcca ttgccagtg      1260
gacctatatt cacggaatcc cctgcctcag ggattgggta cgggcgcttt gtttacgaat      1320
aatcggtata gcctctttat acggaaggcg gttatttgag atatgccgca ggaagagatc      1380
ttcccgttgc gatgtcgagg ccttgttccg ggaaagatat gaaacggagg cttatgaaaa      1440
ttctgtatga agacagggtt ttcggtttgc ggagatagcc gccggcgccct tgggagatga      1500
tgttccgtgg aaatccgcat gcgtgcattc gtatcggaat tgcccaagct tatccatctg cctaaaaagc      1560
atagaggctg tacttccggc tctacgggta ttttttcgac atatccggga ttccgtactg      1620
gatggcgggt caggcacggc tgaccaatgc ttttttcgac atatccggga ttccgtactg      1680
atgctctctc ttccgctttc ttatatagcc ggtaaatgat ggtggtgagg gcattcgaag      1740
cagggggcgt tctgttgccg gaactccctc ttctttgcoo ctttccctcc tgcatacgaa      1800
ggtcaaactc ggacgctcgt acccctgcaa gtggaggaca tccgtgcatc gggggaaagc      1860
cacggttcga aaaggtggaa aatcttttga taggaggagg cccctggca cgactacgag      1920
agacgggttg gcggatattc ccaccgttt tttcgctact acggaatgac ggaaacggca      1980
tcccatacgg ctcttatgcg attgaacggg agggagcttc cgcttggttt gaggcttttg      2040
aaggagtgcg tttccgcccg acgaaatccg gatgtctttg catacatgct ccccatattc      2100
gggaatcgag ttttgacccc gggatatggt ggagctcgta gatgaaaggc atttcggttg      2160
aaggggcgtt tggattacgt aatcaatagc ggggggatca aatttcccc gaggaactgg
2220

```

(2) INFORMATION FOR SEQ ID NO:180

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

tggtcatcgc	gctctctctc	gattcggata	tccaatcgta	gagctatcgc	gccggtgcag	60
gtctgcgcgc	gcggttcagcc	acccgcgcgc	gtataagcgc	gaggtcactg	ctgctatctg	120
tatggctttg	agcgaatcgc	agaatgagtt	catgatattg	agaatgccat	attgactatc	180
cgacgggtgg	agcgagtat	tcacccatgga	gttctaagat	atatggactg	agatctccta	240
tcgaaggcat	atgttcacaa	gtaaacatga	tagacaatga	aagaaaaaga	taagaagctg	300
ccccactaa	aaaagcaaaa	gctactaccc	ccaagaccgg	aaagcgaaga	aaggagctat	360
gacggacgac	atctatgctg	ctatctcggg	ggtctctatc	aagagaccta	tgaagctcat	420
gatgctgaac	ctatgaggct	ccgatcaagc	gtcatcgta	ttctgcttgg	agcatgaaga	480
cacttatgct	cgctcagcttc	ctaaataatc	tcattcaatc	acgacattaa	aaacatgaca	540
aacaatgaaa	gagtataaat	ataaaatcaa	cggtaacgaa	tacaatgtgt	tatcaacagc	600
atcgaagatg	gattggcaga	catcgaagtt	aacggtatcc	ctataaggtg	gaaatactta	660
ccgagaagaa	aaaagcatcg	aagcctcaat	caaacatccg	accgtcacgg	ctgcacctgt	720
agcagctgca	cccgtgctcc	tgcagtttca	gccggaggac	aagggtacagg	cgtcaagtct	780
ccgctcccgg	tgtcatcctt	gacgtttgcg	ttaaggtcgg	agacgaagtc	aagtcggcca	840
aaaggttgct	gttctcgaag	ccatgaagat	ggaaaataat	ataatgcgga	tcgagacggt	900
aaaatcgttg	ccgtgaagg	caacaaaagg	gttccatcct	cgaggggttct	gatatcgtaa	960
taatcggcta	atgatatgac	ggattcggca	gcttcttagc	aaacaatatc	gaggtattcc	1020
tctcttacaa	ggcttcgcca	atgccacact	cggccacttg	gtgatgattc	tggtcggatg	1080
ctattcattt	ttctggccat	accgtatgag	tttgagccta	tggtgctatt	ccgatcggat	1140
ttggaatcct	cattggtaat	atccccctta	aagatgcggt	ctgcagatcg	gtatttacga	1200
agaaggatcg	gtgctgaata	tcctcatcaa	gggtaacta	aaggatggta	tccgccactc	1260
atatttttgg	gtatgggtgcg	atgaccgatt	tctctgctct	tatcgctaata	ccgaagctga	1320
tgtgatcggg	gcggcggcgc	agttcggtat	cttcgggtgcc	tacatattgg	cttgatctct	1380
gggttcgaac	ccaatcaggc	cgtgctatc	ggtattatcg	gggagcagat	gggcctacgg	1440
ctatctttct	ctcgtccaag	ttggctccga	cttgctgggt	gcccattgca	gtctctgcac	1500
actcctatat	ggccttggtc	cgatcatcca	acctcctatt	atgcgtcttc	tgaccacgaa	1560
gaaggaagcta	tgattcggat	gaaaccgcca	cgtgccgtgt	ctactacgga	gaagcagtat	1620
tcccgatcgt	ggggctgctg	cttactactt	ttcttggtgcc	ttcgggttgc	ccttgctggg	1680
aatgctattc	ttcggttaata	ttttgaaaga	aagcgtgtta	ctcgccgttt	ggctgagacg	1740
gcacgtggcc	cgttgatcga	tgtcttacca	ttcttttggg	cgttacggtg	ggagcttcta	1800
cccaggccac	tcattcctga	catggaactc	gatcaagatt	ttcatttttg	gagctttctc	1860
ttcatcattg	ctacgatggc	cgtgtttttg	ttcgtgaaga	ttctcaacct	ctcttgcgac	1920
acaagctcaa	tccattgacg	ggcaatgcag	gggtttctgc	gtacccgact	ctgcacgtat	1980
ttcacagatc	gaaggcctaa	aggccgatcg	acaaactacc	tgctgatgca	tgctatggga	2040
cctaagttag	ccggtgtgtc	ggctcggcag	ttgctgccgg	tatcctactc	ggattcctcg	2100
cctaagaagt	tccataatct	caataagccg	cccattgaac	agacttttct	gtc	2153

(2) INFORMATION FOR SEQ ID NO:181

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 943 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

tacagcttat	gaaaaagtta	ttctctttga	gtgcgggtcat	cgtactctta	tttccttgca	60
ttcttgcgcg	cctcgcac	tcaccgagct	gaacaaacgt	accctccttt	gcccagagga	120
acacctattg	cggctacga	actcgaaacg	gtaagcgctc	cccttcggag	gctgagctgg	180
tagggaaaagt	gaggatgccg	aatccgggtc	atccccggga	gtctctccta	ctcggaggcc	240
gtgcaattgc	tcgcgaagaa	accagaaaaa	gcggtgccaa	tatcctgtac	gtgacaatca	300
ccaacgaccc	tctatcttcg	gcagctccat	gcacagata	ggcggcttat	gctcttgta	360
gattctgtcg	tgaggaacga	gggagaaggt	tacccgactc	gcccctgtac	gattcgggtc	420
aaagggggaa	aatcggtctc	cgatcaaggc	tcccgtacac	gacctctcgc	tccatttcgg	480
cccctctatc	tcacgaatcg	gacaaaaggg	ctgtcttatt	cggagcagca	gctggagaaa	540
agctaagcaa	cggacttttcg	ttcgtactcc	aatataaatg	tcaccggaag	ggaacctcta	600
cggattcggg	ctgatcgctc	ctcgatatga	agccgactca	ctaagaaaat	cgaataccag	660
ggtatcggat	tcgccaatcg	attggatata	tcgctccctt	attcagcatg	agtactgtc	720
tttcggagcg	gtggtgcttg	ggataagttt	cggcttaggt	tatttgggct	tcaaacaac	780
gctgccgaca	tatccgaccc	gaagagggaa	ggttacttct	ccggcagcac	agtggagcca	840
atacggcact	caacgttaga	tacaagctga	acaaacattt	agcatcgggg	gagagatcat	900
gatggtcggg	ggcggttttc	atccggataa	ctaaagatga	cga		943

(2) INFORMATION FOR SEQ ID NO:182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

gaggatgtaa	agaacgacat	cttaccgata	cgtgccgaaa	gaataaagac	aaagccaact	60
ctgcaatgat	caatccccac	agcaatccgg	gattcatttc	atagtatata	tcaacgaact	120
cttagcaacg	agcatggctg	taagagcgtg	ataccgagtg	caccaaacat	ccatgtaaag	180
acatggcgca	tagttgcgtt	tggagcgtac	tatccacata	gacagtggat	tgattgttca	240
attcgtaaag	ttcataccgc	gtttcgttat	ttgcttatat	tttattattc	tgttcctatg	300
gtaattcaac	aaggatctcc	ggtaaagggt	ccaccacttc	acccccctg	catcgaaata	360
ctctacattc	tgatccatca	tacatggctg	gaatcctgtg	ggaactcaaa	tttctcttcc	420
gttgtatagc	ccagcttggg	acagcgtata	cccgtctgag	aaattcggca	aaaataggca	480
acgcagaagc	gccccctgcc	cattggacat	agagtcgaaa	tgacacagacc	tatcctcacg	540
ccaacccaac	agccggccac	aagagaagga	gtaaagccta	cgaaccagca	tcactgttat	600
tctgtgtggg	acccgtcttt	cctcccatat	cgagtttaat	ccatagcgat	acctcagtct	660
gtaccgggta	ccgccatcga	ctacggcttc	aacatataga	gcattcttga	tgccgcttca	720
ggtgggagta	cttc					734

(2) INFORMATION FOR SEQ ID NO:183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

```
ccgtgcgcgt agagctaaaa tcctctatag ggataaaggt cgaatcagaa ctgtattttg      60
ctcaagcaat tggctataaa tagcattctg cgcttattga ttttgtttta ttatctgcat      120
tcccagaggg aagagtcggc tgcagggaat aaggatcgca gtggaatcgg tttctgcctg      180
tcgcacatcg ctacagcaatc cacaggcttg agttgccagc tccctatctg ctcgggcaga      240
tagaaaaagc acccaaaaaga attgccgttg cagcaagcaa caaccaaaaa cgagcatttg      300
attacgcggg ccttccatag aataatcttg tgcgggattt ctctctttgt agaagaatca      360
aaaattgtgc gcaaagataa acgttacaca agaacttgta ttaaccatcc tgaaacgaca      420
ggacaatcgc atttgaaata tagcctgatg atgctccgtc cggaataaac acgaattaat      480
gtgttagaga cctaatagta gaaggaagag accaaggata cagagtacaa cctttcaaaa      540
cgatagccct ctgtcgaaga gaccggcctc ttcggggaat tttctgtatc tgtgttgccg      600
ttactatcgg aaattacaat cacgggtgtc tttctatata agaaatgagt cctgatcttc      660
ccaaacaag
```

(2) INFORMATION FOR SEQ ID NO:184

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

```
tggccgaact ggctcagcag atccatgcag aaggtttctt ctttctcgcc tatgggtcgat      60
gccggtctat cgggtcatga acgtcaggta ggacaaacgg taagactggt cgccccgaca      120
tctacatggc ctttggtatc tcagggtgcat ccagcacttg gccggtatgg aagagagcga      180
ttatatcatt gccatcacaa ggacaaattc gctccgatct tccagggtggc cgatcttggt      240
gtagtggcga cttgcacaag attgtaccca ttctgacggc taagctgcgt tctgcattgca      300
ggacaagtaa gagcctgtta gtataacaaa ccttgtagag gagcgatgag gcgaagggct      360
tttgtggctc gtcgcattca ttcggctcct ttcatccat cgaagagagt tatggaattt      420
cacaatctga tcatccaatc gaagatggta tcacgacgct gaccatcaac aaaccggaga      480
cactgaacgc ctctcctctg aagtcctttc cgaattgaag tcggccattg ccgttatcgt      540
acagaaaagc ctcgagtgtc gatcattacc ggaagcggca aagcattttc gcaggagcag      600
acatagccga gatgcaacat ctgagtgcag ccgagggaaa gcctttggag ggcttgaggc      660
agaggtattc cgaaggatag aagaatgcct ttccctgtta ttgcagccat caatggcttt      720
gctttgggag gcggagcgaa ttggccatgg cttgtgacat ccgcatagct tcggcttaaa      780
gcccgttttg tcaagcccga agtcggattg ggcattcaacc c
```

(2) INFORMATION FOR SEQ ID NO:185

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 803 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...803
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

```

gctgcgatag cgctcagttcg acgtgagaaa aggaaaggga gcttttagcgg cagaggcagg      60
attgctatatt caatatatcg gataagccgg cgaataatcg aaaccggata tcaccataaa      120
aataacggct acgatgcggt tgaaccacgt atgccaacga cattgatacg attgcgtagc      180
aggctgaaaa gataaggata agagaccacc agccaatcgc ccccaaagct atacctaaaca      240
tgccgaggta taaccgacta acatcctccc cggaacatng gtgacgaagt tgaacgggaa      300
tatagagcga taaaaaagaa aatgataaaa gggttggata gcgaaggcca aaagagctta      360
ggacggtatg ccatacagag tagttattat cctatcatcc accttgaagg tgggtgcagt      420
ccgatacaga tatataccga aagaaacatg acgacactgc cgagaagctg tagccaagcc      480
tcgttgcttg caatgaagtt catcaccaaa cctattccca gatacgtgac agtggcataa      540
agagatcgct aagtatggct ccgataccgg tgtagaatcc atcgcgcctc ccctgtgcag      600
agtcccttca atacacaaaa ttccgatcgg ccccatagag ccgacacgag aatgccaatg      660
agaataccgt atagaattga agtggcacca tgcggtagaa aggcaaaatt tccttattgt      720
cctgctaagc cggatgcaaa gataaacatt ctaccctgtt atatcctaatt ccgtttttgc      780
cggattcttg aaaagaaaaa gtc                                     803

```

(2) INFORMATION FOR SEQ ID NO:186

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3910 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...3910
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

```

gggagagcgc atagcccgat ttgcagatat agaagtactc agctatcgac cgacctcttc      60
ggcacattga cccctaagca gaggatgctt tgctaccact atcggaagca gccctgcgag      120
gacgggatat tacaaccata cagaactccg ctacaacctc tgggtacgca gtctgatgga      180
gcgtattttac acccatattag caagtgcgaa cgaaccgacg acttttgccc tgctggaaga      240
atacccttct gcatctgggt tgccaatggc attcaccacc attacagcgg agccaattca      300
ttgcccggtt cagtcggggt ttcttgcggt cagccctgag agagcgggag tggagctgga      360
gccggaagag caggtgcttt tggagcgcgt atgtacgata cccgattttc tacccaaaca      420
gaccgagcag agcggcggaag agatattatc aaggcttctt cggtcatttt ctatgcaccg      480

```

ggtatcaccc	agccccgaagc	ggaaagccat	tacaaaaacc	tgatagaagc	tcttccccgaa	540
acgagaaaaag	ctgtccgcgcg	agcttcggac	tgaataccccg	tctgatccctt	cgacttcggg	600
cgaattgaaa	gacgaggttt	gctgtataga	cggattgacg	gccccgccat	agaagctgta	660
gtcgttccct	tggaggctgc	catacctaca	ctgagaacga	ggaacaggcc	gcatgcatac	720
gactgctgtg	cgactttacc	gcacaggaga	catcaggctg	tacgaccggt	tctgtattcg	780
ctggtggaaa	acaatcgtac	tcggatcgat	tttatcaacg	gattcaccca	agttatgccg	840
atccgatagg	catacacggc	agttgggagg	gactgggtaca	cagcaggacg	aagaagccgg	900
cagacgtacg	cgcatcatca	gcgaacatgc	cgttgggttcg	aagcacattc	gccgatcgac	960
gcacgtttcc	gcaagaagaa	ccccatggta	tatcggctac	ggtgggtcaat	gtactgacca	1020
tagccggcgc	agctatccctg	ccacaccgat	aggaatcaac	ctcccgaatg	ccgactgggt	1080
cgtgccgaac	acggatccaa	gtccgtcact	atcgacaata	tcacggagca	tacaaccatg	1140
ccgcgcgagg	gacaggtctg	tacgaggagt	ttatccccgac	gaggaagtac	gcagacacgt	1200
agagctgcat	gccgacctaa	cggacgcctc	cacaccgacc	tgcacgaatg	cctcggacat	1260
ggcagcggac	agttctcccc	ggtgtaccag	gcgatgcact	tggagaacac	gcctccacgc	1320
tggggagacg	cgtgccgacc	tcttcgccct	ctattttctg	gccgatccca	aatgatcgaa	1380
ttaggtcttt	tgaccgatcc	cgatgcttac	aaagccaact	atacaaatac	atgctcaacg	1440
gtctgatgac	ccaactcgtg	cgtatcaagc	aggagaggag	atagaggagg	cgcatatgcg	1500
caaccgtgca	ctcatagctg	ctacgtcttg	gagcatgccg	agcggccggg	ggcaatgtcg	1560
ctggtctgga	agagggcaag	acggcactcg	tgatcaagga	ctatgaagca	gtgcgtggat	1620
cattgccggt	ttgctgaccg	aggtgcaacg	catcaagagc	gagggcacta	taccgccggc	1680
aaagcgttgg	tagagcgtta	tgccgtccac	gtggaccgct	cttgacagag	gaagtgtgta	1740
cgcgctatgc	caagctggat	attgtccgta	taagggattt	gtcaatcctc	ggttgagacc	1800
cgtatataat	tcgagggcag	gcttacggat	gcaacgatag	aatacacgga	aggctatgcc	1860
gacaaatgct	tcgctacagt	gcagaatata	gcttcctgcc	tacagacagt	cgcttttgca	1920
ggaggcacga	agattgcgct	cgcacctccg	acgggcgatg	acgggtgtact	atcggccagt	1980
atgcgtgaga	aaggactcca	ctacggcata	actttggagt	cactcgcgaa	catctgtctc	2040
gactggctcg	cacggccgcg	cttcgcctcc	actggccgac	tatctgtgga	gacgcgatgt	2100
aagggagcga	agatactcgc	cacgatgatt	tttcggcccg	aagaactgac	tcattgacagg	2160
caacgagatt	gtcccgagag	gccgacaacg	tggaacttcg	cgagcactga	cagccaatct	2220
gctggagcga	atgcccgaa	cgatccggag	catcgccgat	ggatcgagag	caaagagact	2280
actcctgaca	tgatgacggg	agtttgacgc	ttgcagccag	attgtttaca	cgcggcatct	2340
ttccggaaga	cggccggcag	agaaactctt	aacactggcc	attctccatc	tctccgatga	2400
gagcagaaa	cggagcttcg	gcgcgcttcc	gcacttctgc	tcaagcggta	gggcgaggct	2460
ccgcagaacg	gacaaaaaaa	gtgctgtgcc	tattgcccga	tcgagccaa	acacagcacc	2520
ggttttgtat	gaattatgtg	aagatatcgc	ttcgaaactc	acttctaccc	aaaggacgag	2580
taagagaagc	gactatcatc	gatcatcgag	aagcctgtat	aaggcaccag	acagtccggg	2640
atgcggtgcc	atcggctgtc	tgattgtttt	ccagcagagc	agccacgata	cgcggaaggc	2700
caaggcacta	ccgttgagcg	tgtggcaaa	ctccactttc	ttatcgcatt	gcgataacgg	2760
cacttcagac	gattggcttg	gaagctctcg	aaatggacac	cgagctaacc	tccaaccacc	2820
gctcttgggc	agccgaatag	actcgaaatc	gtaagtcaat	gccgaagtga	agctgatata	2880
tcgcgccgag	agcgaaggat	acgccacgga	agteccaa	tatctacaag	gccttggaca	2940
agccgaccat	ctgatcgagc	tgttcgtagg	agtgttcggg	cttgctcgatc	agacgatctc	3000
caccttggtg	aactgatgga	ggcggttcag	accgcgaaat	ccttgccgta	cgaaccggct	3060
tcgcgctcga	agcaagccga	gtaagcgta	ggagaatggg	caattcgtcc	tcggagagaa	3120
tgacatcgcg	gaagatttgg	tcaccggcac	ctctgccgtg	gggatcagat	acaggttgtc	3180
cgcgggacat	ggtacatctg	cccttccttg	tcagggagct	gtcccgtaac	gtagcggaa	3240
cctcattgac	tacatagggc	ggctctatct	ccgtgaagcc	ggcttgccgg	cttcatccaa	3300
gaagaagttg	accaaagctc	gctgcaggcg	tgtcctttgc	ccttatagac	agggaagcct	3360
gctccggtta	tcttgacgcc	ggttcgaagt	cgatcagatc	gtatttcttg	gccagatccc	3420
aatgtgggag	ttgtgcgttc	caagctccgg	cactgtgccg	cctgtcttca	cacagacatc	3480
tcctctgcgg	tcttgccctg	agggacagac	tcattgcggca	gattcgggta	agcagaagct	3540
ggtggcggtat	agcattctcc	agatcagctt	tccgctctcc	agatgggtgc	tcccggcttt	3600
catatcggtc	actttcgcac	ggatggctct	ccctcgtctt	tcttgccggc	tttcatcaaa	3660
gctccgatct	ccttgcaatg	gcgttttgct	ccgccaagcg	agcatccaga	ctctgttgag	3720
tttccgctgc	tgtctgtcga	gagagatgac	ttcgtcgaga	atagcagctg	catgaagtgc	3780
ttcaccgcca	agcgacggat	cacttcttcc	ttgttttcta	tgtttgcttg	agtgtcagca	3840
tagtatatcg	aaaaaaacaa	aaggcaaatc	ccaaggcggg	tacagcctgt	agagattcgc	3900
cccggggatc						3910

(2) INFORMATION FOR SEQ ID NO:187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

gcgatatact	tgatggcata	gtcaagcgaa	acggaaagg	gttcgggtatt	tttggcaacc	60
ctacaaactt	gcctgcatgc	ttgatataag	ggccgaagg	cctacggcta	ccattacatc	120
cgcatectca	tattgtccca	gtttcttggc	aggaggaata	gttccaaagc	ttcctccagc	180
gtgatggatt	cgatggctgt	cccggctgga	gcgaggcaaa	ctgcgccttg	ataccgtttt	240
ccttacccgtg	cgacctttct	gcaccatcgc	tccgtagcgt	cccatttttg	ctacacagat	300
tctccggtea	caggatccgt	accagcatt	ctttcaccga	tctctggctg	ggatcgaact	360
cgcatgcttc	tgccaccaac	gggtggaatt	tgtgtagaac	cgaccgatct	gcttctgcca	420
ttgcagtttt	ccttcggcta	ttgggtcaaat	tctttttcca	ctttggccgt	gaagttgtaa	480
tcatcacct	agggaaacgaa	gccacgagaa	agtcgttcac	cacaagcccc	atatcagtgg	540
gaggagctta	ttccggctct	gtccgttcag	ttccgttttg	atcgtctcgt	tatggctttc	600
cccttggtgt	attccagcag	gatgtattcg	cgtgtttgcc	cggtttgctg	ccgcgtacta	660
cgtattcgcg	attctgtatg	gtttggtagt	gggggcatag	gtggatggcc	tgccgatgcc	720
caactcctcc	atthttcgaac	gaggctggcc	tccgtatagc	gtgccggacg	ctgcgtgaag	780
ctctcgttgc	ttttgcatga	tgcagagaga	gcgtatcgcc	ggctttgaca	gaggcaatag	840
ctgctcctcg	gtatttgtag	agccatgttc	ttcgtccgaa	tctcacgata	gactccgagg	900
aaccgcgtcga	atacgatcac	ctctccttgc	ggctgagggt	ctctgcaaac	ttgtcgggtc	960
cgattgttat	cgctggtttt	cgaggatggc	atccgccatc	tgggaagcaa	tggttctgcg	1020
gcggatcagt	gatatagctt	ttgctctttg	cnggggtgccg	tctatctctg	ctctatgtta	1080
taagtaggac	ggatggcttc	gtgggcttct	t			1111

(2) INFORMATION FOR SEQ ID NO:188

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

tctgcgggatc	agcaacggta	cttcgcgcgac	ctcggcgaag	agtatgccgc	atcaaccctc	60
ctttctccga	acagtgaag	acnacggcag	gcttacagat	cggactctct	tttgaatatc	120
cccattcttct	ctgccatgca	aacgcaaatc	gcgttcggag	cagtcgcctg	caaatacgct	180
caagcgagct	tgcactgtcg	aagagaaaaa	agccctctat	aaagagatca	ggcaagcata	240
cagcatgccg	tggcagccga	taaggccatc	gcagcagccg	aaaacagcaa	ggccctacgc	300
tcaaggcata	cgaatacgct	cgcgacagct	tgcaggcagg	gcgttgctctg	cctacgaata	360
tgccgaggca	aaaacaaaat	acgccctcag	ccagtggaa	aacttcgtgc	caagtatgac	420
ttcatatata	aagccaaagt	ttggatttct	atcagggcaa	agacttctaa	aagactcaca	480
agaaaagctat	tttgaaccct	cagcgagggtg	ttcatgagat	ctatcaggac	cccagacatct	540

aggggtgctgc	gtcaaaattc	gttttgccac	agcacccttt	taacgtcatt	cgacgtaaga	600
aaacgccaat	gaataattct	tttcctgac	agagattatg	ccctaagatt	ctccggcaaa	660
tgtatagggg	gtatcctgct	tctgctggat	cgaaccaaca	ttgaaattcg	gattgctttt	720
gacagaatgt	tgcagccgca	caggaagatg	ggctatacca	cagggcaaga	tgccgggtact	780
ccgtgaggat	gatgggctac	ccccgtatgg	ctcttcgagg	tac		823

(2) INFORMATION FOR SEQ ID NO:189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ccatggcact	ctgatgatcg	ataattccag	tgctttccgt	atgcaggaaa	cgttcccctc	60
gtgggtgccg	aggtaaattg	ggatgatgcc	ttggtacacc	tcgcaatata	atctccaata	120
cgaactgtac	aacgattcag	atgggtgggc	actcaagccg	atagaagacc	tttctcacat	180
acgtcgtgta	cacgtgccac	gtatcaggct	gccagtgggtg	caggtgcgct	gggtatggcg	240
gagttgtaca	gcaggcggaa	gagttggctc	ggggagagaa	gcctaccgtg	gacaattcgc	300
ttaccagttg	atgtataacc	tgattccaca	gatcgacgtc	tttcggacaa	cgactacacc	360
aaggaggaaa	tgaagatgta	tcgcgagacc	aacgtatcat	gcatagcgat	gtgatgggtga	420
gtgcaacctg	tgtgcgtgtg	cantgatgcg	tgcccacttc	gaggctattt	gggtggaaac	480
ggaacgcccg	tcgctcccga	agaagctcgt	gcagcctttg	ccaaagcttc	ccggagtgtg	540
cttgtgccga	tgagcccgtt	cag				563

(2) INFORMATION FOR SEQ ID NO:190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

taggtattta	atgtcggatt	tataactaaat	aagtgggtatt	gggaataactg	aattgcacat	60
gaaaaagccc	tcgatacata	ggtgctttta	ttcattttata	tttgtgtatc	agccgattat	120
tccgtgtgtt	tatgggtatga	tcaatgaaca	aagctatggc	acgacaagga	aaatcatcta	180

atgaggcctt	tgaaaagaga	aggttatcgc	ttaggttgca	acttatacaa	agggatgaga	240
gtggaaccgt	gaacatactt	cttgcggcag	cagcctatga	actcaagaga	gctagaaggc	300
tcttttgac	tttatcaaaa	caatctgcga	gatactgttt	gctacaatat	ctccctaaaa	360
gggacttttt	aggggatgac	tatataggga	gttaaacaaa	gctatatagc	aatcggccca	420
atcctatata	gcaatcaaac	ga				442

(2) INFORMATION FOR SEQ ID NO:191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

ggctgagagg	tcaattcaat	ttccactctg	caccgtcttt	cgtatcttta	tcgtaaatec	60
cagagccgtg	agttcgtcgc	ggatcttata	gcttgctgcc	aatccttacg	agctttggct	120
tcggctcgga	tacttaggag	cagatccctg	ctttgccgaa	ggcttcgctg	ccaccggctg	180
aagacgcctt	ttcatccgca	taccaagcag	gtcgaacagg	aagaggcgga	atgtagtacg	240
cagttctcta	agttggaaga	agtaatggta	ccttggtccat	tgtgtacagc	attattgcgc	300
gcgctgcata	gaaaagggtt	gctattacca	ttggactggt	cagtcacgtg	tcattggcatc	360
gtagcaacgc	ttacgcagat	cgccaacctc	taggagggtc	tgctcggcag	cttcaatcca	420
tcgagcaagg	ctgctgcata	cgcaagcgct	ccaaaccctt	ctctgcgcgt	tccagagctt	480
cattgctgaa	tctacagtgc	ctcgatagtg	ggctccgaga	at		522

(2) INFORMATION FOR SEQ ID NO:192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

gggccaacc	cgtagcagga	atgaaaagaa	gcagaaagag	gatccggaaa	tccggatccg	60
gtgcaaggat	gttttcattg	tttctttcgg	attatcggtt	gtttcgaaca	ggcggtccag	120
actcatttcg	tcttgatca	atacctgctc	ggtttgctac	cgctcctgcg	cgaaacgata	180
ccggcacctt	ccagttgtcc	atcaatcgcc	ctgcacgggt	gtagccgata	ttgaactttc	240

tctggtatta	gaggtagatc	cctgttgtga	gtttactacc	attcgggcta	cttctcgaag	300
agaggatctt	tctcctgcgg	attgaatgct	ttcggtcctc	cctttcacct	tcgggcacat	360
actccggcag	ctcataagcc	gaggtatagc	ttcctgtagc	gaaatgtggg	gagtgacggc	420
ttcgactcc	ggagtatcga	gaaagcgcat	tgcagacgta	ccgtgtcttt	tccctgatag	480
aaaagcatat	tccacggccg	acgagctgat	tggctcccg	ttgatccaga	atggttcggg	540
gtcgatcatg	gagaatactt	tgaaggcgat	acgagcagga	aagttcgctt	gatgataccg	600
gtgatgatgt	ccgtggaggg	ccgttgggtg	gctaccacat	gtgaatacct	gcggcacgcg	660
ctttctgggc	gatgcgggta	atcggagttc	tacctcctta	cccgatgtca	tgatcagatc	720
ggcaaaactca	tcgacatcag	cacgatatag	ggcaggaatt	tatgaccgtg	caagcggctg	780
agctgccact	gataatctga	tcgttgtatt	ccttgatggt	ccgaaccgt	gctccgtcag	840
catgcggtag	cgattgtcca	tttcgatgca	gagagagttc	angtgggtac	caccttggtc	900
atatccgtca	cgatggctct	gtcctcgctc	gaagcctggc	cagatagtga	cgttcgatgg	960
cttcgtagac	ggcgaactcc	gcattctcgg	gtctacgagt	acgaacttca	gttcggcccg	1020
atgcttcttt	acaagaggga	ggtgatcatg	gcattcagac	ccacggattt	cccttggtccg	1080
tagcacctgc	tatcatgagg	tgaggcatct	ttgcaaaggt	cgaagataac	acttcgt	1137

(2) INFORMATION FOR SEQ ID NO:193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...5366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

aacgggggag	agactctgct	ccggcagatg	ggcggccaaa	gaggcggcaa	gtcgggaagcg	60
attcgcctcca	cgaggctctc	ttcgccctgct	ctgaactcat	tcgtatcagc	cggctaaaag	120
gtgggaagaa	aagcattttgc	ctttccctcaa	ttgttttccg	ataaaagcct	tataatcacc	180
ttctcgcaat	aaatccgaaa	ggagttggcc	ggattgttcg	tttgtatgta	tagacgggag	240
gctccctctc	aagcatgagc	tgatagagta	gctgataagc	tcgttcgtag	gcgcgaaatc	300
cgggaaaccc	aatatgctgt	ccagctgggt	gacggctaca	agactacatg	ttcgttatag	360
acttgccctc	tgatcagttg	cgtgccaaaca	agatatccac	ctctttcgct	tccagacgcg	420
ccagagcttc	gtccatcttc	gtcggctcat	ggccatatcg	ctgtccattc	tgaggataga	480
gacgggtggg	aacgtctttt	aagctcttcc	tctattcttt	cggctccata	ccccacaggt	540
gcaggtgct	cggtctctct	acgcccgatg	cccgtttgca	ggagggacga	tgccggaag	600
gggtctgctg	tagccgcagt	agtggcagac	gagcataagg	aatgctttgt	ataggtgaga	660
ctcacatcgc	agtggatgca	acggagtttt	ccccacaaga	gctacaaatg	atatacggag	720
cgaagccctc	tcgatttgga	ggacgacggc	catttttttt	tgccgaatcg	tctcttcaat	780
agctagacga	gggggaaaga	aagcagttca	cctgcaccga	cctgtctttg	acgcgcattc	840
tgcccatgtc	tatgacttcc	aaatcgaatc	gggggcgaac	ccatcgtcgg	gccaggtgat	900
cagttcacag	gctttgtggc	gcacttggtg	ggcacctcgg	cagaaggagt	ggccgaagcc	960
aacacaacag	ggcagtcgtg	atccggccga	gtcgagctgc	cacctgtcgc	gtatggaatc	1020
ggggggcaga	tctgtctgtt	tgtagaggta	ttcctgttcc	tcgtccacga	taatcaatgc	1080
aagcgacgga	atggcaggaa	aagtgcgat	cgaacaccca	gcaccaccaa	ggatattccg	1140
ttgtggccaa	tctgttccac	acttccaccc	ttttggatcg	ctttcaaagg	catgatagga	1200
tagcaaacaa	ctgcccagcc	tctcgccata	cgtgtggaca	gagtatcgct	tcctcctcgt	1260
ttgttcgctt	ccgggagagg	tacaggactt	ggcctcctga	acggacaact	tcttccgtcc	1320
atttaagagt	tgtttttctt	tgcgtcgaaa	gtcatgcgta	tagaggagag	aagaggtttt	1380
tgaggtagag	aagccgatac	tgcggagtct	gtagaactct	ctccgattga	atggcttttt	1440
cttctctctg	gggtgctctc	cacaagcggt	ctcacctccg	ccggccgaat	acatgaccga	1500
gtgtgtaaca	gattcggtatg	aaaaatccct	ttctttttca	aagcggaaag	ggtgactgta	1560
gcatgaggtc	ggactccgcc	agtagccttt	gcggcatcgg	agaggaatat	gggaggggtg	1620
ctctgttatc	agctctgccc	aatgaagcaa	aagggcggat	tgcttgagac	acgatgcaaa	1680

ctatccagaa	gcgaggcaaa	agtcttttcc	gtccgaaagg	ctctgccaga	cgaacgaata	1740
cttctgactt	gggcttataa	cggctttttac	ttcttctcc	agccgtatgg	cccctcgttc	1800
gaccaaggag	gtaaagcgcg	aatcgctcgt	ttgccgacag	ccttttgacg	ggcgtcaagc	1860
gttaggttcg	tccttttgcc	gactccaaaa	tatcgaggag	ctcctcttca	tacgactaag	1920
ccggctgtcg	gcttcgaagt	ccgtattata	atggatgacg	tatggctctc	gggtagtaat	1980
gctgcaggca	gagcagcacg	gagtacttcc	cctgcgtaca	tatgtaataa	gccgacagcc	2040
actgccacag	actcagcttg	aggcagtaac	tgacggctta	tcgtcaggca	ggaagagaac	2100
ctccttgatg	aaatttgacg	attgggacgt	ttgtcggaca	gtccgatgat	aatcccgtat	2160
agtatcgctt	ggctccgaaa	ggtaactacg	aacgcacccc	cacgaagcct	tctcggctaa	2220
cccctcggcc	aatcggtagt	gaaaactacc	ctcagagcca	agggaatgag	gacttcggca	2280
tagcgcatag	ctatcttctc	ccttcacatc	ggagtcacatg	ctatgattcc	gctttcagat	2340
attcgtgcat	ggagctgctg	ctttccgctc	atcgcccatc	gccaatatca	cagtggctcc	2400
gcacgaacga	tgtcaccacc	ggcaaaaaa	tcggggagag	ctgtctgatt	ctctcattga	2460
cgacgatggg	gtcacttcaa	gaccggaaaa	gttcggggaa	gttcggggaa	cgagcggatt	2520
ggcgataaca	ccgatactta	caatcactcg	tccaccggga	tctcctcgat	agcccccggtg	2580
atcgcaacag	gacgacgcga	ccacctgcat	ccggctcgcc	aagctccatc	ttttgcaggc	2640
gcacgcagtc	actcggcctc	gttcattgcc	gatataattcg	ataggattgt	gcagttcagg	2700
aactctatct	cttccctcct	ggcgtgcttc	acctcttcca	atctgccggc	atttccctct	2760
cgctgcgtcg	atagacgata	atggcacggt	ctgtccgagg	cgtttgccg	tacgaacgga	2820
gtccatggcc	gtatttgcgc	cccgatgaca	agctacattc	ttgcccttga	aaacgggtgt	2880
gtcgtgtcgc	gttggctcgc	atgcatcaga	ttgacgcgcg	tcaggatttc	attcgaagac	2940
tgactcctac	aaggttttca	cccgggatat	tcatgaaatt	gggcagaccg	caccacttcc	3000
tacgaataca	ccgcgaaatc	ctgcttcacg	caggctcatgt	atgcgatcgt	tcggccgaca	3060
atcgtattcg	tctcaaagcg	tacgccctct	cttcgagaag	attgatctcc	gaatcgacta	3120
tactattcgg	aagacgaatt	ccggaattcc	gtacttgagc	actcctccga	tttcgtgcag	3180
ggcttgaata	cggtcacgct	atagcccaac	ttggccatgt	ctccggagaa	agaagtcggg	3240
ccggaccgct	tccgatcaca	gccactttga	taccggttcg	agggccattt	cgggaaacttt	3300
gagtgcgccc	tgttcgcggt	cgtagtctgc	ggaaagcggt	ccaagaaacc	gatggcaaca	3360
gccggtttgt	tcattttcgt	aagatgcacc	ggctttcgca	ttgcttctct	tcgggacaga	3420
cacgtccgca	accgccggca	aagagcttgt	ctctcgcaaa	gtagatgctg	cagccagtaa	3480
tcgcctactt	ctatctgctt	gataaaggtc	gggatattga	tactcacaga	catccttcca	3540
tacagctcgg	ttgcggacaa	tcgagacaac	gagaggctcg	gccatagcgg	cctcacggga	3600
caaaccgcga	ttcacctctt	cattgacttg	gagctacgat	agagggggtc	gagttcgggc	3660
atttcagccc	gtggagcgac	atgcgttctt	tattttttgag	cgcgttgcgc	agctcctctc	3720
tccaggttca	gagcgacgca	gtcggataag	ttcttctgta	gtcatgtcaa	taagcagaaa	3780
ataaggttat	tccatctctc	ggtatgcgcc	caaacgcgat	atatctcatc	gaaatccact	3840
tggtgtgcat	cgaattcggg	gccatcgaca	cgacgaattt	cgtctgtcct	cccacgctta	3900
tacgacaagc	cccacacata	cggtgccatc	caccataatt	gtattgagag	aagctatggt	3960
cggtatctct	aacgttttgt	caggagagaa	acgaacttca	tcatacagc	cggcccgcag	4020
taacgcagag	gtctaccggt	tcccgtttga	taacgctttc	cactccaccg	ttacgaggcc	4080
tttcgtccca	taagacccat	cgtctgtcat	gatgatactt	catcgctatt	ggctcgcatt	4140
tgttcttcaa	ggataaccag	atcttagttc	tggcagccaa	tacgacaatt	acacggttgc	4200
ctgctttgtg	gaaacctcca	cgatcgggag	caaaggagcc	acacccacac	cgcctccggc	4260
acaaccactg	tgccgacctt	ttcgatatgc	gtactctgtc	ccagcggacc	tacacatccg	4320
tgatatagtc	gccgacttcg	agttcggcca	atttcttggg	aatttgccca	cggcctgaac	4380
cactaaggta	atggtaccgc	gcttttatgtc	gcctgtgcaa	tagtcagggg	gatgcgttcg	4440
cctttttctc	caacgcggag	attacaaaat	gtcctgtctc	tcgcgatttg	gctatacgag	4500
gagcctctct	tccagcttga	tcacattagc	cgagaagtat	tctttggata	cgattttttc	4560
atagtaacag	tcacatttgc	ccgctgctaa	ccgaagcggt	cggccgaaag	gtaagaataa	4620
tccgggggga	gtagacagga	caaagaaaag	gacactccgt	tggagagctg	agggagcgtg	4680
gcagtcacat	gggaatacca	tcggggaaac	ggataaatat	ggtagttttg	tctgtaaata	4740
agtaagcata	aacccataat	gcgcattgat	ataatcaccc	tgctgccga	aatgatcgaa	4800
aaacactcaa	ctgctcgatc	atcgggaggg	cacaagaaag	aggactgctg	gactgaaact	4860
gcaccagctt	cgcgactatt	ccaccgataa	atggaaacgt	tggacgacta	tccattcggt	4920
ggagagcccg	gcatggtgat	gcaaatagac	cgatcgaccg	gattatcacc	gaactgaaaa	4980
cccagagaga	atacgatggg	tgatattcac	ctctcccagc	ggtgagcggt	tcgaccaacc	5040
gatggccatg	aactgagtct	cctatccaat	ttgattgttc	tttgtggaca	ttataaggga	5100
tagactatcg	tatcagggaa	catttgatca	ctcgtgagat	ttcgacggcg	actacgtact	5160
caccggtgga	gagttggccg	ccgcctgtgat	gaccatgtga	tcgcccgcct	catccccgga	5220
gttctcaacg	atgccggcag	cgcctgtccg	acacctttca	ggacaatctg	ctggcccctc	5280
cggctctatac	ccaccggccg	agtataaagg	ttggcgagtg	ccggatattc	tgctcagcgg	5340
aatgaagcca	atatcgccaa	atggcg				5366

(2) INFORMATION FOR SEQ ID NO:194

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

gttgaatgta	nagactgaat	tgggcccatt	cttcggattc	gaaacgctgc	ggctttctat	60
ttcgacaacg	aactcatcga	aaaaagcttg	ctcacagcga	tgaattgaag	tggtacaatg	120
actaccagca	gtgggtgtac	aagacgctgc	tcccgaactg	actaccgagg	aaagagcttg	180
gctcaaagag	aaaacttgac	tatctaacca	caaaaatggc	attaatacag	agtgttaggg	240
gctttccctt	ataatcggcg	aggatacctt	cctcgccgaa	aatgccacta	ttgtggcgat	300
gtagtcatgg	gcaaaggctg	tagtgtgtgg	ttcaatgccc	gtatgcgagg	cgatgtcaat	360
tccatt						366

(2) INFORMATION FOR SEQ ID NO:195

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

aaacttttgt	gcatcccnaa	ggatgcggta	taggttggtt	tggtgccgca	agcttgagga	60
attatttgtt	ggcctttcga	tatgtcgatt	gccttttcaa	gtattcaggt	ggttataacg	120
ttggggatcc	acctcttccc	attccgacag	agaagttaag	cccaacggtg	ccgatggtac	180
tgcgtcacag	tgggaggtag	gacgcgcgcg	ttttttaaga	agcgtgagag	agaggggggg	240
ataggtctcc	accctcctcc	ccggaaaaaa	aggtgaagga	gagagtctcg	aatcgaggct	300
ctctcctttt	ttattttctc	tctctccaaa	aatcattttg	ptttctctct	attcctctat	360
atgctttctc	cttttccttc	ctttcctccc	tttgtttccc	ttcatcttcc	tttccttttc	420
tcttttcate	ctcagtcgga	ccagcaaagg	ataatcggcc	atttgctttc	ctcccccttg	480
cttcgcgtta	tcttataaaag	tgagttcgat	ataagcgta	tggtgccgac	tctcataaga	540
tttgtcgatc	aatcctttgt	tgggatatta	actataaccg	atcagaaatg	aaagggaaaa	600
agtttgacgt	ctcatcgcat	gtcgaa				626

(2) INFORMATION FOR SEQ ID NO:196

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

ggcaggtcga	gatacagagtc	ggggccggcc	accacatcca	cgtgatgttg	cggatcaact	60
cctccttgac	gcgctcggcc	atgcagccca	ataccccgt	acgagacggg	aagaagccc	120
tcttttcttt	cgtagcgagt	ggtaatatgcc	agccgggttca	gcactttctg	ctcggcattg	180
tcccgtaccg	aacaggattg	accaggatcg	tatccgcctc	atccacgttg	tccgtgaggt	240
tgtagcgctcc	atctgcatta	cggacgctac	cacctcactg	tcggctacgt	tcattggcag	300
ccataggtct	cgatgtagag	tttgcgctct	tgtttattct	cggggattta	gagtcggtcc	360
gatttggtcg	atcatgcttg	tatgttatat	caattgtcgt	attatctcga	ttattaccga	420
caaaagtgtg	taaaactact	tgtgctcatt	atgtttgtga	tggaaaaag		468

(2) INFORMATION FOR SEQ ID NO:197

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ccactgacct	ttcctctggt	caggaggcgt	tcgatgagca	tttcctcggt	actttgcaga	60
ttcagcacta	tgtccacctt	ccatccatga	tgtgcgagat	cgtctccatg	gcttctgctt	120
ggggaatggt	acgtggaaat	ccgtcgagat	aatcccctcg	gtatcgacca	aagtgcgtgat	180
gagcttttcc	atcatgccac	gatcaggctg	tcaggtagca	ggtgtccctc	gttgatgtag	240
ccggcgctgc	ttggcccagt	tcgggtctgag	ctttgatttc	ggcacgaagc	aacttccggt	300
tgaatatatgc	cggaatccat	atcgacggat	cagttcttcg	cttgggtgcc	cttcccggaa	360
ccgggagcac	cgaagattag	tacgttaagc	attattcttt	tattttatag	atgtcctggt	420
acatgcgtcc	cagatcatca	tgtcaaggcc	gtgtcctacg	ataaagtcac	tgccgatctc	480
caagcctaca	aatcggtatg	gatatcgcat	ttgagtgcag	cgggtttggt	cagcatagcg	540
ctatgcgcac	ctctttggct	ccaagctcgt	agaaattctc	ctttacgcac	tcatcgata	600
acccgaatca	atcagatctt	ctacgatgac	cactgtctgc	cacgcagtgc	ggcgcgtcacg	660
ggcataatct	ccttgagcac	gaatgtctct	gcataccgca	ataactggag	tagcggggcga	720
aatccacttg	ataacctcat	cgagagcctg	catcagttcg	gctgcaaaca	taaacgagcc	780
gttctgatac	agacgaatag	gggattgtcc	tcatgcagat	cccgtttgat	ctcgcagcca	840
tcctcttaat	ggcttcatgt	atgcgagtg	ccggaatgta	aactcaaact	ctttgtcttt	900
cagtttgatt	gttctcattt	gtcgcaatga	cttctttatt	gtgcgtgcaa	atatagccat	960

tttgcataagg	gcagctgcat	gaaacgactc	cgtattatat	ataaggagge	gacgtataaa	1020
ggatgcgttg	ggataatctc	gcgaatccca	tggtctgata	gtttacgccc	cgaattttta	1080
tatttctacc	tcctaaaaaac	gtggcgtggg	aaaatttttc	ttttggtcga	gaagtgaaaa	1140
aaacacgtgc	cggaacgaaa	aagttgcggg	tccacttttc	agaaaaacag	tgccacagtc	1200
ggagcgtttc	cggttcgtgt	ttttagttgg	caggttatga	gcatgtgcct	gcaaggggtga	1260
tgtgcaatgt	cgaagtaggt	cggatcagat	aaaaacagct	gccacaagta	ctacacttca	1320
cttgtttaaat	aagtcagaga	cgggttcctt	tctattgata	cctaattggt	tatggcgact	1380
ttttctctgt	ggagaggttc	tcgggcgga	tggaataaac	ctgaattttt	ccgaaaagag	1440
tcggttgcat	ggaaaagtct	gtacctttgg	agaattataa	accaaaaatt	ttgcaccaca	1500
tggctaacga	taagacgcaa	ccgtgcagat	gctcaagcac	gatttggact	atttgggaatt	1560
gctctcggga	gtttcccgac	agcgacggaa	gcagctacgg	agattatcaa	tctcgaacta	1620
tattgaatct	gcctaaagga	acagaacact	tcctggcgga	cattcaggcg	aatacgaagc	1680
ctttatccat	gtgctcaaga	atgcgtccgg	tagtatcgga	gaaaggtaga	cgaggtcttc	1740
ggtggtcagt	tcgcgcaaaa	tcagagcgag	agctgtgcac	cctgatctat	tatcctcgcg	1800
agaaactcga	actgtgaagc	aaagtgtatg	gcggatggag	gactggtata	tggtcacgct	1860
gatcagctga	tcaaatgtgt	tcagaaagct	gcagagaaat	atactcgctc	caggtacgta	1920
agacccttcc	tcccaagtac	agctatatca	ttcaggagct	ctccacgaag	atggtgtcaa	1980
tcccaataaaa	tcggcttata	tcagcagcac	tttctctcta	taatatccac	aggggtgtgcc	2040
gatgacttta	tcattgcctt	agttagacca	tccagcggct	ggtcacgcac	catctgcacg	2100
ttggtagggg	tgtctttcga	ccgtggnccc	ggagcacata	tcataca		2146

(2) INFORMATION FOR SEQ ID NO:198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ttttctcgaa	ccggaaagaa	atttttacgc	tcgtaaacga	aaattttttg	cacgtgtttt	60
cgaattttta	cgaccgcgaa	tttgatgatt	tctggttctg	tttgtttggc	ggatcttcnc	120
cgttccgtcc	gaaaaggatg	ggtgcttgcc	tgaggcgaga	ggtcgcgtgt	agtatggcac	180
atacacgata	gcttcaatgc	tgaaagcaca	cagcacgaga	tctgccctac	gacagcctca	240
aaagaagaaa	cggggactaa	tggaacgat	ccttctgtcg	cgccgaagaa	tgcaagcag	300
attcaggaaa	agatgaaagg	aggggctcgc	aagccatggg	atgtcttgct	tcggaggggtg	360
tataaaaagc	gagatattct	ccgtattcgg	gacggccgaa	agatcatcgg	tcgggtgtag	420
caatagatcg	gctacggcaa	aagaataggg	aatacatgga	tgtgatgggg	atcggtggcac	480
tcttcgcaga	agaatatctg	tgcttgagtc	gaagttccgc	accggacagg	tagaagggtt	540
ggctacgcag	gtcggttcgc	tatgagtgtg	ctctttgtcc	gcaggggctt	ctcatgacaa	600
tgttttgcca	tgagacatgc	catacctttg	ttgtgatatg	atggggcata	ataccgatga	660
tcagcacgac	aagggaggcc	aagccttgaa	gaatatggag	agcttctttc	tcacaagcga	720
tcggtgtttg	gaacaaaata	agagttcctt	cttatatcaa	gtgttttttt	gaccgatttc	780
cgtctaatac	cgaacttgct	tgaacgtgtg	accagatttg	tcgataatat	ccgtgctatc	840
agactctcct	gactatagcg	tcgggcatag	atgtctccgg	ccaaccgtgg	atataattgc	900
cgaggacaca	ggctgaagca	ggaagatagc	cgaccccaat	aggccggtaa	tgatgcccat	960
gaggacatcg	ccgcttcctc	tgtcgccatg	ccgggggttg	ccgtattgtt	gaatacgacc	1020
atgccgccgg	catacaggtt	gcactgaatg	ctcctttcag	gactacatag	acatgatgtg	1080
acaggcgagg	aatcgggctt	ggcgcagccg	ttcatagtc	gtattgcat		1129

(2) INFORMATION FOR SEQ ID NO:199

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1946 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1946
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199

cattatcggt	acttatccag	tcaataatca	tatattgagt	gggaatatct	ttattttggc	60
agatcggtatg	gcctgaggaa	aaatttttatt	cattaccttt	tttccaacca	cctgcatcgg	120
ccgtcattcg	aaagttgaat	tacatccttg	tcagaaatcg	ttgttatttg	attgaaattc	180
ttttgttaag	catttgaaat	tagtcgttgg	gactttgtcc	aatgaagtgt	tttgatttaa	240
ctctgccggc	tgctcaatct	taatcgtcga	tatatatctt	tttccatant	ggaccattta	300
tgtcaacaga	agcacatagt	gagttccttt	gatataagta	gaatgcatca	ttctttcttg	360
tctgctgggt	ttattcttca	acattatgtc	atgatgatga	ttagtagagg	aacatccaac	420
tcaataaatt	ttagaacatt	cgattcatgc	aatccattat	gtttgtaaaa	ccttttagtg	480
gtatttttgtg	attacatgcc	caatcgctat	tccagcttgc	ctaataagct	cgatagtcac	540
atgaaaggga	ggtggtctaa	ttcatgggtca	aaacaaaata	cacaatcagc	ttaggaaaagg	600
caactaagta	caaaaacttg	caatttttcat	ctttttccca	tcattattca	agtaatttcg	660
ggaacttcct	ttatttcaga	aatcaaacat	aatctttgtt	cactttatga	acaaaagcat	720
tttcaatttt	cttgagttgt	gtgcatcagc	atcctntgca	agtttgctga	ggaagtcctt	780
ttgatactac	aattttccat	atttgtaatt	tattggatat	attgtactat	gcaaggatatg	840
aaaatctatt	aaagtcaatc	ctctgaagcg	tgaagaactt	tgttttgtgc	acatctatcc	900
tctaacatgc	acttgatat	aattgtatat	tgttgtttat	gaatttctcg	tagttgtgga	960
aaaaaattat	tttttgagaa	aattcttggc	gatccgattc	tttttcgaga	cttttatatt	1020
agtatatatt	actatattcg	tttttgaaac	gaaaaagcac	atgcagattg	aagtccttta	1080
caaactggat	gatgggattt	gaggatatga	actttgagag	agttttatgc	tcatgatgaa	1140
aggtttgggt	ctaaatgttt	tacaccctct	tttttgaggg	agggcttatt	cgcaatctta	1200
aattttccgga	gtttgtttag	ttctcgacag	agtacacatt	caatattttt	attacctttg	1260
aagcttattt	agctcaaaa	ggaataatcc	attataacta	tgagtacaaa	aaacacgaaa	1320
gaatggctct	tttagaggcg	tttaagttgt	tttcggaaaa	accttacgac	aagttactta	1380
tacaaacctc	caggagaata	ccggattaag	cagaggcagc	ggttgcatca	tacaaaatca	1440
aagtctgctc	tttttgcaac	agtgttaagt	agtttatact	cgcaagttcc	attcctgagc	1500
gttctttttga	aaatggagaa	gcctcaaagg	ttttatacaa	cgcttcacgc	aaaattgtcg	1560
tatagagcaa	agacttttga	aaaaagagga	attgagaaca	taaataaatc	tatgctcact	1620
tatgttctca	aactttttac	tactgcccaa	ttatggcaga	acgatagcag	aatggatgaa	1680
aaaccagcaa	aggacttggg	ttaaaataat	tagaatgcga	tggataggaa	agaaataaga	1740
agtgatgttg	atgtggaaat	ggttcattct	tatttcataa	tctgtattta	ggattttcct	1800
tctccggtag	cacgaaaggg	gggggtacga	cttaaatttt	cttgaaaaag	agttcggctt	1860
cattactcct	ttctatttaa	agaataaatt	ctaaatccgg	cgatcgttca	agggagaaaa	1920
gtatcaggta	tatcttctgt	atctct				1946

(2) INFORMATION FOR SEQ ID NO:200

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

atccggaatc	tatcgaaacag	gccatgaagg	ccaaggagct	gatcgacaga	ctacacccac	60
gccggccccg	aagacttcta	cagagaaaaa	accgaataaa	tcgaaatcga	tcttcatgcc	120
ggcgaaactac	tcgaaacgac	ggcagggtga	agaatgggga	tatattgcag	taccaactgg	180
acaaattcca	cgaagtatga	aacaatacgc	ctcctgttaag	ggacaaaaga	ttgttttcat	240
tcatgcaaag	gtgaaggcat	attgcggcag	gcaatagaaa	aagaactgcg	caccgctaca	300
aacaacatcg	ttttcaggat	gcctccttcc	gagaatatgg	tttggtgcta	cgatgggtgat	360
cattcattga	aggatagtag	cagttcctgc	cgatggaaat	agaaagaaaa	ttcctggtct	420
taaatgacga	tttcaaagcc	aggctacggc	ggtacacaac	attatacaag	cttatctcgt	480
ggctgatgaa	gatgcac					497

(2) INFORMATION FOR SEQ ID NO:201

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

aattttttatc	aatcgaaatta	aaagtgtgtc	cacttatttg	tattaaattg	gccttaactc	60
taaaaacaat	gaactaggcc	aatcttttta	cctcatttcc	cataaatgga	ggcaaagaga	120
gcttcttccc	ttcgggatgt	tcattgcttt	tgatagaata	atatatgtgt	tagagatttc	180
caaggtctat	gccacaatgt	aattcgatca	ttttatagat	tgctcataaa	aaaatattaa	240
gtgtaggaag	ctgaaactta	cagtaggcac	atctttattt	ttccttttca	gtggattaca	300
tcgaaaagag	agggtatgct	tcatataacg	agaggacaga	tataagaagt	ttgataaact	360
gttttcggca	gtcaagtcct	ctcaaaaggc	aaacttcgag	ataggagcct	cggaagaacg	420
ctacaatgaa	tcacctatgt	tatccttttg	cccgaagagc	cctcttcgga	acgaaagaaa	480
acccttcggg	taccactatg	aattgagcga	cacccagggc	tcttacaaca	tctctgtgaa	540
attgatggag	tctctacgga	cctactctct	acaacttgag	aagatagcgt	atctgtattc	600
gatacgggtg	tgggaacggt	agcctacttt	ctccgcacga	taagcacacc	tctttcgaag	660
acatactccg	catcaatgac	tcgggcgacg	catctaccct	gaatatatgg	cgaaaggaga	720
cagattagcc	gccaaaattc	ttttcttgcc	gaccgtatct	atgggagttt	aggagtgtctg	780
gatttgacga	cgacttccgt	caattcgaag	aggatatfag	tcatacgaat	atcttctccc	840
ccccgaccat	atccgtcagg	tgttcggggt	accaaccaag	atgatcgaac	ggaagacgat	900
gggtgccaaa	agttcgtggt	tcatcaagag	acgaacggaa	agacatcatc	cgcattctccc	960
cgtttatgga	tgataggatg	tctttataac	ctactaccat	agcccctatt	atgccaaaaa	1020
gttgagaaga	aaccgaaaaa	ctttaggaga	aagagagaat	acaacatcta	cgaagaggac	1080
gctttg						1086

(2) INFORMATION FOR SEQ ID NO:202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

gcacgtcgg	cagcacctcc	acgggagtat	gcggattgag	cgtgacgccg	atttcatgcc	60
ggccttgca	atcgccgcc	gtgagcgatg	caggtgcgac	tggcttcata	gtggacgttc	120
atcatataaa	cgcccagttc	ggccaactgt	ccacgaactt	catcggtcc	acgatcatca	180
ggtgaacatc	gagcggttct	tgcaaatcgg	tccgatagcc	tcgagaatgg	gaaaaccgaa	240
cgaaaattgg	ggacgaatac	gccatccatg	acgtcgatat	gcagccagtc	ggcccgtgc	300
gattgatcat	ttcgacatcg	tccggccagat	gcangaagtc	ggngacagca	aagannggag	360
atacgatagg	ttgcataagt	atagtatcgg	gttatttttt	attgattcga	tgctcgcaaa	420
gttatgcctt	tcttgccgca	tccctgtaat	tttcagacgg	gctatcctat	ggttttacaa	480
aat						483

(2) INFORMATION FOR SEQ ID NO:203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2884 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

gccttcttat	ccgtctcccg	tgcggcattg	cgcgagtcgc	cgccaatggg	gcggagcgga	60
agactccctc	tctcctaccc	cttcttttcg	agcattctat	aaaggaaagg	ggttcgacta	120
cagactattc	acaagcaata	aacttaagt	tttgccacag	gtaacagccg	atacatcac	180
aataaacc	caatcacaa	gcaatgaaac	gaatcgtttt	atcatctttc	ctgttcgttc	240
tgctctactt	tctttgatgg	cacagaacaa	taccctcgat	gtacacatat	ccggacgatc	300
aaggatgcct	cctccggcga	accagtgc	tatgccactg	taacatccgg	ctgacaggag	360
cagataccac	acaggtgttc	cgacaagtga	ctacggcaac	ggctacttcg	tcataggcct	420
gccggcgagc	ccctcctatc	actgacagct	tcgttcgtag	gtatgaaaac	ccataccatg	480
cagattagtc	gggaaatgga	cagcacgaca	tcaaattccat	cgacatttct	ctcgaatcca	540
ggacaaacaa	ctctccaccg	tcaccgtatc	ggcagcacga	ccactggtaa	gatggagata	600
gaccgcctgt	cctataatat	gaaagatgac	cccgcagcaa	gacgaacaac	ctgctcgaaa	660
tgctgcgcaa	cgttcctttg	gtaacgtgga	tggtcagggc	aatatccagg	tgaaaggatc	720
ttccaacttc	aaaatcacct	caatggcagg	ccctcgacca	tggtagagcag	caaccggaag	780

gaggtcttctg	ctccattcct	gcccatacga	tcaaacgggt	ggaggtcatc	accatccggg	840
tgtaaagtac	gatgcggaag	gcacaagtgc	catcctggac	atgtcacgga	agaaggtaa	900
aagctggaag	gatatccagg	ttccatcacg	gcagtgtcag	caacaatccc	acagccaacg	960
gtagtatctt	tctgacggca	agtcgggcaa	agtcgggctg	actaccaact	ataactacta	1020
cggtggcaaa	acaagggctc	tcgctacttt	accgaacgta	ctacatccat	gctccaaaga	1080
tagaagaagg	caaagggcaa	gaaacctttg	gcggacactt	cggaatccc	tcctctcatt	1140
cgagatagat	tcgctcaatc	tctttacggg	ggcggaatg	tacgcctttg	ggagatgacc	1200
accgaccgga	acagcgtaga	aaaaactttg	ccggcagcaa	cctcatgtcc	tacatagaca	1260
gaaaactcaa	aacaagatgg	atgccggatc	atacgagctc	aatgccgact	atcagcacag	1320
caccgcctgc	cgggcggaatt	gctcacgggt	tcctaccgct	tcactcacia	tctaataata	1380
gcgagacctt	cattgaccaa	tggaagcgcg	atccgctcaa	ccagctaata	cgatccagta	1440
cgccggccaag	cactccaaat	ccgatgcggg	atggacgaac	atacggcaca	agtggactat	1500
acacgtccct	taggacaaga	cattcttttg	aagcaggggt	gaagtacatc	tatcgtcatg	1560
ccacgagcat	cctctctatg	agatacgacc	atccgaagat	gctccgtggc	agcccgggtc	1620
ctatatgcac	agaatccgtc	gaacggaaag	ttccgccacg	atcaatcatc	ggagcagcct	1680
atgccggcta	caactatcgt	aaggatcagt	attcttgcaa	accggcctcc	gagtggaaag	1740
cagcaggctg	aaagcactct	ttccgaaaac	gcagcagcag	atttctccca	caactcgttc	1800
gactgggtgc	cacgctcacg	ctcggctata	ccccctcgcc	catgaagcag	cttaagctgg	1860
ccataacttc	cgaatccaac	gtcctgcaat	cgcccaactg	aatccctacc	gctacagacc	1920
aacgattatc	aagtacagta	tggtaatccc	gacctaaagt	ggagaagcgt	caccacgtcg	1980
gtctctccta	taatcaatac	ggagccaagt	catgcttaca	gcacgcctcg	actacgactt	2040
ctgcaacaac	gccatccaaa	ttacaccttc	tcggaccggg	ccaatcccaa	tctgttccac	2100
cagaccttgg	caatatcgga	cgagagcatt	ctttcagctt	gaatacctat	gccatgacac	2160
gccggccgta	tgggtcagga	ttatgctcaa	cggaaatata	gatcgacatt	ccaaaagagc	2220
gaagcactcg	gcattgatgt	caattcatgg	tcgcgatggg	atactcaggc	ctgatgttca	2280
ccctgccga	ggattggact	gtgatctctt	cggaggttat	tatcatgggg	gaagaagcta	2340
ccagacgaag	tagatgcgaa	tgtattcaac	aatatcggtg	tagccaaaca	gcttttcgac	2400
aaaaattgag	agtctcgctg	agcgcaaaaca	acattcatgc	gaagtattcg	catggaagag	2460
ccggaccatc	ggcaatggat	ttactattta	ttcgaaaaag	ccggtataca	acggagtgtt	2520
tcctcagcc	tcacctacag	cttcggtaga	tgaatacaca	agtgcgcaag	gtagagcgta	2580
cgatcgtaaa	cgacgactca	agcaaaactc	atcccaagga	cagcaggggtg	gcggacaagg	2640
aaatccaccg	gcaattgata	aagaaaacac	gtaaaaaaac	accatacaat	gagaaaaaga	2700
ttttcgccgg	ccttgctggg	ctcatagcca	cagcactgat	agccgtgcat	gcaatatcaa	2760
attcgacaac	aaaggcaaaa	caatcacccc	caaggcgatg	ccatcacgga	gactcgcaac	2820
atcggtacat	tcgacaagat	cgtgtcgagg	atgcattcaa	catccactac	aaagccggta	2880
ttcc						2884

(2) INFORMATION FOR SEQ ID NO:204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

ggacaagggtg	gtggagaatc	tgagcatctt	cggttgctgca	gctcgttttg	cggcgaggcc	60
ttggatcata	cgctgctgca	tggccctccg	gggctgggaa	gaccacgttg	tcgaatatca	120
tagccaatga	gcttggcggtg	gggcttagat	cacttccggg	cccgtcctcg	acaagccggg	180
tgatttggcc	ggactctcac	ttcgttggaa	tccaacgatg	tacttttcat	agacgaaata	240
caccgctgag	ccctgtagtg	gaagaatatc	tctactcggc	catggaggac	tacctataga	300
tataatgctg	gacaagggac	ccagcgcgcg	ctccattcag	atcatctctc	ccccttcacc	360
cttgtgggag	ctactacgcg	cagcgggtttg	ctacggcacc	ccttcgcgcg	cgtttcggga	420


```

tcaatcttca tctggagtat tccgatgtgca tactattacc ggtatcgtgg agcggagtgc      480
acgcattctg aggtgtcctg ttcgcacgat gctgccgtag agatagcggg acgaagccgg      540
gtacgcctcg tatagccaat gc                                          562

```

(2) INFORMATION FOR SEQ ID NO:205

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 749 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

```

gctcgaatgt tcttgaatac ttgttcggtc tgctctgtta ctccgccggt acaaagttcc      60
ctgtggtagg atcaaggcct aattgtccgg aagcataggc atattaccca tcaggatagc      120
ctggctgtat ggcccgattg cggccgggca ttcttcgtgt tgattacctt tttcattacg      180
tactgttttt tatttgatta ttaatttgat gattgcagtc tttgctgtcg cactacttcg      240
taaatacaat gccggccgca acggagacgt tcaatgagcc tatagccccc atctcggaat      300
agctactatg ccatcggcca tcctaagcgt atcagggtgat ggccgacatc ctccgcccc      360
atgactatac ccaaaggcag cttcatgggt actcgggtata tagatctgca gccttctccg      420
aagcagcgac tatgcgtata cgtattcttg caggctgcgg atggctccgg gaatggaagt      480
cacgcgacaa ccggaatacg atgcaaagct ccggcagagg tcttgatagc atctcctcca      540
ccgaaacgct tcctctttcg ggaatgatga tggcatctac ccctgcacct ccgccgtacg      600
agcaatagcc ccgaagttcc gcacatcggt gataccacga gtagcangag gaagggtgcc      660
ttaccctcct catagagcat cggcatagtt gatccaaacg ggtatatctg atagccgaaa      720
gaatggccac cacccttggg gattcttgg                                     749

```

(2) INFORMATION FOR SEQ ID NO:206

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

```

gagtattaaa atttctcgag agagccattt ttctagattc caatataatc cttatatcta      60
ttatactaga ttgggtagta cgatgaacca attggatccc aaaaaagaat gagggcaaaca      120

```

gaagatttcc	tccgtatcga	aaagtctgga	aggaatgggt	caacctagat	tctccagagc	180
ctaatagcta	tgatatctca	tgctaagaac	agggaccaat	atgctccatc	gtaacctgct	240
gaacttgtaa	gaaactcaaa	cttctcgata	tctaccaagc	tcaagctgta	tgctagtaca	300
gaaaaaagg	tgatatttcc	tggttttata	acggatatag	aaggatccct	atgtagggtg	360
cacttctgtg	agagtctttt	ggaatacaat	agaccgttct	tatatcttat	tttctttgtt	420
ctccattgtg	gaagagatct	gaagaagatt	aagaaaatag	gcaattaaga	atgtaaacct	480
tatngagagt	gtctatgcag	cagatattat	taggggggag	tggangtata	tccctttact	540
cagc						544

(2) INFORMATION FOR SEQ ID NO:207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

tggtgcgtta	gaaaatggaa	agtgcagata	tggaacggctt	gactagggga	tagctttttg	60
tctatgtagt	ataagataat	tctctgtgat	tctgcgaatt	atgacccttg	tcttttgcct	120
cgtatcttgc	tttcagcctt	ttcaataccc	ttggctatag	tcttcttttt	tgatgatttc	180
tagcaaacct	tctagacaag	tttccgattc	tcttggagag	aaaggcaatt	caaattaagc	240
gtgattttat	atcatcattc	caagacttat	ttgcactaga	tattgttccg	tcactcttga	300
gctgatgcta	agaaacagtg	cgtcggtaaa	gagattaagt	gtatctcctc	atccttcttg	360
gagcaatcgc	aatgagcgga	gccctgactc	tgccactgca	acatgcaacc	atattgctat	420
aggatagttg	ctgggcaggg	ttttggctac				450

(2) INFORMATION FOR SEQ ID NO:208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

ggccatgcc	cactgccacg	cgtgcatcgg	ggacttcacg	ttgtactatc	cggcgatctc	60
ttctatatta	tctattcggg	tgtggacgat	aaagaccttc	cgttgcgagg	catctcgaaa	120

ttgacagctt	cccgaacaat	gtcgggggtga	atcgtgccag	tccggtggca	acgggatagc	180
gattcggcgg	tggggtttga	tattcgagag	gtcgcgtgct	cccatcagag	agaattgcaa	240
agtacgggga	taggtgtagc	agacatggtc	agcgtatcga	cattgacctg	tagttgcgca	300
gctttttctt	tactgccaca	ccgaatttct	gttcttcac	gatacaagga	ggccgaggtc	360
atggaatctg	atatcgttgc	tcacgagcct	gtcgtaccta	taattatata	gatccgacct	420
tctgccagat	cgtgcagaat	cctttaatat	ccttggccga	acgggcgcg	gatattgatt	480
cgatacgcac	gggaaatttt	gcaatctgtc	cctgaacgtc	tgatagtgtc	gataggccat	540
acggtagtcg	gcaccagtat	cgctacctgt	ttgccgtctg	tggcggcttg	aatgcggcac	600
gaacagccac	ttccgtcttg	ccgaaaccga	catcgcccag	ataagccgat	ccatcgagcg	660
atcgctttcc	atatcggtct	ttaccttgcc	gtggcacgct	cctgatcggg	cgtatcttcg	720
tacaggaaag	aggctccaat	tcgtgctgta	ggtagctgtc	cggactgaat	gcaaagcctc	780
gctctctttc	ctttgggcat	agagccggat	cagatcgcca	gcaatatact	tgaacgcttt	840
ttggctctct	ctttgagctt	ttgccaggct	cccgtcccga	gagactcagt	tctacctgcg	900
catcactgtc	accacctttg	tattttggaca	attatggagg	ctgtgcagat	tgacgaatat	960
tatatcggtt	tttcggtaaa	gagtttgatt	acttctctgc	gcttccctcc	cacatcggtc	1020
gtgataaggc	ttccgaaccg	ccgataaccg	gatcgatatg	cacgatatag	tcgccttgga	1080
gaattgggtc	agctccttca	gtgagagggt	cactttcccc	gaacgggttt	gtcgcttttg	1140
agattgtatt	tgtggtaacg	atcgaaaagc	tggtgaccgt	aagcagaccg	atccgaagag	1200
cttcgtccga	aaaaccctca	tgtaagtgtg	cgatactctt	ttcggaagga	gcgaagagct	1260
tccacgctcg	gaaagatctc	ttccactctc	tcgtattgct	tatccgaggc	tgtggccaaa	1320
agcttctgtg	gccggc					1336

(2) INFORMATION FOR SEQ ID NO:209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

gggtgggtcct	gcctgtagac	caattctttt	tttttgccca	atatgtaatt	ctcatggcca	60
aaaaatgtct	tcaaagactt	ctgatcaaag	aaggatttat	gatttgggaa	agtgtaaacc	120
gatctgagcc	actcggtagg	actatcccca	cggtttat	tttaactttgt	tcggaaatag	180
cctctgaaaa	aacgaaggat	attgtaagta	tggccgataa	agctccttgta	gtggagatga	240
gagattgacg	ctctgtcagg	aggaaaacgt	catttttcaa	aatttgaaatc	tgacctttcc	300
gccggagact	tcgtctatct	gataggctca	gtgggatcgg	ggagagcact	ttgctgaagg	360
ctttgtatgc	tgaggtgcct	atctctgccg	gtatgcccg	gtgatagatt	atgatctggc	420
aaagttgaaa	cggaagcagt	tcctatctct	cgcaggaatt	tgggcattgt	gtttcaggat	480
ttccagttgc	gaacggacgt	actgttgccg	agaatttgga	tttcgttttg	cgagctacga	540
ctggaaaaac	cgagccgacg	gcgagcagcg	tatcgaggag	gttttgaccg	tgtgggaatg	600
tctcggaagg	cttataagag	accgcacgaa	ctgtccgagg	ggagcaacaa	cgtgtgggta	660
tagccagagc	tttgctggcg	aagcctcggt	gatcctggcc	gacgaaccca	caggcaacct	720
cgattcgggtg	accggttgca	gatcgcttct	ctgctctacg	aaatcagtaa	gcagggcact	780
gcagacttat	gagcacgcac	aacagcagcc	tgtctgtcga	tctgccggca	cggcattggc	840
cgttcgtaag	aatggcgatg	cctcctcttt	ggtcgagctt	gatgcagatg	ctgtttcaag	900
aaaaaatacg	gaaatagatt	agcacgataa	gtcaggaatt	gaaagttctc	aaatttggcg	960
gtacgtctgt	aggagatgct	aagcgtatcc	gcaagtgttg	cccgaactgat	tactttcggt	1020
aaaagggaaga	aaatttatgt	cctttcggtc	atggccggaa	cgaccaattc	gcttgtcgaa	1080
tagcctcaca	ccttgtcaaa	cgcaatgtgg	cacagggcaa	agaggtgtgc	aggtgttgcg	1140
agagaaatat	catcgcgaaa	taaagtctct	atacaacgtc	cggatacctt	gagcgagcc	1200
aagaaggccg	tcgactccct	cctcgtctct	tgggtcatat	gtgcgacgtg	gagggttca	1260
cactcttcga	ggaaagcggtg	tgttgatcct	cggcgagctg	atgagcacga	ccatgatgca	1320

gattatttgc	aggagatggg	tgcagtggta	gccatgctgc	cggctttgga	gttatgcgta	1380
ccgacaagaa	tgcagagccg	gacaaagact	atatccggaa	gatctcttgc	cgatgataga	1440
ggctcatccg	gatgaggata	tgctattcct	acggagggtt	acatttgtcg	gaatgccttc	1500
ggagagatcg	acaatctcca	cgtggcggca	gcgactacac	ggcctctctg	atcggagcag	1560
cactgaatct	gatgaaattc	agatatggac	ggatatcgac	ggcatgcaca	acaatgacct	1620
cgtgtcgtag	acgttacggc	acccgttcgc	cgtctccatt	ttgaagagct	gcggaactgg	1680
cacacttcgg	agccaaaatc	ctccatccga	cctgttcaag	ccggccaagg	agaagaatat	1740
tccggtacgt	ttactcaata	cgatgatccc	gatgcacccg	ggacgctgat	ttcactggat	1800
accgaaaagg	atztatcaag	gccgttgctg	ccaaggatgg	cattacgggt	atcaaggtaa	1860
aggcagcaac	aaactccttt	catggcactt	tatgcgcaag	ctcttcgaga	tttcgagttc	1920
taccaggagc	ctgtggatat	ggtcgctacg	agcgaagtgg	tgtttccctg	accattgaca	1980
atgacaagaa	tctgcccgat	attgttcgtc	cttgcccgat	attggagatg	tgacgggtcg	2040
taaggatatg	gtcatcattg	tatcgtaggc	gatatggagt	gggacaatgt	gggcttcgag	2100
gctcgtacat	caatgcgctg	ggt				2123

(2) INFORMATION FOR SEQ ID NO:210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

gggaaatgaa	tgccttgagg	gttatgggtg	atatatcgca	tgcggctggt	cpactgttcg	60
tgatgtcttg	caaatcagta	gtgcccctgt	tgtagccatc	attcatcgtc	ccgcgctctg	120
tgtaatcata	cacgaaatct	gaccgacaag	acgcccctgc	catagcccgt	agtgggggag	180
tggtgcaggt	ttgtcttatg	cgggatttat	ttccgagcag	gaggaagagg	gctccgtaca	240
gcatgggcag	accatatcgca	ccactttgtc	aggttgttgg	gcacgaaca	tgtagtgtcg	300
gttccgattt	tgatggagat	ggcgaactgg	taggttgccg	agggccaatg	acctgatcaa	360
tttgactgtg	gagcttctac	gtcgtggcta	tatcgggatc	agctcggatt	gctctggggc	420
gagaattttc	ttcgggtgat	gagaatgtac	agcagaaagc	aaagtgtcag	tagaaaacagg	480
ttttcaaggt	tttcgggttg	caaagatccg	attttgggtg	acaattattt	gcaaatgtga	540
aataacctct	atctttgcgt	cgtgggtttt	tcataatagt	attagattta	aggttaacaa	600
gaagatcgaa	ggctgtcggg	agacattctt	tagattggag	atcccggcct	gtacttatcg	660
tgcagggcgg	gtttttgttt	tgtaccctcc	ggcgtgggtc	gcgaagaagt	cgagaatgtc	720
gattaattct	tccaactgag	actgttgcat	gggattttca	ttgagctctt	ttgctgcaga	780
gctgtttctt	gtgccttttg	gaaagatcaa	acctccggta	tatggacatc	gagaaacaga	840
aattttccca	agttttccatt					860

(2) INFORMATION FOR SEQ ID NO:211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

aaaggatgta	atattgtgag	cccgcaaaaa	gaggggaatc	catcagactt	aatatcccg	60
ctctctttct	ttgcggaaaa	gggttcaaac	ctgatttcta	aagcattaca	taatgataac	120
tcttcaacta	atcgaaccgt	gtactatg	gtgatcggtg	cgtcgcaaga	tgtgacaaaa	180
cccggtggaa	aagtatacaa	aacattctga	acggctcgtt	tcagggtcgt	gtattgggtg	240
taaatacgaaa	gtgtctaacc	tacagggagt	ggaatgtgtg	cccgatgtga	aagactaccc	300
caagtagatt	tggctatttt	ggctattcct	gcacgtttct	gccacctacg	atcgaggtgt	360
tggtgaaaga	aaaagggaac	aaaggaatca	tctatttctt	gcagggttct	ccgaaatggg	420
tgcagaaggc	aaggctctcg	acggcaaatg	gccgaactgg	ccaatgaagc	cggagctacc	480
ctgatcggcc	caactgcgtc	ggcgtaatga	atccgctgca	ccaatcggtg	tttaccactc	540
ggtgccggta	cttacgccta	agggatgcga	ctttatctcc	ggttcggggc	aactgctgta	600
tttatcatgg	agtcggctct	gagcaagggg	ctttcttctc	atcggtatat	tccggtcggca	660
acgtcgctca	aacgggtgtg	gaagattgct	cgaacatttg	gacgagacat	tcgatgtctg	720
cacttcttct	catacctgct	cctatatata	gagactatct	ccaaaccgaa	acgcttctctg	780
aaactgccag	atcattggta	cagaaaggct	gtcgcattgc	ggccatcaaa	tcaggacgtc	840
ttcagacggg	ggacgtgctg	cagcttcgca	cacagggtgcc	atctcaactc	cgatgtggct	900
gtagatgcac	tcttccgcaa	agccgggtgt	ggcgctgcta	cagccgtgaa	gaactggcta	960
ccgtgggtgc	cgtacttcaa	atccgggtact	caccggtaag	aatatggctg	tgatcacaca	1020
tgcaggcgcc	cggccgttat	gctgacggat	gctctctcca	atggaggtat	gtccgtactc	1080
cgattcccg	agaaaagact	cgcacattgc	tgtcggagtt	gtttgacgtt	cttccgtggc	1140
taacccgatc	gacattctcg	ctacgggaac	agcagacaat	tatcgaaagt	gatcgatact	1200
tgcgagaaa	atctggacac	gatagcggta	tggtcgtgat	tttcggtagc	cccggtactc	1260
tcgatgtgag	cgatcttacg	atgtgatacg	cgaacaacag	aaaaaatgca	agaagccgat	1320
ctagccgtac	taccttctgt	gatcaacgcg	aaggaaaggaa	tggagcgttt	catgtctcagg	1380
gaggcatcct	ctttgaagag	gaagtggctt	tggcacgtgc	ttctgcaagg	tctaccaaac	1440
gcccgaagccc	gaaatgactg	aagagagcga	ttgcccacaa	cagcagaaat	ccgcgtctctg	1500
ctcgccggca	agagcggtag	ctcggaaccg	gcgatatgct	ccagctgttg	gatttgaccg	1560
gtatcactgc	ccgcaagaac	gtctggtgac	aacagagaca	gaagctctgg	atgcagccgt	1620
agtatcgggt	tcccattggc	tatgaaggta	atgggactgg	cgcacaaatc	gatgccggag	1680
gtgtaatact	gaacgtttcg	accgaagaag	gcgtaaagag	agctttggca	agctgatgca	1740
aatcaagggt	gctgaagggt	tacagtgtca	cagatggaga	gtggcgtgga	agtcttcac	1800
ggggtaaaga	aaggggacga	ttcggtcatc	tgattacctg	cggtttgggc	ggatatattcg	1860
tgaagtgatg	aaagatatct	gctgtgctct	ggctcctctc	ggcaaaaacg	agcactggaa	1920
atgatccgtt	cgctcaagtc	ctatccgata	attcgcggta	tcgcggcaaa	cagggcatca	1980
acgacgaggt	aatcgccgat	acgctctgta	gatctcccgt	ttgctggctg	cagtgcccg	2040
gatcgaggag	atggacataa	tccgctgatg	ggacgtggag	aaagactatc	ggccgtagac	2100
gtggtagtgc	tctgagcgat	gcgaagtaag	agatataaga	aattcaagaa	cacagtaaaa	2160
atatcaagag	atgaattttc	caatcgatga	aaaactgatt	cgtgaaagca	aaacgaactg	2220
cacatcaaa	acctcggcat	ggcttcgata	cgagtctggt	agctttgggt	accaatctgg	2280
aaaaggctac	cggcactaaa	ttcgccgtat	ggaaatgggt	gtgcccggac	ttcctgcacc	2340
tcagatcggt	atgagacgga	gatacaaaa	ctacgcgaag	gagtagcttc	gatttatccc	2400
atttggtatg	tctgcccga	ctcaagcagg	aggcatcgcg	ctttgccaaa	tctttgtcaa	2460
tatcgacata	ccggcacgtg	cttgcggtgcc	tacggtaggt	cgatgcaggg	atgcttcgta	2520
tctttcctcg	tggccaatcg	cacacacaaa	accgtgaata	cggtagcgtc	ttttatcgac	2580
cccggttca	aatctgacaa	gctaca				2606

(2) INFORMATION FOR SEQ ID NO:212

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

gcggttgggt	cagtagcttc	ttcagccttc	attgcagcag	aatcgatctc	atagcagccg	60
tatcaactac	aggagctgca	tcttctacca	aagtggcaaa	tccatagccg	tagagtcagc	120
agcttcttca	gtcttagcct	gagagttcaa	gaagcgaatg	atacagctgc	gattacagct	180
gcaaaagcaa	caaattcttc	atttcctttt	gggtttaaaa	gtgtaattaa	tggtctataa	240
cggcgaaata	tacagtttct	tttggtagca	ccaaaaaaaa	cgaccaaatg	ctgttgcat	300
gagccctttt	atccggaagc	cttacgcctg	gctattcctt	ttaagacggg	ggcaccgat	360
cttgcgcaat	caagtataga	ggaaacgttt	gagctgtgtt	tgggtgtctt	ctcgaactct	420
tctgcatggc	ggacaaaggc	cttattttct	cgtatgcacc	cacttgcccg	ttcagttcgg	480
ctcggtctct	tccatataag	cccatgcttg	atccggagag	atccctttat	gctctatcgc	540
tgtctgtccg	gcacgattag	tgcgatcaag	cgcccgcttc	gctctgtgcg	atactttcga	600
ggacatagga	taattgttga	tcttcgatcc	tattcc			636

(2) INFORMATION FOR SEQ ID NO:213

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1063 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

gcagaaaggt	tggcttatcg	gtgggcagca	aaacgtatca	ccttctgtca	ctcggagagc	60
aattcattcg	agatcaagat	gacgctcgaa	ccgattcaga	actgcgcctc	aacctcacag	120
ccaacagaac	cgatacccca	caaacgcgac	ccaatacgtc	tatgccggca	tgccacgtac	180
ttatggagga	aatttctgat	gacgaccatc	ggactgaaag	gcattgttcag	cagttcgtcc	240
ggagcacggg	ctatgcctcg	caagccttca	atcagttcct	ccacaatcgg	gagaaatcgc	300
agggcgctatt	atggctcaat	atcatggagc	cacttatccc	tctccggatt	catggaagga	360
agcagtctgg	gccggccagc	cggtttctct	ggaaccagtg	ccgtttctct	caactcagcc	420
gacgtgctta	ttccggcttt	ctcagtgctt	atactcagag	gtcagtgagg	aaaatcggcc	480
tgtccggcat	ccccctcatg	ccttccattc	ttcccaactg	gaatgtcaga	aacacagccc	540
aagcaaaaca	gaaaaaccca	acaaataaag	aaagaatgcc	cgaatcaaca	agcaaacagc	600
cttaccgcgg	tatatacaac	gtagatagct	atagctctac	ctcgggtggg	tgggcttgac	660
cgatggtagc	aacctgggct	ttatccagac	ccgtcggacc	ccagtaacgt	gactcccgtt	720
gcattccatg	cattcacatt	ccgtttgttc	gtctcgaaga	cagttttgct	cccctgctcg	780
gtgtgaagtt	acgtttatga	gtggattggg	aatcaatacg	gactacagaa	agatcgccgt	840
ctgaatctga	atctatcggc	ttatcagctc	gtggagtcca	ataagatcag	ataaccgtag	900
ggatgagcta	taaggcagag	aattttgcca	actcatcgcc	ctgcaacgga	caagacccac	960
gaggaaggca	aaaggagggc	aaagaacaac	gaagaccatg	gcttcgcgta	ccgggtggggc	1020
actgactctc	gagtggacta	tgcttacaag	ccgacactga	cgc		1063

(2) INFORMATION FOR SEQ ID NO:214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

```

ggcgagtcag tacttcgcga ataacgacca agcctatccc ctgaccattg gcttggtgct      60
gaagaatggt gtaaagagac ggggtggcaac gtcacgcgca taggctgtcc attatcctct      120
acgagcagat tgtgacgac caaacaggca gaaccgtctt tggtgccgag acagccagat      180
cattttgctg tgcaaaactct ctatagcggt gcgcagcaga ttgatcacca cctgctctat      240
ttgcttgcat cgcagcggac taagcacgaa tcttgctctt tgcacatctt catttcacac      300
ccgtttcgac agccaaaggc tgcacagca gtatgcacg ctccatagcg gtaccaagtc      360
tacggaagat agggtaggat caggtagctt gacacttcgg caaatcgtgt gataaagcga      420
cttcaatggc catcacccgg tgcggcagag agcgatggct tcggacactt ccccttcggg      480
agtatgagga tgtcgtcgaa agcatcccc acggcattta gcacaccgat tataccggcg      540
tactgttatt gacctcatgg gctatcagcc tgaacagttt ttcatagggt ctttctccgc      600
cgaatgcaac tcctcgggtca gggtttcgat actgaaaaga gacgggtgaa cgaacgatcg      660
aagaatctca tccgcgtaat cctcctacct cggccgtagg caatcgccat gtacgggatt      720
ccccttcgcc cagctgtccg gaccgaaagg gatcttcgcg catacttctt ccaacgggtct      780
ttcgtcggga tataatcatc gggtaagtcc aacagcctgc gtgcggcagg attaccgata      840
caaccgcat gtcgaaatcc aaaacgacga agcccacggg cgaacatcca tcacgagcga      900
aaggaaaatt tccttttctt ccagtctcag ttctccttct taaggctgtg catcagcgca      960
ttataaagtt cgaccacccg tctgcattcc gctgaccgac aggagcaagg gtagtggtcat     1020
agtccgtgta cggagcatat ccattccatc gcctacggct cgtatcgga atactaccta     1080
ttatatagga aaccgagaaa gaagaggaga gcaacctcta tagccagatg aagaagagcc     1140
cgcctttctc taccggagga tataggagag tcatcgcata agcaatagag agagcaatac
1200

```

(2) INFORMATION FOR SEQ ID NO:215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

cagcgggggat	gctgatgggc	aacttaccaa	ttcttgacat	aattccgtac	tcctttatca	60
ataaacgtaa	cacaatactt	ctcccccaac	tttcaactac	gagcttcttt	atcagtcac	120
actcctcgtg	gggtagaaac	aatagcatac	caaggccgtt	caatacgcgg	ggcatatcac	180
gataaccac	atacttcgaa	ggccgggacg	agacacacgt	ttcaactttc	tggatggcat	240
ttactttatgt	gccaaatcat	actttaaggc	aacttttatt	atgccttgag	agtcttctcc	300
tcgaacttat	agttcaggat	ataccctttg	tcgaaaagga	tcttgtgatc	tctttcttaa	360
tatttgacgc	cggcacactt	accacacgat	ggcagccata	attgcattac	gcaaccgcgt	420
caaataatct	gcaataggat	cgtcattttg	aattacaatt	aaattgatcc	ggaaagccgg	480
acaatatatta	aactcttacc	aactcgtttt	ttttacgccg	gggataagac	cggcagaagc	540
atttcacgaa	attgaatacg	ggaaatacca	aattggcgca	tatagccctt	ggacgcccag	600
tcacgcagca	acgattatgc	aaacgaacag	gagaagcttc	ttagggagca	actgcaaggc	660
ttcataattt	ccttcagcct	tgagtgcgct	ctctttgcag	catatttcgc	cacaagcttg	720
gcacgcttca	cctcggggct	ttcattgatt	ctttagccat	atcaattttg	tttttttagcg	780
ttctgaacgg	taaaccgaat	tctttcagaa	gggcataacc	ttcttcacgc	gatgcgcgca	840
agtcacaaaag	gtaatatcca	ttccgagaat	cttcgtaatc	gctcgatatt	tatctcgggg	900
aaaatgattt	gttcattgat	tcccaacgta	tgttacctct	tccatcaagc	ttgctttcga	960
tacccttaaa	gtcgcggatt	gaggcaaaagc	gatgcgcacc	agacgttcca	agaaactcata	1020
catttgctcc	gacgcagagt	aaccataaca	ccgattggca	tcttctttct	caacttaagt	1080
ttgagatgtc	tttcttagat	accgtcggta	cagctttctg	tccggtatag	ccgtcaattc	1140
gcttactgca	acatcgataa	tcttcttgct	accggtgcc	taccaagacc	ttggttgatc	1200
acgattttct	tcaacacagg	gacttcacat	cgctcgtata	accgaattgt	ttcatcaggg	1260
caggtaacgat	tctcttgat	agtctttctt	cagattggca	gtggcactca	ttattttaat	1320
tccctctctga	tttttttagcg	taacgaacta	atttgccatt	ctcattgaga	cgcgcccaat	1380
gcgagttgcc	tttctgtttt	tgggatcgac	aacattcagg	tggaaatatg	tataggagct	1440
tcctttgata	tgattccacc	ctgaggattc	tggcgctagg	cttagcatgc	tttttgatca	1500
tattcagccc	ttcaacgatg	cacgctgttc	ctttactaat	acctccaaaa	cgcgaccgga	1560
gtggccctgt	cttcgccact	gatcaccatg	acggtatcac	ctttctttat	atgtaattac	1620
tcattttctgc	ttgcttaatt	ataaagttat	aatacttcgg	gagcgaagaa	acaattttca	1680
tatttgttcc	acgcgtatcg	cgtgcgaccg	gtccgagata	cggctgccac	gaatatcacc	1740
ggctgcattc	agcaagacac	aagcttgctg	tcaaaacgga	tatacgatcc	atcgggacga	1800
cgaacttctt	tctcgtacgt	acgattacag	ctttggagac	agcacctttc	ttgatatcgc	1860
ttaagggata	acactcttga	ccgaaaaccac	gatgatatca	cccacagagg	ctaactctctg	1920
cgcgtgccgc	ccaaaacacg	aatacagaga	gcttcttttg	tccgctgttg	tcagcgacaa	1980
cgagcttga	ttcttgttg	atcattctat	ttgccctttc	gattatttca	gttagtctcc	2040
atctctttgt	acgactcaag	gacgcgtctc	catgatacgt	accgtatcac	cgataccgca	2100
ttcattctct	cgtcatgtgc	gtggtatttt	tttgtcttat	tgacaaaact	accataatag	2160
gatgcttctc	tttccacttc	acagcaaccg	tgatagtctt	atccatttgt	tgcttgagac	2220
aacacccaca	cgttcttttc	taagatttct	ttcctgtgtg	cactctatct	atctattgag	2280
ttcgcgttgg	cgcagcactg	tctcatctgc	gcaatcatat	gacgttgatg	ctttagttta	2340
gcaggactat	ccaaggcgaa	accgcattgt	tgattcgcat	ttggtcataa	gcagccactt	2400
cgcattccaat	cgtccctgga	gctcttttgt	tgcaagctct	tttaatttcg	aatcttcatg	2460
acaattacgc	attttgattt	tggatatcat	aatcgtgaca	accacgaact	tagtcgttac	2520
ggggagcttc	tgagcagcca	aacgaagact	tccttagcta	tttcgtaagg	cacaccttcc	2580
acttcgaaaa	tgattcgccg	ggagtaatag	gagcaacgaa	accttcggga	gcacccttac	2640
ctttaccata	cggacacctt	ctcccttctt	ggtaaatagg	ttgtcaggga	aaatagaacc	2700
catacttgct	cttgacgctg	catatagcga	gtcactgcaa	tacggcggcc	tcaatctgac	2760
gaccggttat	ccacttgctc	tgcaaaagact	tgatccaaaa	gaaccgaaag	acaactgggt	2820
acctctctgg	gcaaaaccct	tctgcgacct	ttctgctgtc	ttctaaactt	tgtttttttt	2880
ggttgtaaca	tttgtctgtc	tttctaaatg	ttagcgatta	ccttttcttc	tacggttgcg	2940
tcaccgccac	ggttgttgcc	gccctgtgca	ttgggacgac	ggctttgggt	ttggccactg	3000
caaaattggg	ggcgaggtcg	cgtttctcgt	aaacctccct	ttgcaaatcc	aaa	3053

(2) INFORMATION FOR SEQ ID NO:216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

```

gcgacattt ttacgcggtt tttcaaagcc aaaaagacaa taactccaaa taataaagaa      60
gaaaatgaac gtatcgatca agaatacggg tgcgcgtcat ccattgctac ggtagcaatc      120
gagaaggctg attatgccaa cgaagtgaag aagctctgcg tacctatcgc caacgtgccg      180
atgtccccgg attccgaagg ggatgggtacc gatgggtatg atcaagaaaa tgtacggtaa      240
gggtgcaaag cagaggagat caaccgcgta gtcggtcgtg aactctatcg ttattagcag      300
agaacaaact caatgtactg ggagagccta tgcctaacga ggattgcaga aggagtacga      360
cttcgatacc actgacgact ttgaattcgt atcgacctgg ctctcagccc cgtgggtggac      420
gtagtggtag acaagagcat tgtgtacctt attatacgat ccaaccaca gaggagatga      480
tcgaccggca atcgaatcta tgagatccag ctacggacat tcggtggaag ccgatgaagg      540
actgccaacg atgtagtga ggggcgtctt tgcgaattgg aggatggcaa ccaaagaag      600
gtggtatctg tgtggaagaa gccatgttgc ttccggctat atgaaggacg aagaggagaa      660
gaataaattc gtcggcgctg ccaagacagc gttgtcgtat tcaatccctc gaaggcatac      720
aataataatg agtacaactt tctccctcc tgaagtggga caagtcggct atcggagagc      780
atacggtgac ttttctttcg aaatcagcag tatctcccga catgaaaagg ctgactgaat      840
gaagagttct tcaaacaggc ttccggcgag gagacggata tcaaacgaa gcggacttgc      900
gtgttaaggt aaccgaaggt gttcgcgagc attcacggcc gaaagcgact acaaatttct      960
catcgatctg cgccgcgaat ggaagctcag gtaggagagt tgcagttccc cgatgccttg      1020
ctgaagcgcg gctgaaactg tcgcacacgg agtggagtga tgaagaactg gaaaagcata      1080
ccctgccatg atcaaggatc tgactttcca tgtgatcaag gaagatcggg gaagaagaac      1140
gacatcgtgg ttacgcgcga agaggtcagg aatttcccat cattgtagcc aagaatcagt      1200
ttgctcagta tggcatgtcc gccgtcctca ngatgctctc gaacgctatg ccaatacgat      1260
gatggagaag gaagtgcctg tcgcaatttc ttcgaccgtg ttacggaaaa taagctggct      1320
tgcgcgttga aagaaaagct cga

```

(2) INFORMATION FOR SEQ ID NO:217

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

```

ggcgtgaagt acagcgatat taaccaactc ggcaacgaag cagagcgcgt gccctcaaag      60
agagctatag ccacctggct aagctgcgcg acgaagtgtc gccatgggca tcattcccgc      120
gatcgctgac tggaagacgg tgaatccaac ctctaacagc agttcttcgc aaataatact      180
cttgagagag ggggagatcc gaatgataag ttttcgggtg tcttctctct tcttatttcc      240
cgctcttttg ctttttgtgt ttatccgcca catttgtcag ccggtagaga tgaccgattt      300
cggcagcatg taaacgggca aaaagagaaa agtcgtatcc tccttcgcgt tcggacataa      360
agaaaaagcc gaaacctctt tgcatcgaag aagtttcggc ttttcggccg gaggcaaagc      420
actatcaaag actattccag gaggagcaaa ctatctccat aagtcctgtt ccactgncct      480
attgagaaa gcttactcgtc aggcgtgccc aatttcggcc g

```

(2) INFORMATION FOR SEQ ID NO:218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

```

ctgaaaaatt tcattcgctc agttttacaac caaagcaatg cgaagaggat ttagatggca      60
aactgggata cgtgctactg atcggaaaaac cattgagcaa tatttggctg acactgataa      120
tacaaaagtc ccaacctctt ttattcaaat gtctccttaa ttccaagtca tccaactttt      180
ggttccatat gcgcctcgac tattttttta gttgtgtttc gccccttgat actgtcggcg      240
atattgttatc ggtcgattta gcngtcacca atgctcatga attgcacaat ctgatgaaaa      300
gactatcaac aaagaaatct catataatcc tattgcacac aaaatattct ttacgcagaa      360
nggaaaggct gcgatgctcc aatcttacgt gtttcttaaa aagaaatcgc cttctgggta      420
cacagtcaac tctatcttaa atctaa                                     446

```

(2) INFORMATION FOR SEQ ID NO:219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

```

gctttcatct tcatggcttt ccatgtagag atggccggag ctgcatcaa gcaatgacag      60
caggacgcaa tcctcgaaa atggctgcaa tgattttgtg tccctcatct gcgcaaagaa      120
catggctaca gccagaatga tcaggaagag ggaagaatag tccccaaggc gcaaacggct      180
gctccggcat atcctcgagg cgatagccta cgaagatgga tatattgacg gcaaatactc      240
cgggcgggat tgcgcaacgg caaaaagatc cagaaaatcc tcctccgata gccatggtgg      300
ttatccacta tatcggcctt gatcagtggc aacatggcat aacttcaccc gaagggtgaat      360
cccgcgata ccggaaaaag gtgagaaaga aggatagata tggatttcac ggcaaaaaaa      420
gaagaccact                                     430

```

(2) INFORMATION FOR SEQ ID NO:220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

```

gcccgaataa cggaaaatca aacaaaatgt ttcactaaca aaaaagataa cgaacatgaa      60
aagattatta ctctctgctg ctatcctaag tagtatgggt tgtttaatgt caatgcacaa      120
gagttgaaaa cctctgctga catgaaagtt cttttaagaa gaatgtggta ttggagggtat      180
ttactgccga atggtggggt actgtccagg tggaaaagag cgcattgcaa aagcaattga      240
aatgtggatg atgaatataa ggagcgtggt tttcagacat ttgttcatta taatatggga      300
tctcaaaaaa atggcctcgt gttggccaac ttttcattgc attgatcaaa cattgggcat      360
tccgggtttt ccgacttttt cagtttgccg taggagaaaa aaggtgaaaa tctttcaata      420
ggtgctccaa tagcaattaa aataagatta tgaaagggtt tggatgatgt acagcccctg      480
cagaggtaaa cttaaattga ccaaagggtg aacaccggaa gatgtatgta cagctacatt      540
actggtaaaag tcgatgctga cctcataggg aaacctctta tgttgactca tatgtattga      600
aaaacaatat gaagc                                     615

```

(2) INFORMATION FOR SEQ ID NO:221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

```

atcgccaagc agaagccggt catggtactg gcttcggggt ggcaaaacag atgagtacga      60
aggattgtct gttcgccggt gctttggctg ctacgatttc cggcttggag aaggagggtca      120
tttgcaaga cggagcgtca gttttccaga actctggggt aactacaata cgcagtgagaa      180
gctgatggcc tacctgacgg tcgcgatcat tacgaacgcc tgcgcgccaa taaattggaa      240
agaaggttcc ctattgcact tcaactcaat tcacagaaat tgttcccga ctgacttcaa      300
aatttctgcc gcatcaacgg attgcccggc taaccgactc ttctaccggt cactccacct      360
ttctaaacca tccgaacaaa tcttgtcggg gtcggcatct tttttcacgg caaacatcc      420
cttttctccc tacgtctctc gcaatacctt ttggtacgag attgaagatt atgccgagga      480
atacgaagaa tggtgaaaag ccggtacgaa acacttacga tcgtaggcgt acgatgcacc      540
ctgcacgatg caggagacca gcgtaggcgt acggtgctca ttacaacagc taattaccag      600
tacattatgg acaattaaag taaaacgaga acgacctgga aattttc                                     647

```

(2) INFORMATION FOR SEQ ID NO:222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

```

gaaaacttcg actctatttg atccccgcga atttggaat gaatacagtc agccataacg      60
tcgggcatgg tcatgaaaag catcgcgag tccgggatgg ccgatacacc gccggccaag      120
gccacttggt tgatgctatg atctttgccg cttggcgaag tttcttcata aagatgtcta      180
tgaccgtgtg ctgaaggatg cgcacagatc ggccttggtc tttctatga agtcgggatc      240
ttcggcaggt tggtcgcgca gagtatagag gaatgatgtc ttgagtcgcg tgaactatag      300
tcgtaaccgg acacatgagg acgggcaaag cggaaagcat cgggttgccc tcggaagcca      360
acttattgac gatggggcct ccgggataac ccaccccatc accttggcac atttgtcgaa      420
agcctctccg gctgcatcgt catcgtctgt cctattacct ccataatcgt aggggagcga      480
accagaataa ctgagagttg cccctgaaa ccaacaagca caggaatggg aaagagggag      540
ctgtgactcc tcacccggct cacgaaggaa gttggccagg acatgggctg aagatgatga      600
cttcacgcat cggaatgccc aatgaaagag acaatccttg gcaaagctgg tgcctacaag      660
gagcgatccc agcaaaccgg gtccacagtg aaagcgatgg catcaatttc ttctttgcga      720
atgccggcac gtttgtagct tcgctgacta ccgggacaat gttctgctga tgcgcacgcg      780
atgcagttcg ggaaccactc ccccgtaggc tttgtgtaag gctgtgccg cgacacgttg      840
ctaagcatag tttcgttctt gaccacggct gcagaggtgt cgcacaggag ctctcgatcc      900
ccaatatgat aatgtctttc ttcatgtctg tttttttct atctgcaaaa aaacgaataa      960
aaccttgttt gagccaattc tcctccgagt gttgtgtgtt tcaattgtga taaggtagtg     1020
ccatgagaaa caaggagaat aatggaatgg gaacagacat ccgaaccatg ggagatactc     1080
tcttttagagg aaattccggc ctctttcttc agttgagtat agacagcaaa acgacttaag     1140
gcttgtgtca taa                                     1153

```

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

ggcttttttc	gcaatttttg	cgatggcttg	tgcattgccag	ggagggacgc	cggcaagtgc	60
ttcaccaact	ctacaggatc	tccggggcgaa	atgatgctgt	catggacgac	caatatctgg	120
gatcgctgt	cggcgaagcc	atctacgggc	aatgaccgag	gtggctccgg	ctctgaacca	180
aaacgagccg	atcatgctgt	ttcgcgcgta	tccgaaaagg	attttacggg	cttctccgc	240
tatatcgcaa	tgtgctgcag	atcgacatca	accccgatat	attcaccaag	actttctcaa	300
atacggctat	gaccagtggg	ctaacgggtca	gctcgctcgtg	ctgtcaacag	tctgcgaca	360
gattcactga	cggcctacgt	cgaatccaac	aatcggccat	acagaacctc	tttatccgcc	420
acgagctttt	cctcttcggc	cgttttgga	gaaagactgc	agtgcggatg	ccgaccagcg	480
cgtacagcgt	tgttcggata	ccatatcaat	gtgccggccg	atatactcag	ccacaaggag	540
gcaaagactt	cctgtggatg	tccaacaatc	agatgcgccg	gcgcaagggt	ttttggtata	600
tactttcccc	tatcgcgag	catcgatct	gggactcatc	gtatggtgga	ggtgcgtgac	660
tccgtgctca	aagccaatat	agaaggtcgg	acgcagggtc	ttatcccgtc	acggagcgta	720
tgctactgaa	gcattcttacg	tctacccggg	cgacccaaaag	cagg		764

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

gggaatgggt	cttccattga	ctatgatttg	atgaaattaa	aatccggcca	c'caatcggtg	60
atgccgaaaa	aatcagctcc	acaaaggtaa	gattatcagc	aaacgaaaaa	gatgctttgc	120
attcagagac	cattgttttt	gctctgagct	atcggcaaat	gtactcatcc	tgcaaaaaag	180
aagagggcga	cccaagatat	ttggatcgcc	ctctgttctt	tatgctaact	tcattcagag	240
ggctgcggct	cctcctgaaa	aaagtgttgt	cagatcatat	aactttattt	tttgcattca	300
ggctcgcact	gatgaaattg	ccctgtgcat	cgaacagcaa	atctactcct	tgttggtgta	360
cacgatttcc	gccttgatg	tgcggttga	cttctttcga	tgtccttgat	aaatgcaccg	420
gggtagttcc	ggttgacgta	atgatgatct	tagccttgat	gtgagcagga	atgttgctgt	480
catcatcctg	tcgctacgt	ttccgctgat	gaggttgccc	tgtgcatcga	acagcaagtg	540
tactccctat	tgggtagta	aatttctacg	tcataagtac	cattggagta	cgctcgatac	600
tgtgaatgac	agcttcccgg	taattctgat	gacatagtga	tgatcagagc	ctgatgttgg	660
cccgaatgtg	tttcgatg					678

(2) INFORMATION FOR SEQ ID NO:225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

```

ggctggagaa taacaagaaa taaaaagacg atgaatcaat tgaccttcac agaaaaacga      60
accttaacga ccaatcaagt ataaaagcga caaaagctcc ccggtctcct tcttcgtcaa      120
tgaatcgaag ttatagtcga gcgaagccat tgaacaatgt ttcgggcgga aagattatct      180
ttgctcccat tcttatgaca ctctgtttag cgaagttaaa atttatgagt cgcagatttg      240
ccgaaacgag agcttggatt tgtcccgtgt caatgaggag gtgttggccg attgatgcaa      300
caccgtcttt ttgaagaaaag tctgaaaagt cgcgagggtg cccctcgttc gttttttatg      360
agggacctcc ctctgccaac gggatgcccg gctccaccac gtaatggctt cgtgccatca      420
aggacactat ttgtcgttac agacgatgaa ggggttttccg agtggaccag gaaagcccgg      480
ctgggatact acg

```

(2) INFORMATION FOR SEQ ID NO:226

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2746 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

```

gagtaccgtt tcgctgggtg catgtacccat gacttctacc atatcgccgc tttgaggaac      60
tggacgcccgt cgatgcttgc acccggtatg gtgatctgtc gaacgtttcg ggggtgcatga      120
agttgtatcc catctcgtcc tgatagagta ctgatagggg cgctcgttcta ttctgacctc      180
ttcgacctng acgcgctggt ccagggtctta tcgaggatac gtcctgtagt cacgttcttg      240
agtttgtgcg gacgaaagcc gggcctttgc cgggcttgac gtgaaggaat tcgagatgaa      300
gtagtactgt cctcaattt cgagacacat gccgttgcga aagctgccgt ttagaccatt      360
tgggtataat cgttttttta atgatgacga aagggtaggg ggcggttctc gaaatgctgc      420
cgatccttcg ggatataggc aagcctcctg ttgcggaggc aaaaataaga aaaattgtcc      480
gcgaggaaga agtcgattat tttcaaattg agtgtacatt ccggtatcaa gaaagacata      540
taagagaagg catcctgctc atttgatgtc gggttccttt cctatccttg tcgaaagtgt      600
gtttggtagg gcaatttgtc ctgcctgctt tgcagtaggt gtgattttgt ttgcatagtc      660
ttaaaaaatat tgacataatg acaactcaaa agatttgttt tctatatattg gagtgcgccga      720
tattggctta aatacaagggt gtagggcatg ttggtttgat gtgcctgata taccgtccta      780
attcactacc gaatcaatta tggttttgtc agaaaaagca aagtattatg ttgtcttgag      840
catcgctacg gtgtccacaa ctatcatccg ctgcgagggt tatctctcgt ggtcagggag      900
cttatgtgtg ggatgtggat ggggaagcgtt attcgacttc ctttctgctt atagtgccgt      960
caatcagggg cattgccatc gaaaatcata gcagcactga aggagcaggc ggaaaaaatc      1020
tgtctgactc acgggctttc tacaacgatt gtttgggtga atacgaagag tttatgcaca      1080
ttatttcggc tacgataaga tgttgccgat gaattcgggt gcggagggtg ggagacagct      1140
ttgaaactct ctgctcgttg gggttatcgt gtgaaagaat acccgaagag aaggctgtca      1200
tcactgtagt cgacggcaac ttccaggccg caccatcagt atcgtttcca tgagttccga      1260
tcccgcagag tatacagatta tggcccttat acgcccgggt tcgtcaatat accttataat      1320
aattagaagc tttggagaag gcattggagg aacacaaaaga ccatgtagct gctttgtcgt      1380
ggagccgata cagggtgaag ccggtgtctt tgttcccgat gtggttatat ccgtcgtgct      1440
gcagagcttt gccgcaagta ccatgccctc ttgtggctga tgaagtgcag accggtatcg      1500

```

cacgaacggg	acggatgctt	gctgcatca	tgatgacgtt	cgccccgata	ttgttgctgct	1560
cggtaaaagta	tttccggcgg	ggtattgccc	gtaagttgcg	tattggcaga	cgatgagtta	1620
tgcttacgat	caagccgggc	gagcatggtt	ccactttcgg	gggattcccc	ttgcctgcaa	1680
agtggcgatg	gctgccctta	cggtggtaaa	agaagacgct	tgccggagag	agccgaggag	1740
ctggggcagt	atctcagagg	agagtgtctc	aaatcaagag	ccctctattg	aagttgggtcc	1800
gcggacgagg	tatctcaatg	ctattgtcat	cgaaccgcac	aatagacacg	aggcatggga	1860
cggtgcgagg	caatggccga	acgcggccct	ctggccaaac	cgacgcacgc	catatcattc	1920
gcttggctcc	gccactttgt	atcacacgtg	aggagctggc	caagccgtgg	agattatcaa	1980
ggaatccatc	aaggtttttag	agtaaccatc	atggctctta	ttcgcaagca	ggccacgaac	2040
cggttgctga	tggtgcgcgc	gctctttttg	gattttaatgc	cgaaacggcc	agaaacaaca	2100
gcttccaaaa	gaaacgggag	taccggaagc	agtagcaagg	gaagcgaaaa	aagagttgac	2160
aactacgtca	atctattgcg	cgaatacggg	gtagatgtat	gggtcttcag	gattcgaaga	2220
cacctcatac	accggattcg	atattcccga	acaatggttc	agcacgcacg	tcacaggcga	2280
attggtgctt	tatcccatgt	atgacctaac	aggcagcaag	agcggaaaatt	gcccgactcg	2340
gctactgttg	gtaaatggaa	gggtggtatc	gtatcatcaa	tctctccggc	tacgagcggg	2400
aaattgtttt	ctcgaaggca	cgggcagtat	ggtattggac	aggggtcaatc	tatagcttac	2460
tgctgctctt	ccgaacgtac	caatccgaag	gtattagaga	atcttgctcg	gaattggact	2520
acaaaggatt	gattttttacc	gccacagagc	gaatggtgct	cccatctatc	ataccaatgt	2580
gatgatgtgt	gtggcttgcg	ctatgcgacg	gtttgttttg	agtgcacacg	ggacgaagcc	2640
gagcgcgtat	ggtggtgaat	agcctgaccg	ctaaccggaca	ccgcatcata	gccatagtag	2700
ggagcaggtg	gagcacttcg	cgggcaatat	gctcgaagtg	gagatg		2746

(2) INFORMATION FOR SEQ ID NO:227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

acgccaaacc	ggacttcagc	gacgaagacg	gtacacgggt	agcagagctg	aggacaaatt	60
cgccgaaatg	gaaggctgga	atgccgagag	cgatgcagca	tggtgctgag	cggacttggc	120
atcaaagagg	atctgcacta	tatgctgtga	aggatctgag	cgaaaagcaa	aaggtgcgtg	180
tgttactggc	gcgcgcctat	acggtaagcc	tgacaacctc	ttgctcgacg	agccaacgaa	240
cgacccgacc	tcgagaccgt	ttcatggttg	gaaaactatc	tgagcaactt	cgaaacaccg	300
tgctcgctcg	aagccacgac	cgccacttcc	tcgattcggt	ctgaccata	cggtggacat	360
cgacttcggc	aaggtacaac	agttcagcgg	cactacagct	tctggtacga	atccagccag	420
ctcgctctgc	gccagcaaca	gagcagaaca	agaaggccga	agagaagcgg	aaggagttgg	480
aagagtttat	cgccgcttca	gtgcgaacgt	agctaagagt	aagcaaacga	cgagtcgcag	540
aagatgcttg	agaagctcaa	tatcgaagag	attactccct	cttcccgtgc	tatccgggta	600
ttctcttcac	accgggtcgc	gaacccggca	ataagatctg	gaagtaaagg	ggctgacca	660
aagtatcgaa	gggcaacttc	ttttcctgat	ctgaacttca	atgtcgaaaa	ggacgacaag	720
attgtcttta	tcagcgagat	cctcgtgcga	tgaccgcctc	attcagtatt	atcaacggag	780
agatacacc	gatgaaggta	catacgaatg	ggggcaaac	attaccacgg	ctttctgcc	840
ctggacaatt	cgggctatct	caatacggat	ctgaatctcg	tgagtgggtg	tctcagtttg	900
ccaaggatac	gaacgaaatt	tttctcaaag	gttcctcggc	cgtatgctgt	cagcggagag	960
gagattctca	aaaggcatcc	tcctctccga	gggagaagat	ccgtgatg		1008

(2) INFORMATION FOR SEQ ID NO:228

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

caataggtga	gcaaaaaaga	taccttcttg	ataatcttct	ctttttgcaa	ggtttctata	60
attctatttg	agaaggtgca	atctgtagag	cagggagacg	aggcgggggc	taaaggttca	120
gtcctccggg	aagtttgtgc	gtcaggagac	ggtatcacca	tcagtggagt	actgccagga	180
ttctttcatg	acgaaggtat	tgctttgagc	acgacgtcgg	gatggtgatg	cagttctcgg	240
cagattccgc	aatcagtagc	taggggtgtt	cttcgggtcaa	acgttgctcg	aggaatgtag	300
caagtgcgcc	acttcatgat	gggtgcagtt	tccgtctttt	ctcttagaca	tacgtcgcat	360
agcttgagc	tgtgggactg	ctcctcgccg	aataggccag	aagcatgccc	ctgcgacagg	420
tgttttcttc	ctctatgtag	cgagcgactg	atcgattcgt	gctttaagcc	gatcgcgacg	480
gtcctcgtaa	ccgcacgagg	tatctggagc	aattctgcac	cctcacgtct	tgtgagaaat	540
aaattcgtgg	cagattcttt	tgtggaatat	agttcactat	gccggcttgt	tcagaagcag	600
gagttgctga	tagacctgat	cgacgctaag	ccctgtcttt	cggccaattc	gctttccact	660
atggaaacat	aatccgcaaa	caacctctgt	atgtcctcat	cagggcagtc	agcacgctgt	720
cggaagccctg	ttcgctctca	tgcggtatag	ctcgtcgccg	tgcacctgta	ttgtcaggcg	780
cgaggcgctct	tttctctccg	atactcccaa	atcccggtca	catcgaggat	gcgatcgacg	840
ccaatacttg	tgttggaac	atcctgaaat	tccggcaaaa	agatcgatgt	cgaagtcgaa	900
agatcgctcg	aatccctctc	cttctcttat	cgcaggtagt	tgcaaatccg	attgtacacc	960
gtggcgatgt	attcacgtgg	ggaaactcat	tgctcactcg	ccttttcagg	ttgaatatgt	1020
cgctctccct	gccagtaaga	cggcataaag	cctctctccg	tcccgaaccg	cgcgaccgcc	1080
tcttggaact	actctctccg	cgaagagggc	atctccatgt	gaagtacaat	cggacatcgg	1140
gcttgctgat	ccccatcccg	aaagcatttg	tgcagagatg	atccgcgttt	cgccttccat	1200
ccagcttttt	tgccttatth	cccgttcaca	tgggtgagac	cggcgtgata	gaaatcggcc	1260
gagaagccgt	tttcccgagg	aagcgtgcca	gatcgccgcc	cttatctcgg	ttgcgacagt	1320
atagacggcc	gaaccgtcca	cgcgactgag	gatatgcagc	agcatcgtct	cttgtctgcc	1380
gtccggcgga	tgaatacga	cagattgggg	cggaaaaagc	ttttctcagc	acgttcgggt	1440
ccggaatctg	gagtagcgt	tgtatgtcgt	gatcaccggc	cgtgtagccg	tagcagtcaa	1500
tgccaatacg	ggaacatccg	cagggcctcc	ctgatgtctg	ctatcgagag	gtatgccggc	1560
cggaagtcta	gccccactgg	gatatacagt	gacattcgtc	tacgaccagc	agacttacct	1620
gagagcatgc	agacggctga	ggaaaagtgc	cgagcccaga	cgttcggcga	aacgtataga	1680
aattttagtc	ggccgtaaat	acagttgtcc	agcgtgtgat	aatctgctcg	cgcgctatcc	1740
cggcatgaac	ggctgtcgcc	ttgacctctt	ttggcgcaat	cccatgatct	ggtcccgcac	1800
cagagcaatc	agtgcgttac	cacgagagtc	aaaccgggca	gtagcagccc	ggggacttgg	1860
aagtataact	cttaccacca	cccgtgggca	gtagtcccaa	tgtgtccttc	ctgccaaaac	1920
ggattcgatg	atcgggagct	gcacaggcct	gaacgaaggg	agcccccaata	gtgtagcaaa	1980
acctcctccg	gcgtatgcag	agacggagct	cgatctcatt	ggaaaacctcc	tccggcatag	2040
gaggaagaaa	gtcttctctt	ctctcccgat	ctcatcactc	tgctcatggg	cgtacacttc	2100
cccgtgcaat	aacgatcggg	aacctctttc	atatcgggtg	agaggggata	gagacgtcac	2160
ccggtgacaa	gtgttgagc	tcttcgtctc	tctttgttct	ggttcgtatt	ctatatgatt	2220
ctctgcattc	caaattcaga	cagcctgtgg	actaccccgg	ataataatcc	ggtgcagcgt	2280
gtgaaaatca	tacacgaaag	tacaataata	cgcccaatcc	tctgtctcga	acctcagccg	2340
atctccgaca	atccggaacc	gcaaaagctg	cgattgcggg	tcgtgttttt	gggaaaagtg	2400
agcgagatth	ttttcgttgt	ggcgcgtaaa	tttttctttt	ctcgcaccaa	aggaaaactt	2460
ttacgcgccg	catttttagg	gccggtgagt	cgccgttttt	ggctcgtgaa	aagggtggcg	2520
tccccagccg	gttcttcttc	ggctattttt	ttcccatctt	gtcggatctt	ttggcttaat	2580
cctctcataa	tcaggtgtca	tctttgagtg	gtttgtctct	cgattcgcac	tttggctctc	2640
tccgttaggt	ctgggttttg	gagcttgttt	atggtagcct	ttgcagtgcg	attctgaggt	2700
atthggctct	tttatactta	tctaagaggg	ctttacgtac	ttctccttat	cttgccgatg	2760
agthtttttt	gtacctttgc	aagaaacgta	gatacggtaa	aagaatggat	tccaaaaaaa	2820
ttctttacat	atcccaagaa	atthccccca	cttgccggaa	acggacatat	cggctcgtttc	2880

gcgcaaattg	ctcagacccat	tcaggagcga	ggcaacgagg	tgcgcatTTT	tatgccccgc	2940
atggcatcat	caatgagcgt	cgcaatcagt	tgacagaggt	gatacgctt	ccggcatcaa	3000
tatgatcatt	aacgacaacg	accatccgtt	gatcatcaag	tggttccat	ccagtcggcc	3060
cgcatgcagg	tttatttcat	cgacaatatg	atttcttcaa	gcgcaagacg	atgtacgaca	3120
tcaagcccaa	gcaggaaatg	acaacgatga	gcgagccatc	ttttttgtgc	gcggagcact	3180
cg						3182

(2) INFORMATION FOR SEQ ID NO:229

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2568 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ggcgaatcgg	tttcataaca	atgagaccgt	tgcacaaaaa	cccttccacc	cctcatatca	60
atcaagacag	atacaagcat	tgatttgacg	aagaaaggga	gcttcatgcg	gtctctctgc	120
aaacctcaag	aataccccga	tgaaaactgg	gaaaatttct	gtttgtttgg	tgcccatatg	180
tttgagggtt	gatcttccgt	aaaaacactt	aagaatcagc	tctgcggcaa	aagacttcaa	240
tgaaatccta	taaaatagtt	gcaaacagct	gatagttagc	gcattgatgg	gagctaatac	300
gctgacaatc	gtttcttatt	tctcgccctat	ttgacgagga	aagagtactt	ctctaattgga	360
aacttgggga	aatttctatt	tgctcgggtgc	cctataccga	aggtttgacc	tttcccgaag	420
acactaagaa	tctgctctgc	acaaaagaac	tcaatgaaaa	tcccctgcaa	cagtctcaac	480
agtgcgaag	cgaaataact	aaatatgttg	tgttatgaaa	agggagctat	atcagaatcg	540
aaaaaatggc	gaaaatcaat	ttgttggtga	agcaaaactt	gtaagttgac	tttaataact	600
aagcattgcc	attaaccaat	ttatgcttta	atctttattc	gtctgaatat	cttacctttg	660
gtgaaattct	tttacgaagc	tatgctgtaa	atagaaacct	gaaatcaata	gacgcataaa	720
atcataatta	caatctaatt	tttgctcatc	tctatgaaaa	gaaaattcgg	ttttctctgt	780
gctggctgct	ggggatcgct	gtggcgactc	ctaaggcaga	ggcttgacc	aattgatcgt	840
agccaaaggg	gcttcgactg	acggttcggt	aatcatcagc	tatcggcaga	ttcgcatacg	900
ctctatgggg	agttgtatca	ctgggctgct	ctgattgggc	tgaaggaaac	atgcgcccac	960
ttatcgaatg	ggacacgaac	aaccacttgg	attcattccc	gaagtagcgc	atacctacaa	1020
tgtcatcgga	atgtgaacga	acaccaagtg	gctattgcgc	agacgacatg	ggcgcgactc	1080
ccgaattggc	cgaaagtgat	ggtatcatgg	actatggcag	cctgatcatg	tggtcttcca	1140
gcgttctaag	acagctcgtg	aggctataga	cgctatacca	atctggtaaa	ggaatacggc	1200
taccatagca	gtggcgaaaag	ttttatgttg	ccgataagaa	cgaagtgttg	attctggaga	1260
tgatcgggca	gggtaggggc	gcaaagggtgc	tgtgtgggca	gctgtgcgca	ttccggacaa	1320
tgcattagtg	cacatgccaa	tcaagctcgc	atccagcaga	tcgatttcaa	gataaagatt	1380
atctctattc	tcccgatgtc	gtttcatttg	cccgtagagat	ggattcttcc	aaggaaacaga	1440
caaggatttt	agcttccaag	aagcatataa	ccttataccg	aaggtggtct	tcgtgggtgt	1500
gaagctcgtg	tatgggcttc	ttcaataagt	tcaattcgca	atgggtaag	tatgaagctt	1560
ttatacggat	cagagcaagg	ataaaatgcc	tctctatatt	gttccggatc	gcaagcttct	1620
gtcgctgatg	ttcgcgatat	gatgcgtgat	cactacgaag	gtacttccta	tgtatgacga	1680
acgatccggg	tgccggccct	tataaagtac	cctacgttgg	cgctccgatga	gcttcgaagt	1740
ggatggcaag	gagtagctta	atgacgtgcc	attgccactc	agcaaaaccg	atttgtttcc	1800
gtagcccagt	tgctaatttg	ctccccgatg	ccattggcgg	tggttaattg	tttggcggtg	1860
acatgccgat	atggccgtta	tgagtcogat	ctattgttcc	acaacgcgtg	tccggagtgc	1920
ttccgctcagg	gtaatggcga	tatgatgcac	ttttcttggga	ttcggctttc	tggatccaca	1980
attgggtggc	taatatggca	tatcaccgca	tgatcagatg	atagccgata	ttcgccctgt	2040
acagcgtgaa	ctcgaagggc	ttgtgaccgc	atacttccga	ctatcgacaa	gcaagcacaa	2100
gagctatcgc	tctggatccg	gccaaagctg	tagcattcct	gacaaattac	agcaacaaga	2160
ggcagagaaa	gcaactgccc	gttgggaagcg	tcttggggaa	tatctatggt	aaagtacatg	2220

gatggcaatc	gcaagaaaga	ggagagtggc	cgatcaagac	aaatggatac	ggtttcagtg	2280
ccatgcctga	tttccccggt	tatgtcagga	atactatcga	cagatagcaa	catctgaagc	2340
ggccgaacgc	ttctcaagaa	agaaaaggaa	caacattaag	ttggttttatt	ccctatcttt	2400
gccccgaaat	aaaaagagac	aagaccgac	aaggctcggtc	ttgttctttc	gctctgtagt	2460
tcaatggata	gaatagtggg	ttcctaaacc	atagattcgg	ttcgattccc	gacggagcta	2520
ccaacctgaa	aaacactgaa	atcaatactt	tcgctcatatc	tactgatg		2568

(2) INFORMATION FOR SEQ ID NO:230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

tgccaaactc	cttgaagtag	tcttctatcg	tatggcgacg	gaagtgcaga	tggcttccaa	60
tgcatcccca	tcggcaaagt	atcctccaaa	gcgattgctg	tggcaaacgc	cctgtccgga	120
aactccgggt	agccgagacc	gagcaactga	acaggcgggc	gatatagtcg	gagtaaacga	180
tgcgacaagc	ctcgccctc	ccacattgta	tgcccgcccc	caaagagaag	ctttgtgatc	240
gtatgcttca	cgcaggcaga	ggcaagatcg	cggatatgga	cggctctcga	gcgttgcca	300
atggcataca	gaatacagag	ctgttcagca	aggacgaatc	gtgccgagga	taatacccgg	360
gcggtagatc	gtccattcga	ggctggattc	cttaccagct	tttcggcttg	caacttggtc	420
agagcatcgt	agtcgcccac	gaggggcagg	tcatattgtc	cgcactgatc	ataggagctt	480
tcagtctgtc	ccatataccc	ctaccgtgga	aatgtagagc	aggtaggcgc	ccgggggagag	540
cgttccagat	tctcgatgat	gtagcgcgta	cccacgtgtg	tgacgtccct	gccagtcgaa	600
gacgcttata	cgcattggct	ttctcaaggc	tctggcatga	atcacaaaat	cctgtccctt	660
acaggcctcg	acggtattat	cctgtaggaa	cagtcgccgt	agaaaaatag	aatctccttc	720
ttatactttt	cgaagaagcc	atcgtagtgc	cacgcttgat	atccnaaacg	gaaatctcga	780
agacttgccg	atcgtaagga	gtagagccaa	aatctctctt	cccagcgtgc	tgcggctcct	840
gtcagaagaa	cttttatctt	gtagccata	actatttttt	ctgtctgtaa	gggattatta	900
tttattgtgc	cctcaaatat	aaggaattag	gattagttgc	caagcaggaa	cagccggaca	960
gaggcaaaaag	cactccttac	ggattgccgt	acgcagtcct	tttcaagatt	gtacttgtag	1020
gtgtgggcaa	atccccttag	cgttgaccgc	cgaagaagtc	tgctatagcc	agcagcagat	1080
ggcaccacgc	gtggaggtgg	caagccttgc	caagaagag	cc		1122

(2) INFORMATION FOR SEQ ID NO:231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

```

gttcgaaaaag cgttttaatt cctgtatggt gcaattgaaa tatgatagag agataggact      60
cgcgctcacc gatacgtttt aattcctgta tgggtgcaatg aaatctcccg gggtgggcag      120
cacggctttg aggaattggg ttttaatcct gtatgggtgca attgaaatcc gttacaaata      180
taggcttttc tgtttgatgt gaggagtta cgaaggggtg aaacccaaaa ttcagacatt      240
catagtgtcg atgtctgatt ctatgaaaaa ccaaggggtg tgacgactga tatatttatt      300
gattatcaat catttcaaaag atcgccggag gttaatcatg gcaaaggctt gatgaatttg      360
ctcgagccga cgcttcaaaa gatagatagc ggagctgtat cgtgctgtat tatagaaata      420
tatccgttgc agaacgctct tgccaattat ttctttttcc aaccaacgtt cttgtctgga      480
agaaaatatg tcagactatc ttcttttttt tccataattc cggctgctct gctcttcagt      540
ctaagagctt gacttccgat atttccccct cgaacacaga gttctgaacc aattcagata      600
ttttctgcac agttttaaca ttttgccaac acgctttcac cgatatcgta cactaaaata      660
atatacatca cccaatacat cttaa

```

(2) INFORMATION FOR SEQ ID NO:232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

```

ggcgagcttt ttcacgcaat tggatcangc tctttttactc tttccagtta aaactcatat      60
tctttttctaa atagtttaggt ttgctatttc atgacataag gcatactcgc cggaaagcag      120
tcggcactgt ccggtcgccc gtaggggtgtt actattattt atgatcacat acctcggtca      180
gcacacccat agtactttcg ggtgcaagaa accgatattc aagccctctg ctccctttgcg      240
agcttttcgt cgatcagctt aatgccttta gaggcggcat cggccaatgc ttctgtggcat      300
cttccacaca aaaagcaatg tgatggatac cttctccacg ctttctatga atttggcaat      360
agggctttcg tcagaggtcg gctccaacaa ttcagcttgg tctgccctac catcataaat      420
gcggtacgca ctttttggtc ggtacttcct caatgctgta acacttgagt cccaatacat      480
tttcgtagta gggagggctt cttcgatact tttgaccgca ataccgagat gttcgatgta      540
gataaattca ttgctctcta ctttttttatt gtgttgactc ttctaccatg tccgaagatc      600
ttaatgcaaa gcatttttcgc aaatgtagaa attattctga tggactgatt aagtattgnc      660
catataatc

```

(2) INFORMATION FOR SEQ ID NO:233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

tcctaaacct	ctttccgagc	aatcatctga	ggggtaaata	tgacagagaa	taaggtatta	60
cgggtgtgatt	acatatat	gtacttaaat	aatccactca	aaacggatga	aaacgattgc	120
gaacgagtct	tttcttcttg	atacaaagtc	cccgaaacct	ctctgaggcg	tcttccctgg	180
tatttgtctt	acgtccgctt	ttgcatgcgg	atggatgcga	gtcgggtgtct	tccacgcgga	240
tcgctgtgccc	gtaggagtgg	atgcttcgct	cgtggccaag	gatctctcct	atgttcggtg	300
gatggggcgta	cacgggtagg	gtaccgggtg	gcgacatgg	tggtgtgctg	aacgactttc	360
tgggcttttac	gcaccaccac	cgtgctttcc	tctcggggtg	ggaagtctgg	gtgctgcttt	420
gttgcaggac	tcgggtttgc	gcacttcggg	ttggagattg	ccgccgggtt	cgatgtgaat	480
ccggatattg	ggacactaat	atcaatggca	tcccogttta	ccataagagc	cgggttgcca	540
gttgtgcgct	cgagagcggt	tggatatagg	tattcttacc	gttccgatcg	ggcggcacag	600
tcgatggccg	atgagatgat	agcagcaggg	atcaagggtat	ttggaatttt	accccttggc	660
gcatacagtg	acccgaaggc	gtggtctaca	gaatacgtcg	atgtatgccc	agttggctgt	720
gatgtttcaat	cggataaatc	gctaccttag	gtctccgaag	gctgaacaat	cctcctttgc	780
cctttttata	ataagggtct	tcgctcgctt	tggaaacgatg	aagataattg	ctgcggcatg	840
aactatgggtg	cgcattgtcag	cgaaatgcga	cgtgcggaca	tcttcccggt	gctccctgtc	900
cggatggagg	gggagccgat	ttttgtgtgg	agaacctgtg	cttttctca	aggccgactc	960
cttgttgcgc	gaagggcata	ccttttctat	cggatttttt			1000

(2) INFORMATION FOR SEQ ID NO:234

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

caaagagaaa	aggcgtgtag	atggtatgcc	tggcacacga	tctacacgcc	ccggagtatt	60
tcgcttctga	gatcgctcag	tacttcgtcg	tacttgtccc	gatctcttcc	accatatctt	120
cggtgattcc	cttcattttc	ctacggtctt	ctggtagcga	ttcttggctt	cataatagcc	180
ttccaccacg	ctatccttac	tttgtcggct	gtactgttga	tgtcttcaac	gaagcgagta	240
cgttttcacg	atcagcgaaa	taagcagcgg	tagccnaat	agcaaggccc	actacagacc	300
gagagaaaac	tttccttgtg	agtcataaaa	aaatcctcct	tacttattaa	atgctttgaa	360
tcaattttgt	cagaaaacca	attcacncca	atatgaatcg	tttcgt		406

(2) INFORMATION FOR SEQ ID NO:235

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 791 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

aaaaagggttt	tgggaaatgt	agcctctatc	ggcaatgagt	ttgccaaaag	attcttgggtg	60
aatgttccgt	ctttcagagg	ttctctgtca	tcacaattcc	cggtgtgatt	tgatagttga	120
tgatttcacc	cctgtcgttg	ataacaaatg	cagtttgaat	ccataaaacc	aacccatggt	180
gcttttgctt	ttttgaccca	tccccctcatt	gtcctatgcc	catgagctcg	tttgatatga	240
caagcttcag	tggggtggaa	tcgatgaaag	agatgcctgt	acattgaccc	aaacacacat	300
attgagaaat	gctatcagct	tgaacccac	cctgctttgc	agccacaaa	gcgattataa	360
gagacaagat	tggggaactc	ggatcgacaa	gatagggtgat	gtattgaaga	taaaaagctt	420
tcaaattctcg	gtatcttgac	aatgaaacag	gatcaggatg	gtcatgacct	cactgtccga	480
catcttaaac	ttctattcct	gcgttttttg	tctgcctctt	cgagggtctt	tttcttgatg	540
cttcatcaaa	aagcttggag	aaatcatcta	tgatgcaaaa	aacatcaata	tatttgtctt	600
cataaagtag	cgttttgttc	gttcgtatct	tattgatatc	aactgctaag	atacaaaataa	660
ttcgctactt	tttcaagcat	aatgccacgt	tctttgggcg	tttaacccta	atcaaaaaac	720
aaattcattg	gtgtttctta	cgtcgaactg	acgttctacg	gaataccgct	atgctccttg	780
tggttagtta	g					791

(2) INFORMATION FOR SEQ ID NO:236

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 664 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

agcagattat	gccatcacgg	cctctcactc	ggagggtttc	ggtctgaata	tctggagggt	60
actgcttgtg	gaaaaccggt	tgtagccact	gatttgcccc	attcagagaa	atctgcggca	120
caggctttca	ggacaacgaa	ttgttttttc	tgtaggaaac	caaaaagaat	tggaggattg	180
cataactaaa	agccttgtca	tacgttcaac	cctcaaaaag	tctccgatat	caggcatcat	240
ttctcgcgga	aacaatgtct	gtacaatatc	agaactatta	tacggagcta	tcagtccact	300
aaaatgaatt	caatgaagag	tgcattgtcc	gattattact	gctcaatcgt	actttataaa	360
agcaaaccgg	atattattcg	ggatgtcatt	actccttttt	ctctgatacg	gtaactaaga	420
agaagcttat	cctcatagac	attctccgac	tgacagtctt	cgtgtcctcc	aagaagaaag	480
accggaggat	ttcagggtatt	tctttaataa	ccgcaatata	ggattcggat	cagctcacat	540
atcgggtatta	gagaggcagc	tcgcttcaat	ccttcttattc	attaattcta	atcctgatgt	600

gcagtttggc cctgaagtgg tgccgacatt ggcttcaaca tggaccgaga atcctgatat
agga

660
664

(2) INFORMATION FOR SEQ ID NO:237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...3236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

tccccgccac	ctcctgaagg	aaatagttgt	gcaatctgtc	cgtgactgcg	gaaaagatga	60
ccccatagaa	aatagaatcg	ataatatcc	cgataccgcg	gcaatgatca	gagacaaaca	120
agagagaaaag	gcgagtgtat	gctctcgttt	cgtaccaatt	tggccaataa	atagatacaa	180
aagcccatgg	caacgagcga	aagagactca	agaagagttt	gctcccta	tctataccga	240
aagcctcccg	ggattttcca	cgaaattggat	ctgaaaccaa	ggggcgacaa	cgtggactgc	300
cccagtagcca	tagtcgtctt	cacccatata	ttgatcacct	gattacgacc	agaagcaaga	360
caatgagagc	tgcgactact	tttccctgag	gcgacgggag	agaaaagaag	ccatctacta	420
tttcttctcg	ttcatttttg	ctctatgctc	agcgtagcat	gaggtagcgc	gcgaagtcgt	480
tctttgggaa	aagtttgccc	gtttcgcggc	aaacgcgcta	agtcttattc	tcgatacggt	540
cagagcagct	tgcaagtttt	ggataaaact	catcagtcgc	tgtgccaacg	tccggattcc	600
tctttcgaca	gtgtggctgc	accctcctcc	aacacctgaa	cgtgggagag	gtatcagaca	660
catcattacc	tgctgaattg	ctgacgcgcg	acgcaactgc	tcgtagtcct	tgcgagcctg	720
atccaatttg	gccaaattat	ttgcttgaat	tcttccaact	cttcgctcgt	gtagcgtggt	780
tttttaccat	ttgtatctaa	ataatcgtaa	gtggaacaga	tttctcggca	gacgaaaatt	840
catatctgcc	tccgaagtct	atccctgatg	tttaacaact	tgatgctaag	gacaaaatca	900
tcgaaatcca	gctccactcc	atcgctgaca	gatcgctgat	ctccaacgat	tcggcctgga	960
tttgctgggc	gatatagtca	ggtgctctgc	caccacttta	tccataatat	cgttagacaa	1020
gagaaggact	ccaccttgtc	cgacacttcg	aaaccgcttt	gcttgcggt	attctgcaac	1080
gattcacaag	ttcgcgagcc	agtccttcgg	agcgaagctc	atctgtcctg	taatatcaag	1140
ggctacggtc	agattgcctt	cgttggctac	gaagcctccc	ggaatatctt	ccgagacgat	1200
ctccacatcg	gccaaattcaa	gctctccgga	gtcccggcca	cttccatccg	gaaagtgccg	1260
gccttctcga	gggacgtatc	tcttccctgcg	tcatggccgt	tacagcttct	gccaaagcct	1320
tcacactttg	ccgtagcgtg	ggccgagtcg	tttgaagtc	ggtttgatcc	gttgaccaga	1380
atacccatcg	gtcatccac	gaatcgagc	tctttcacgt	tacctacta	aggatcagcg	1440
gctgtacgga	ttcgatacac	ctgcgctgct	atcgtctata	gccggtatca	tcagtgtagc	1500
caatggtttg	cgtaactttcg	attcactctt	cggcgaagtg	ccagcaccat	agacgaaatc	1560
tgctgagcat	ctgcatgctc	tgttccagtg	cacggtccac	ctgactttga	tccggccggg	1620
gaagagcgcc	aagtgcacgc	tttcgtcttt	gcccgtcaga	tctcggacag	tcggtcagca	1680
tagaaaggac	tgatcggagc	catcagtttg	gatacgtaa	caaggaggta	taaagcgtct	1740
gataggcaga	gagcttatct	tcggcatatc	tccctgccag	gagcgacggc	ggcttgagac	1800
gcacatacca	gtctctagat	tctcggagac	aaaatcgctg	atggcacgac	cggcacgtgt	1860
agctcgtagt	cgctcagttg	atcatccact	tcacgaatca	atgtattcag	tcggaaagta	1920
tccagcggtc	gatctccggc	ctcttggcga	aaggaatgct	tcttcttctc	ccgtaaagcc	1980
gtccaaatta	gcatagaggg	caaagaacta	tacgtattgt	ataaggtacc	gaagaatttc	2040
ctgcgtacct	cttccactcg	tccgtgtcga	atttgagatt	gtcccacggg	gaagaatttg	2100
tgatcattac	cagcgaagag	gatcggagcc	gtatttcttg	atggtctcga	aaggattacg	2160
ccgttgccga	gaacgttgct	catcttattg	cttttcttat	ccagtccaag	ccgttggaata	2220
gcacaacttt	gaacgaactc	gttccctgata	tcatgtggct	atggcgtgaa	gggtgaagaa	2280
ccatccacgc	gtctgatcca	cccttcggct	atgaagtcgg	caggggaagac	ggaaccgtcc	2340
tccactcggt	cggattctcg	aaaggatagt	gcatctgggc	ataaggcata	gcacccgagt	2400
caaccatata	tcgatcagat	ccagctcgcg	gcgcataggc	tgacccgagg	gagcaaagtg	2460

tgatcccatc	tacaaaaggc	ctatgcaggt	cgatcttgga	tagttctcct	cggtgtagac	2520
accgggcttg	aagcctgccc	atgggttggc	tccatcatac	cggttttgac	ggccttctct	2580
atctcgttgt	acagctctcg	accgaaccga	tacagatctc	ttcggaacca	tcctcagtag	2640
gccaaagggc	aatggcggtc	cccagtagcg	actgcgagaa	aggttccaat	cttgagattc	2700
tccagccatt	tgccgaagcg	tcccgtaccg	gtgctttcgg	gtttcaatat	atcttaccat	2760
tgttggttat	catctcctct	ttgcaggctg	tcggcggata	aaccagctat	cgagcggata	2820
gtaaagaacg	ggcttggtcc	tctccaacag	tgtgggtagt	tgtgtgtcat	cttttcgatg	2880
cggaaaacgc	gttctgcac	ttcagcatca	cgcagagttc	gacgtcgaga	gtctcgctct	2940
ctccgtcttt	ccggcatcgt	acgcattttt	cacgtagcgg	ccggcatatc	gtcatagagc	3000
ggcagatcca	tgtgcttctc	tacaaagaca	ggatccaatc	tgtcgttggg	aaatagcggc	3060
cggccagatc	caccataggg	cgcatatccc	ctctttgtca	cgaagcatca	agggagggc	3120
accgcttttc	ttggcccgcg	gtcatcgtcc	gcaccgaacg	taggtgctat	gtgcacgatg	3180
cgggtccatc	ttccgtggtc	acgaaatcgc	ctgtgatcac	tcggaaagca	ccttgc	3236

(2) INFORMATION FOR SEQ ID NO:238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

tggttcgctg	ccccaaagtcg	ttgtacgatac	gtcttcgcga	agaggatagg	cgcgtttccg	60
agtaccgctc	gatattctgt	ccgatgagga	cgatacggcg	gtacggaaga	agacccttc	120
aaaaacacgc	tggtcaggca	tcaggatgct	tcccctactt	cgccttgca	tacttcgatc	180
tgaagaaagt	cttcactccc	tccgcttcca	tatagatttg	ggcacctacc	acttcgccat	240
atacagaaga	acatcggcga	gcagccggaa	gaccgccatc	tgacgcgcaa	cctgacggct	300
tcggccgaat	acaggatttc	gccgaggagc	atagaccga	agatggaagc	gtttggtgcg	360
ggatttggac	tacttcgaga	ccggcgacaa	gcctatatca	cccaaaccac	tccgcactat	420
catatcgaga	aaggaaagat	cggctgaggt	tcgtgccgga	agggcagctt	ctttggccgt	480
cgccggaggt	ggagcaaccc	gaacgggacg	aaagcaaata	cgcccaagac	aaacggttcc	540
ggcagaagcc	ttcctgagcg	tacatgagct	gatgcccattg	atgtctatac	ttcctgctga	600
gagaaaagta	ttt					613

(2) INFORMATION FOR SEQ ID NO:239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

```

cactgtttttt ggcattgctg atgggatcat ggatgtcgat aggttcgtgc agatattgta      60
gtcaccgcac  aggatcaagt tagggcgact cttgcggatt cattgacata agattggaag      120
tgctccagcc  aaaccatctt gaaggccgac gctcatcgcc actcgtcccg gatggatgat      180
aaacgcttac  gatagaagat cgccgaaatc ggcacggata aaacgacctt ccgcatcgta      240
ttcttcatac  ccatgccata ttctatatga tcaggctgat gctttgtgat gataccacac      300
cgctatatcc  tttcttttga gcccgaaaaa aagatacgag ccgtagccca gtgcttcaaa      360
tccttcattt  ttcgaattgg tcattctgca tctagtttcc tgcaggcaca agcacatcag      420
gattctcttc  tcgaagccaa cgatcagatc ttttcttca      459

```

(2) INFORMATION FOR SEQ ID NO:240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

```

gtgaatagac  tcacgattgt cctcggcata agcatagcca gagcaaaacg agaaagctga      60
ccagtagatt  gacgccacaa ctgtagcgat aggccgactc acccgtcccg gatttttagc      120
cccgtagttg  aaacctacga tcggctgata ccctgagcca caccgatgat aatcatgaaa      180
aagagcattg  catagcattg ataatcccga atgctccgat ggccaagtcg gtagcatctg      240
ctgtccgccc  taggatacga aagaacgatt catgatgata ttgaccagac tgccgtaagg      300
tgcatggcga  aggggtgctac cctatagcc  gttatgccgc cgacaccggc agggacaggc      360
ggaaagccga  gcggtggaaa cgtagcatac tgccttacgg aaaaagtgcg aaaggacgta      420
gaccgaacat  actatcatgg aacgacagtc gctatggcgg ctccgcttat ccccatcccc      480
aacggataga  gaagatgtag tccagcacca cgttcgatc agccccgatg atcatcgtat      540
catggctttg  cgcgtagtc  ccgaaagctc tcatgatagc attgtagcga agcttcagag      600
ctgagaaaat  attggcagga ccacgtat      628

```

(2) INFORMATION FOR SEQ ID NO:241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

tgcttcttcg	agacagtcgg	aatgagtcgg	atccacaccg	aaatcattgt	gaatatgagc	60
gtattcttcg	tgatgtcgtc	cacgctcggt	cgttcgtgtc	gctggtagga	gtggcgaaaag	120
caccgttctc	gtcgcgatag	acaggcagcc	ttcgatatcc	aattcgccac	gtccgattcc	180
gacaaaaggt	tcgtctcata	tcccacgccc	aatacaatgt	cggagcctac	cttatcacgg	240
tcgaaacccc	gatagagtac	cctgtacgaa	gagataaaaag	gttgccctatg	tccacaaaagc	300
attgatataa	taaagcccca	atccgcgtac	tacacgtcgg	gacactgctc	ggcagacggc	360
ctgtagcggg	taggatacct	gccggtagct	tttagcagct	gcgtgtggct	gctatggcag	420
ggatttcttt	gatggccggg	agtcgcaagt	ctgtatcagc	cgatcaagcc	tctccgttca	480
tctcatctat	agagtggatg	gcgaccggcc	tgctgcaact	ttggccgtac	cactcctacc	540
gaaaagccgg	acaatgatgc	agaataggta	cgtaaaagct	gatcccgggc	atcgtctcct	600
tcgtatcgta	ttcgatctcc	aaatcaaaat	caatgtctcg	agaccttctt	catcctcgtc	660
gtcttctatc	gatgccggaa	caaatctcct	cctcatccca	tgtaagactg	gtcaaatcaa	720
gagcttggcg	tactagctgt	ccggctcgtg	aagggtctcc	ttgctgagtt	ctttccacaa	780
gtatctttag	ctcttccagt	ccctgttggtg	ccacggcaga	aatgaaaact	acgggcaagc	840
ctgtcggcag	ctcctcccga	agcatctcgc	acagctcttt	cgcgatgagg	tcgcacttgg	900
ttatggccag	cactttgcgc	ttttgtgcca	atcttcgttg	tatgccacca	gctcccgaact	960
gagtatctcg	tattccttgg	aatgttgctc	gtatcggccg	gaatcatgaa	gaggagcaaa	1020
gcgttccttc	gatgtgccgc	aggaaacgca	gtcccagtc	tttccccgat	gaagcccctc	1080
gatgatgccc	gggatgtccg	ccattacaaa	ggatcgcttg	tctcgatggc	tacgataccg	1140
agattaggtt	ccagcgtagt	gaacggatag	ttggcgtctt	cggctttgca	gcagtgaagc	1200
ctgatagcag	tgtcgatttg	ccggcttggg	aaatccgacc	agaccgacat	cggccagcat	1260
cttgagctgc	atgacaccat	acgctcctgt	gccggctcgc	cgggctgagc	atatcggggg	1320
gccgattggt	agcggctctg	aagaacgtat	tgccgtgtcc	gcctcggcct	cc	1372

(2) INFORMATION FOR SEQ ID NO:242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ttgcagtgat	gggtccgagc	ggagctgtag	aagtaatttt	tgccaaagag	tggcagcagc	60
cgagaatcct	caacaagcag	cattggaaaa	ggaagaagat	atcgtcaggc	tttttgccaat	120
ccgtacaatg	cagcctctta	cggctactgg	atgatgtgat	cgagcctcgc	aatactcgtt	180
tccgcattat	tcgtgccttg	aacagctctc	tacgaaaag	caaactattc	cggctaagaa	240
acacgcaatg	tgccctctta	ataagaggag	tttagtgcat	cgaccatgaa	tattgcaggt	300
ttagccatat	ccttctgact	ttgtttgtca	tagcctccgg	acactctttg	cccagcaggc	360
agcacagctt	cgcttgaatg	aagtgatgac	ccgaatgtgc	gngactatca	ggacagctat	420
ggcaatcata	agccgtggat	taaaatatac	aatcctccan	ccgctacggg	ggatatcaaa	480

(2) INFORMATION FOR SEQ ID NO:243

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 444 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...444
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

ctggaattgg	ttttactgag	gaaaataaga	attcttttga	tacatacaga	gtggcttcaa	60
aatgtcaaaa	ggaggtaaag	gcttcggtcg	atztatgtcc	taaaatactt	ttatcatgtc	120
tcaattgaaa	gtatcttcta	tgaagaggca	aatataaaca	acgtagtttt	acatttggtc	180
acgcagatga	gataatgaaa	atgagcaaat	tgtagatatt	gaatccgact	ctgacctgca	240
tacagtacag	ttttacatct	ttcttccatt	aagtcttttg	atttagataa	agggttgaag	300
ttattgccag	aaaactcggtg	gagcgtttac	ttgtattctt	tgtcctggag	gggaatatac	360
tccaaagatt	acgattaaag	aagagaatgg	ctcaattcaa	tagtattgaa	taactatatt	420
ggagacaatt	ctgatattca	aaaa				444

(2) INFORMATION FOR SEQ ID NO:244

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 456 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

tgcaaaaata	tcctttaccg	gctaaaactc	agataaaatg	tgtttttcat	gcaaggatat	60
gcgccactga	cctgtcgaaa	agagcgtgac	aactactcaa	attgaacgta	agcataatca	120
ttcgggtgcg	tgcccgactg	atagactggg	atagatcaac	ttataatcat	ccaaaagatc	180
aggacgctcg	tgtgtgtaac	atcgggaaaa	ccaaagctaa	agcgcagttc	ggggcacaat	240
ttgaaaaagg	caggtaaaaa	tcgcatccga	gaccgatctg	caccccgtaa	tcgtcgcttt	300
ggtataaatc	tccaaccctt	tctttcgccc	cagctccata	gtcagtaagg	cccgccgatg	360
aggtattgga	cgcataattg	gttcaagcgc	cggaccata	ttttcaataa	ttagcggaaa	420
ttccaaatat	ttggatccga	acggagaaaa	gaaggc			456

(2) INFORMATION FOR SEQ ID NO:245

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: UNKNOWN
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...474
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

ggcttgcggtg	tggatgagtt	cgggactgaa	ccacatacgg	ctctcttttt	cgtggacagt	60
gtgcgggtgtt	caaggaaatg	cagaaaggca	ggtattttct	cttcaccctt	tgcaggaaat	120
ccgtgtcgctc	cctctctatc	ctccctatct	tcttacccaa	tagcgcgctc	cccctgcgtc	180
gatgatgacg	ggcagggttc	gttgttggag	catagtacaa	acttggcaaa	gaacgaaatc	240
tcgtcctgtc	cttatccctc	gcctccacct	tgtaggaaaag	ggtgggtgctg	aggtccttgag	300
ccgctcgctg	tcctccctgc	ggtcgagaag	cacctngtcc	acgggatgag	cagtttccca	360
gcctagtccg	agttgaactg	acttcgaaaag	tctcgttggt	gttgaagggtt	acattgctgc	420
ccaagagggc	tttgaggaaa	gttgagaaat	tgtgctnttg	cccgtgtttc	gctn	474

(2) INFORMATION FOR SEQ ID NO:246

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: UNKNOWN
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...476
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

ggctgcgaat	agcttgtaaa	tacgattgat	ctcaacacct	gcagctttta	ctcattttaa	60
tactggacgg	ggttttcata	cttcttaaat	gcattggtag	tgatacctgt	gtcaatcgga	120
ctgttttcaa	atctgtggca	ttcataatgg	acgtgcagat	acactgactg	taaaatgacc	180
ggctttttct	gtgctattgt	cctgcttttc	tttactgaca	tagctatttg	ggcaaaaact	240
tcacgttttt	cttattaata	aaatactggt	ataaatctat	atcaggaata	cgagtgcagc	300
agatttcaat	tgtaacgact	cttttaccat	cttgatcatg	ttatgacctc	tttgacatac	360
tggttggcag	cgttaccttc	caaatatagt	tcatcaaagtc	tttcaagagt	gcttttagtg	420
aaatttcgga	caaaatgctt	atgatgaatc	tttttgtaga	gttgcgattc	taataa	476

(2) INFORMATION FOR SEQ ID NO:247

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

ggcgtaaaaa	tcgttataga	accacttacc	acttcaatga	caatacggaa	aggcatcccg	60
cctgatacga	tcatatacgg	tggaacatgg	catggctttt	ttgacctctc	tgcggttatg	120
gggggagagg	ctgaaacccg	acaatgggtgc	gtagcgggct	gatgcatacc	gatcatatac	180
attatacggg	gggtggtata	cccgatcatgg	aggactgggtg	gccgatgcct	tactcggtctc	240
tattgccgtg	gcaaaatgga	taggagcgac	cagtccaaac	tctaaaataa	aagaagtcca	300
agatcgtgca	ctttttcgat	tcgatggata	tatcccgctt	gtggatatac	tacagtatga	360
tgcttctgcc	cccatgattt	tttcgagtgg	gagttcttca	tcctctttct	tttgttctct	420
ccgctataca	tcctgctacg	cggcaaacccg	gactgcgtat	tgtatacgta	tctctctttt	480
ctctttatct	tactataaga	gcagcgggtct	tttcgtctctg	cttcttttgg	ctgctgctag	540
agcgacttcc	tcacggtcgc	gctttttgtc	ccgtcagcag	atccaagt		588

(2) INFORMATION FOR SEQ ID NO:248

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1014
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

gcgctctcga	cggttcttcg	ctgtgatcga	gagcaccgag	aggcggtcac	gacactctcg	60
atggcccgcg	caatggctcg	cacagtgtct	atcgccctcg	gaagataacg	agtttctgct	120
ctggattacg	ctccagactg	agcagacagg	tagcagctgt	cgcttaaaat	cgtctagttt	180
gggatcgctg	gagtagtgct	ccactgctca	tctagctggg	cgatgagggc	tagatcctga	240
cggagagatc	aatgtattct	ggagcaaagt	cctcacgtcg	atactctcta	tttccccctt	300
ctcattcgat	ccagaggagt	tgagcttggt	gatctttttg	cgtgatccct	ggcacactct	360
tcgaaggaga	acaatttcct	cgtactatcc	catgcttacc	gggattgagc	tctgcattca	420
catctatctg	tgggcagatg	atatggtatc	gtgctcccac	atatccacca	tattttgggt	480
gtaacgcttg	gatttttgag	cgagaccttg	aaggcggaga	agctactctc	gatgcgttta	540
ccaggccaat	ctgcataatg	cgtgctagct	gatgggagaa	tcgctcggat	ccatggttgcg	600
ccccgagtag	agcttacgcg	tgctctcgct	tctcaggact	caatagctcg	atatcggtag	660
tagcatagag	aggtagagct	gtcgaatgaa	aattctcttt	cggcgcaatg	cagtcctatcg	720
tacgagcgaa	gagttggcaa	ggctcttgct	catacgatac	tcaaagctat	gagggccact	780
aatccgggaa	aggtaagttt	ggtctcaggg	tagtacttac	ggatgtcggt	tcggtgcgtc	840
tgacgagtat	atcctgtagg	acgcagctct	ttacgcgact	agcaggtcat	tgagttagttt	900
cctactctgc	tgtatttgct	ctgccgttgg	gcttcgtcgt	agcgagagta	tatgacagat	960

tgatattcac gagctatatc gcaaaaaaac tctccagatt gccaccattg gcct

1014

(2) INFORMATION FOR SEQ ID NO:249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

agaccgttcc	gattatgaaa	gcagctacta	cgcgcagccg	tataaggatg	ttttcatcgt	60
tgttttcgtt	tatgcaattt	gttcatataa	agcctctcat	tacagaaaga	gcctgtttta	120
gtgagttccc	gatagccata	atccgtttga	ttttgtcgat	tatcttatcg	gcttcgggct	180
tttccaatgc	gaataatatg	cctgtaaagc	atcgtaagca	gtataattct	tccaatcttc	240
tcctatttcc	ttgccaattc	tctgactttc	tcataatcgg	gatgatatgc	tttgaatcac	300
gcataatcgt	gtcgggtggca	tcttcatcat	atccatcgca	aaagttatgt	tgttcaaata	360
gctggcatgt	tgaatgnaag	tcgatacacc	cacccgaata	g		401

(2) INFORMATION FOR SEQ ID NO:250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

ggtcgaagct	cgtagccact	gctacatgct	tggcctgatt	caaatacgcta	acggcacttc	60
ttccggaata	accaacacag	gtaccttgct	cgaatctata	cttcggctgc	aacgcttccg	120
atcagatccg	aatccttgcg	cgatttgctc	gcgtccccat	cacgatcatt	acgggtctgt	180
gtcgcttgca	gtaactagga	ttacatcttc	cggagcaccg	tccaaaagga	cagaggagaa	240
agatattcgg	gaagtccctc	tcgcgttatc	ctttcacgca	gctctttctt	gagctgttca	300
tcagacgttg	tacacgctgg	tattctttgc	gcaggctgac	ttcttgctga	gctggaacac	360
aagccgtatc	gccaccgta	agaagggtgtg	gaaaaaatgg	actgatat		408

(2) INFORMATION FOR SEQ ID NO:251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

atattggatg	tgcccgtgaa	agatgagaaa	gctgcctgct	ggcatgtctt	tccatcatca	60
cggacatgta	tcagcccaat	ccacagcgaa	tgaaggacgg	atctccatcc	ccaaaagcaa	120
cggttatgag	tcgctccacg	ttacggtatg	ggaccgcaga	atcgggtggg	ggaggtgcag	180
attcgctccc	gtcgcaggac	gaggtggccg	aaagaggatt	ggctgctcac	tggaagtaca	240
aaggttcaag	agcgagagcg	gattggatga	gttcctcact	tccgtacgcg	agaccttgag	300
gcacgcgata	actcctcgga	cgattcggcg	gagacggtga	aaacttcaag	atgaacctct	360
tcaccgatga	gatctatgct	ttcactccca	cggagaaactg	atcaagttgc	ctcaggggagc	420
ccagtgtgct	ggacttttgc	ttttgcccat	ccattngcgc	atcggctgtc	aggccgtcgg	480
agcttaatgt	aatggaaaaga	atgtgcc				507

(2) INFORMATION FOR SEQ ID NO:252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

tccgcatgca	agacgagcag	ggcttctatg	atttcaagga	ggcgattgtg	tgcagcctta	60
tcctatgccg	catttcacgg	ttattgatga	tcagacgcca	ccctccgtat	tgtctctcag	120
gtcgaacagc	tgatcgaatg	ccttattgcg	ttatccatct	tatcgatcca	agcagatata	180
tttacggttt	gtacgtggaa	gcatgtttat	cgcttcgcaa	tacctccacc	agcttgtaga	240
tcagccgggtt	ttgttccgat	agctctttct	attcagggtta	ttatagggtt	tgagagaata	300
aacagacgtc	tcgctgcttc	gcgatggctc	tcttcgggtc	tgtagtctct	ccctggatac	360
agcctataaa	attccgaaac	gctttgctgc	gacagcatcg	agagcgggta	ttttctccga	420
gtattcgctt	gtcttggtca	tgcaatacct	tttttgaaag	tagccagcac	cttggtccagc	480
tcattccaaag	aggaataatc	tcattttttac	tgaagagtgc	gagcatcttt	gacctcatca	540
tcataaaaatt	cagaagctc					559

(2) INFORMATION FOR SEQ ID NO:253

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...4542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

tgctcgcaaa	caaaaccaac	tctattcgac	actggagcag	aaaggattca	ccgcccctcc	60
actacgatgt	ggacttatga	cgatcatatc	cgcgacgaat	gaacaaagcc	atgagcctac	120
tgcgcgaaaa	agactacgac	tccttcctgc	agcatacaaa	gagatggcta	tcgttctgcg	180
tgacctgatg	gaaaaaaaga	gcttatcctt	tatccaacct	ctctgaagct	catttccgac	240
aaagattcga	agaaatgaaa	catggcgatc	gggaaatagg	cttcttcctt	atcgcatgcc	300
ggaattagat	gcaccggcca	agcaatcaaa	agaagcccac	ggcaatcatt	tatggcagaa	360
ctgggagcct	tacttgccaa	acatgggatg	ggacagggcg	acaagacgac	aaggcgatac	420
tggatgtagc	cgaaggaaaag	cgactttgga	gcagatcaat	ctgcttttcc	gtcatctccc	480
tgtggatatt	cgttcgtgga	cgaaaacgag	ctggtttggt	tctatacgga	cacaaagcaa	540
gagtattccc	cagaagcaag	ggggtgatcg	gcccagagaat	acgcaactcc	atccgcccac	600
gagcgttcat	atagtagagg	agataatcga	taagttcgac	gtggcgaaaca	ggatcgcgca	660
gaattctgga	tcaataagcc	cggagtttca	tctacattgt	ctatgtggcc	atcagagacg	720
ccgacgggcg	tttcccgggtg	tgatggaaat	gatgcaagac	tgacacgga	tcgtagtct	780
tgaagctcgc	gtacacttct	tacttgggac	gaagagcaaa	gtccggcaca	aggtcgaaaag	840
aaagcgaatc	cgatactgcc	ggagaagacg	gcattcggcc	ggcacgaagc	tgaagagtct	900
cttgacgcgg	tatccgcaac	tgatggatga	ttgccaacga	tcagttccaa	gttcaccctc	960
cttcgttctc	cgatggccaa	gtaattcttc	ctggtgccac	cattaaaatg	atgagcgaaac	1020
gcgcccacat	ccgtcggata	tgctcatcgg	caaactggaa	tcgctcatcg	cttcgtacat	1080
aaaccggatc	gatcgggaaga	gaaatagcat	gaagaaggag	gtgtgtcata	atcatggcgc	1140
acctccttgc	attaatatgg	gacggtcggg	tacaccttat	tcagagactc	ctaaggagtc	1200
cctaccgaga	ccctaagga	gtctcaccaa	gacctctaag	gagtcctccac	cgagatccct	1260
aaggagtccc	taccagaccc	ctaaggggtc	ccaacagaga	ctccttaggg	gttccctcaat	1320
gcttacttca	ggaggggttc	gtgcggtcct	ataatccatt	cgaatggaga	cacggggaga	1380
gtgaccggcg	aaaggaagcc	gaagcttagc	gaatcttacc	gcgaacagat	tgatgatgcg	1440
gcccgcacta	cgtgcacgtg	gtcggagtg	gtcaccatga	cgatgggtgc	accttcgcga	1500
ttgagacctc	tgagcagttc	atgacatcgg	ctccgttttt	ggagtcgagg	ttaccctggtg	1560
gttcatcgcg	aggatgagct	tcggattggc	caccacggca	cgggcgatag	ccacgcgtgc	1620
tgttgctcct	cgagagagctg	attggggaag	tgcccgggccc	ggtggcgatg	ctcatcttgc	1680
gcagtgcctc	ctccactcgc	tctttccgct	cggagccttc	acacccagat	agacgagcgg	1740
caactccacg	ttctcgctta	ccgtatctct	tcgatgaggt	tgaagctctg	gaatacgaag	1800
ccgatattgc	cctacggacg	gcagtctctgt	ctttttcccg	gaggttgccc	actttctgcc	1860
cacgagcttg	tagataccgg	aagtgggatt	gtcgagaagg	ccgaggatat	tagcagagtg	1920
gacttaccgc	atcccgaagg	ccccattatg	gcgataaatt	gcctttgtcc	actttgagcg	1980
atagccatc	gagggtacc	gtctctattc	ttctgttctg	aaaaccttgg	tgaggttgc	2040
gatttcaatc	attgttttct	tgtttttatg	aggtgaaagg	aagagcgaca	agccggacaa	2100
tgcttggtta	tgaatccgcc	gtttgcccga	ttgtcgccgt	atltattcgt	atcggaattca	2160
ttgacagggt	tgcggcgagc	tatgcgccgg	aggttgatga	caacgccaat	gcaataatca	2220
ggaggacgaa	cagacctaca	aggaggaaaa	tccgcggttc	aattcgattc	gatagcttga	2280
acttctccag	ccagttccga	ccgagagata	agcgacgaaa	agtcgggcaa	gcacactcgg	2340
caggctgagc	cgaaaatgga	gcggaggaag	agtcgcgaaga	tgctgccttc	tccggctccg	2400
tgatcttgcg	aatggccagc	tccttgcgac	ggcgattgac	ctccgtattc	catagccgac	2460
cagcccgatc	agagcgatca	ggatagccac	gacactgcca	agaggatcgt	attgcgaaaa	2520
gtcttggtcg	cctcgaagcg	actgagaact	ccatctccac	accgaggaaa	gaagctcct	2580
tgtagggatc	ggcttcgaga	ggatgccatt	cacgcgatgg	aggagccggg	catcgatcg	2640
gcgaagcgga	tcgtcagata	atgcagccaa	tcgtcccat	agacgatggc	ggaaggagct	2700

tttcggggta	agggctcagg	tgctgacggc	ggagcatgag	atcgcgtaga	caccgcgaat	2760
caccactcgc	ccgaaggaag	tcaggatgat	attttgccga	tgacaccgtc	tttccaattc	2820
atcagccgag	ccaattcggg	agcgctttct	tgctgagcat	gatctctctg	tccttttcgg	2880
ttgcagcgtc	gagttttttc	cttcgagcaa	ctcgatgtcg	tagactttca	gatagtgttc	2940
tccacgtaga	agaggtcggc	cacattgatc	agctcacgat	ccgtaacggg	tcgataaggt	3000
tatctccact	ctggccggaa	gaagccggca	aggcgggtctc	agcgtgtagc	cttccacttc	3060
gggcagtgcc	ttgagctttt	cgatcacaca	gggagttgct	gctgatccag	cgactcgatg	3120
gggacataat	acagtcggcg	gctttgtatc	cggcatcctg	ccctatcatg	tgccgggtatt	3180
gcagacggtg	atagccaaaa	ggccgaagag	gaaagtggcc	gccacaaatt	ctacgccagc	3240
agtcocagct	tccagagccg	attgtgtgtc	accgacttgc	gaagatattc	atcaccgggtg	3300
tacgggacag	ggagtagccg	gggatccatc	cctgaagaaa	gtagccatgg	ccaatactcc	3360
ggccaaggct	gcggctacgc	gcacgagatc	agatgcagca	gcggagtttc	gatcagagcc	3420
tccatcggct	gcggaagagg	ataagggtca	ggagggccag	cacgagagag	aggaagagaa	3480
gaggaaggtc	tcccagatca	tcgtaccctg	tatctgcacg	ggcatggccc	gtaacacttg	3540
cgaatggcag	ctacacgccg	gcggttgacc	atygaggggag	ggtcatgagt	acgtagtcca	3600
gcagcgaagt	aagcagcacc	gctatgccac	gatctgtctg	attcgacgca	tattgaccaa	3660
agtgaggatc	tccagcgcaa	gcggttgaa	ggcgtaagg	aatagtgcga	ttccactcct	3720
gcttgccgaa	gacttccata	tcctgatgcc	gcttttgcat	ctccaggaga	gctcgtcgag	3780
gctctcgggc	gacacaccgg	gacgcagacg	gacgtaggct	attagcggtc	gttgccgatc	3840
cagttgttca	ggctctcggc	cggcatccac	gaatggggcag	gagcatatcg	gcttggtatg	3900
tgctgtttg	gggcagatcc	cgaatacacc	tccgatcgtg	atggctcggg	ccgatttgct	3960
ttctgcgggc	gcaaccgttt	gcccaggaca	tcgcccccca	tcttccgggc	caaacttttg	4020
agatgaggca	ggtcataattg	tcgcgcaagg	cactatcccg	gacgcgcgca	tgagttctac	4080
cccgaacatg	tcgaggaaag	ccggttcggc	cagcagggtc	tggtctcgta	ggttttggtg	4140
tcttcgagta	tcattcttcga	ggtgcataca	gagtcgttcg	ggtagccagt	tccacacccg	4200
gtatttcttc	ctgatggcag	gggcaacgcc	tcgctgacc	tgagagaagt	cgagttcttc	4260
cggttatccc	cctcctgact	ttggcgcggt	ccatgcgtct	tgacgatgca	gagcgatcat	4320
gatgggggaa	atcccgttgc	tagcttcgct	gatagatgac	gtagagagca	gaagcacgct	4380
gacggaaagt	ccgagcgtaa	gcgtcaggag	ttgctgatac	tgtgttcgcc	ctgtcgggag	4440
agacggcgag	cagcaagttg	agaggtaaca	tgatgtgcta	tatgtcgttt	aaggttggtta	4500
ttcgttttga	ggtaatccac	gggattggcg	caggctgccc	gc		4542

(2) INFORMATION FOR SEQ ID NO:254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

actgcactga	aagactcgcc	atacagatct	cgtcccgatt	ctttgggcga	tacaatttcc	60
tgttcatgga	gcatcagctc	atcgtagtag	tcgatcaagc	ctcgcccgac	gcacctccac	120
ccgtatattg	ggacatctgc	aaagggtgtc	ggcagcatcc	gacaggaagt	agtagccatg	180
cgtactgtat	gtattcccg	atgctccatg	gtggtttttg	ccggattgta	gaacctatgtc	240
accggccac	ggcataagaa	atacagcgca	tttgccctga	cggagtaccg	gtacggaggc	300
aaatcgctctg	tcgtgatccg	gctcagatct	tcgggaagca	ccctccacca	taaccgaaca	360
cacctacctt	ggacggatcg	gagaagccat	tgacggagc	tgttcgtccg	taaggcgata	420
cactccactt	gcatcgacac	gatcttgacc	caatgtcccg	aagccattag	cgaacggtcg	480
gccgtcttcc	catagctcgt	tgcgctttcg	caggcaaagc	aagggcaagg	aagagagaag	540
gaatgcgact	attggaagta	ttcgtttcat	ctgagaaata	gcttatttat	ggatatgtcg	600
agcagttttt	gctcttcgag	ataggcttcg	aggtgctccc	gatagcaatg	gggcctaccc	660
ctgccggagt	ccctgtaaag	ataagacccc	catacgaagt	gtgaagaaac	gactggcata	720

agcgatcaaa cgatcacgga aaagagcata tcccggtgtat tgccctgctg caccgtgcgt
nccgctatat ccaatcgag gcccaattcc tgcacaccgt gcccg

780

826

(2) INFORMATION FOR SEQ ID NO:255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

ccaagatgag	atcaaaagca	actatgcgga	cacgaaaggc	ggattggaaa	gcagcgaatg	60
atatacgga	tcatcaagag	gatcatcgac	caaagtatcc	acgcgaagta	atcgacaaga	120
cggactttca	atgggatccc	ctgagcatat	gctctacgac	ccggccggca	ctgctatccg	180
aggatcatgc	gaacccatac	gcgatatgaa	tatttcctgg	ccaatttccg	tgcatgcaa	240
gcacagatgc	atacatgccc	catcagccga	accagatcct	gcgtgcattc	gaggagagat	300
ggagattccg	caagaagacg	tcaaacagct	attcgaaaca	ctgtctcctc	tccacaggta	360
aagaaggtgg	ctcaactgat	cagcaaacga	ttggacgccc	gttgagccg	ttcgacatct	420
ggtacaacgg	ctttcgctcg	cgtcgggtat	gccagagagc	gaattggaca	aaatcaccgc	480
agctaaatat	ctacaccgga	agcactcaaa	gccgatctgc	cgaacatcct	gcgcaagctg	540
gattcgaaag	caaagatgcc	gagcggatag	cttctttggt	gatggtggtc	cttcgcgagg	600
tgccggccat	gctgcaggct	cgatgatgcg	caatgacttg	ctcgcctgcg	cacacgtatc	660
gccgatacgg	ggatggacta	caaaggtaca	atatagcggt	acacgaattc	ggacacaata	720
cggagcaaac	catcagatga	acgatgtgga	ctactacatg	ctcaacggtg	tgccgaacac	780
atcctcaccg	aagccgtcgc	tttctctctc	cagaagcggg	atctcgaact	cctggtgtca	840
gcaagcccga	tgcacagaag	gagtacaacg	aggctctgac	cactttttgga	attgctacga	900
gatcatgggc	gtatccctcg	tagacatggc	ctttgggaat	ggatgtacac	gcattcctgaa	960
gccgatgcac	acgagctgaa	ctcgcggtca	tggacgcggc	caaaaccggt	tggaacaagt	1020
actacgccgc	attctcggag	aaaaggacga	gaccattctg	ggcatctatt	cgcatatgtc	1080
aattatccgc	tctacctgcc	caattatccg	atggggcata	tcacgattt	cagatcgaac	1140
agtacatcaa	gggcaaatcc	ttggccgtgg	agctgagcgc	atgctcgtac	agggacgact	1200
ggtgccgcag	tactggatga	aacaaccgtg	ggttctccca	tatcggtatt	gcctatactc	1260
gaagccgtgg	acgagccctt	acgaaagtga	aataatccgg	cgactctccc	tcctccttta	1320
gacagggagc	tttaagggaa	taattatcgt	actgtacgga	aaaaagagag	atgcacctcc	1380
aattctttta	tgattgtgag	atgcgatctc	ttttcttatt	ttttcgatac	tttcagaaaa	1440
atcggttcta	tcactctata	aagttg				1466

(2) INFORMATION FOR SEQ ID NO:256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

```

ggctcagtc cc ggacaggaga aggccaaaga gggaggggct ttcgatcagc cattgtcaaa    60
gggcgaaagg ccatccacct gcacagtatt cgtaccaacc ggagcgtaag caaggttggc    120
agagcgatcc caaagccgta gctttccgaa caaaagagaa tacaaccgct ttctgcacaa    180
tgccctggatg ctctgtggcaa atcgcagttc tataatgccg atttctctga ggcgcaggct    240
acatttctta tatcgacgc ttatacagcg acgaaccgat aatccgcgat gaagccgtct    300
ttggcaggta cgctgctaca gtgagatggg gtggctgcat gaagggagcg tttgctcgag    360
cgcatcccta aagatcttcc gcatgtcgat cgagagggtt gtattctttg gcagtggcag    420
agcgttcgat cctgtcgggt gcaagcgcg cgccatacct tatctccaac aggcagcaag    480
acaagagaaa acaagcgaca acgcgctcgt atgtattatc tgctcggaca gcttttacag    540
aaaacaatcg gccggaggag gctcgcgaag cctattccaa agtggttcgg cttctccgcc    600
tttcgctttg gactttgccg cacggatcag gaagatgagc tggagggtga acggaatccc    660
cgtacagtag cccgctcgat tggaacgatg gccaaacaaa ggcaagttcc aaaggatgta    720
ttgggatcag atctttatgc aagcaggca                                     749

```

(2) INFORMATION FOR SEQ ID NO:257

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic);

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

```

cgtgtctttc cattcagata aaatcaaaga ggcgaaagag gatttggtg cttcgagaaa    60
cgagtggaaac gggatgcaga gggacttcca atcaacaact cacaattaag ggtgtagaag    120
gaagtacgga catcaagggt attgctgtcg cttgcaggag atcgaggaga aagcacgcac    180
caagggtgaa tacaataaat cggtgagatt tatggctttt ccatcatggt caagacggaa    240
aactctcaaa gagttgttcg actgtctctc caaccgcttt tcgtgaaagg gcanagagca    300
tctactatac ctacaataac gggaagttgg cttctgatcc caacttgctt gtcagaactt    360
tatcaatgct ctcgagcgta ttccaaaggt gatgaatcac accgagaaag ataaggaaaa    420
ggtttctgca aacaaggagg ttatatgacc attgcgggtg ggtcgtggaa gaaagaggac    480
gagcttcgct tctcaaagga caggcagccc gaactgggat agaaaaattg cactcacgcc    540
gcacctcccg gaggaagaga aagaaa                                     566

```

(2) INFORMATION FOR SEQ ID NO:258

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

tcagaagaga	atatttatcta	tctctatttg	caaaagaaaa	agccaacatt	atagaagaag	60
aaaatttgat	atatttgact	aaaggatttg	ttgcaggcta	aataaagact	ttataagtgc	120
atctcatatc	ctaattgcat	atttagacat	gcgttgcgta	atattgctga	aatcaagaaa	180
ggaaacataa	ctacttagag	aaaaaacgac	aagaggctcc	ttcttttaggt	gtaattttcc	240
ctatgttcaa	ggtgtaattg	aagaagaaat	actgtatgaa	atagaatcct	ttctaatacat	300
gggatagatg	tcaatttttag	gaataattta	tctcatggac	ttcaacccct	tttgaaattg	360
aaaaatatgg	gatttatattg	tggtggatat	gctaaaaacta	tattttgaag	aaaagaatat	420
gataaaaaatc	gctccctaaa	ttataaaaaga	gataaagaat	tactagcctt	acggcctctg	480
cgaggctttt	aaaaccagat	gaaagtgaat	aactttgcat	tttggcatca	aaattcttgt	540
gaatccaccc	taagtgtgca	aaatatctct	gtaatcttat	ccttggtatc	atatgggtgtg	600
taattcgtta	tttttcaaga	ccaaaacaca	caaagtaccc	tgtaattccc	aacttctata	660
agacttttct	tatcctgaac	tcacgtattc	tttaatgcga	agcaaaaagt	gtccgaaaga	720
aattttgttt	ccgtaataaaa	agattcctgc	aaagctgcat	agtcgttctt	ccaatccttt	780
atacttctac	aggaggataa	aactctattt	ttccggataa	tctttatcac	agtagcatag	840
agaaccggac	ttacaagacc	gaaaagcgta	tatactccga	atcatcgaca	gaaatacaaa	900
aacaagtcgt	cattttccac	cgataagaac	gcattttaca	aagaacaggg	acgagcctgc	960
cattttgccg	gggacgacgt	tcgttccggg	taggacgacc	ctccgtctgt	tttaggtcga	1020
cctgactttt	gtcagggtcg	gcgtgtgtgg	tttattgtct	cgtaatgtgc	aggtaagaga	1080
gggttaagag	tcgatatttc	gggaacggat	aatctttccg	gatttcgcct	cggnatgcgt	1140
tccgatatat	aatctcccng	gggatggcat	gacnggcaac	agtcttctga	aaaccgcac	1200
atctctgcgc	tt					1212

(2) INFORMATION FOR SEQ ID NO:259

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ggccgaactc	gtagaaaacc	ccctctatct	gggttgctct	attgtaaagg	tggagatgcc	60
gatggactga	ttgccggcgc	acagaatact	accggcgagt	acttcgtccg	gctcttcaag	120
tcatcaagac	agctccgggc	atgactacgt	gagcgggtact	ttcttactct	tcaccaaagc	180
caaagaatat	ggcaaaacgg	acttttgctt	gttgacagact	gtgctgttat	acccaatccg	240
acagcgatga	gttggcacag	atcgctgtcg	ctacggctcg	tacggcgaaa	gccatgccga	300
tattgaaccg	cgtgtagcta	tggtgagctt	ctctacgaaa	ggcgtgcaaa	acatgaaatg	360
acagataagg	tcgtagaagc	tactcgtatg	gccaaagaaat	ggctcctgat	ttngtgatcg	420
atggcgaaat	gcaagcccga	tcagcttttg	tagaaagagt	ggcagcactc	aaagctc	477

(2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

```

gatcgcagga tcagattatc cccgtgaagt tgagtgattt aagacggata caaaagagtt    60
tategccaac cccacgaatc gtgccgatct tcccagagagg aaaagcgcga ggtagtaggg    120
cttggtacca tggaactggt tacttctctt atgctatttc gatcaaaaat cagatcgaga    180
ccagctatca gatgtaatca gtgtacaaaa tgaactcatt gctgcatata acgaagtttg    240
ggacgatttg ctcaaaagta tttccacaaa ccatacaagg agcttactcc ttccagcaga    300
aggctgtttt agaagcatat ccgntgcaca tttcagaaat gccttgctta atctcaagta    360
aagaataagg aacaaaatgg gaaagtttaa taatccggcg gccgtgaaat gcccgaactc    420
aatacctcgt ctttgccctga ctggtttttg cgttcctctt ctttatcatg atggtaacga    480
caattcgtga gtgacgcccc aggtgtcgta taataacctn cctaaagcga ctgaattgac    540
aagc                                         544

```

(2) INFORMATION FOR SEQ ID NO:261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...5293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

```

gcaaaaaact gcagagaaag ttaggcccta tctccatagc cactccggag ctctcttgaa    60
tgcgcatgaa atgctgagag acaagatgca ctacttcacg agcagacgca atgcagtgtg    120
ggatttttta ttcacgtggt attcaagatg cgggtaagggt cttgctcctg atggagaatg    180
aagggtgacga agaactctcg cttatgctcg ttcgttggct cgcaacaatg gcagtgtgct    240
cgatgactac ccgagaccga tggtttaccg ccgactctat ccatgggaga aaacgactga    300
aagccggatt gccatcgaca atcaatatca gcagctacca cttatgctcg tcagctaccg    360
ctattggttg cgctttgccg gtgagtgtcc gatgtgatcg agcacttgcc ctctaccatc    420
attatccatc atcgaaatga cgctcttcga cattgaaagc tgcaatgata tgagaataat    480

```

cgaacaagat	cttggctgcg	cccataatgaa	tcagtaataag	aaagcagact	gaagtatgcc	540
gcaaacgaga	gacggatttg	accggaggaa	gatccggagg	attgagcgct	tcgccaatgg	600
acatctctat	tacgggtcttc	atcaggagacg	ggatttcgggg	tgattcgtga	gttcgcgccc	660
gaagccacgg	ccgtatatct	gatcgggaac	tttcgcgctg	gcgtagattg	ccacagtttc	720
ggtttgcgcc	tgtggtgaag	cgggttcacg	ggaattgcga	ctttcatgcc	gactgcttcc	780
gcatgctctc	gctacaggct	cttcttcgaa	tggcccgggtg	gcgaaggaga	gagataccgg	840
cttgggtgcaa	ccgtgtagaa	caggatcctg	aaacttatct	ttctacgccc	aagtgtgggt	900
gccggatact	ccctatgaaa	tgaaacaccc	tatcctaacc	gtaaggacga	gcctttgcta	960
atztatgaat	gtcatatcgg	atgtcgtccg	aggaggagaa	ggtcagcaca	tacgaagagt	1020
ttcgacggat	atcctcccc	gtatctgcaa	ggacggctat	aatgccatac	agctcatgcg	1080
atacaggagc	atccttatta	cgcgtcgttc	ggctatcatg	tgtcaggttc	tttgctccga	1140
gcagtcgttt	tggaaacgccc	gaagatctca	agcgtcgatt	gatgaagccc	acgctctcgg	1200
cctctacgtg	atcatggatc	tgggtgattcg	catgcagtc	agaacgaggt	cgaaggcttg	1260
ggcttgtag	acggacgcac	acccttttct	tccatgacgg	caatcgcgga	ctccatccgg	1320
cttggtattcg	tattgcttcg	actatggtag	ggacaacgta	ctgcacttcc	tctttccaac	1380
tgcaaatact	ggctgacaga	gtttggttc	gacggcttcc	gttcgatggg	gtgacgtcca	1440
tgctatacta	tagtcatgga	ctcggcgata	gttcgacaat	tacgacagct	attacaacgg	1500
ccatcaggac	ggcgtatgctt	tgcctatctg	atcttgcca	acaaactcat	tcacgaactt	1560
tgccccgagc	aatcacgata	gccgaagagg	taagcggcat	gcccggatt	gctcttccct	1620
ggcagatggg	ggatatggct	ttgactaccg	tttagccatg	aatatcccg	tttctggatc	1680
aagctcatca	aagagcatcg	tgacgaagac	tggaaacccg	cgacatctgg	tatcaactga	1740
ccaatcgccg	tcaggaggaa	aagagatcag	ctatgccgag	agtcacgac	aggctttggg	1800
cggggacaag	acatcatatt	tcgcctgatc	gatgcgata	tgtattggta	tatgaacaag	1860
caagtgtgtg	acatagcgtg	gacagaggca	ttgcactgct	gaagatgatc	ctctcttcac	1920
tgccacgacg	atgaatggtg	gttatctcaa	tttcatgggc	atgaattcgg	acatcccag	1980
tggatagact	tccctcgcg	agggaaatgg	ggctgtacaa	gtatgcccgc	aggcagtgg	2040
gtctggccga	tagtcttct	tgcgctatgc	aggctctgac	ttgtttgatc	aggatattgat	2100
agccatgtac	gatcgggtgga	gagctttcac	aaactccctt	tgccgcaata	ctggctaaga	2160
gagaagagca	ggtgatctgt	tacggctcag	cgcatctctt	cttcgtttca	attttcaccc	2220
cgaacgttct	tattcggatt	atccccatcc	tcttcggccg	gtaagtattc	ggtagcgatg	2280
agtaccgatg	cacggaagta	cgaggtttcg	gtcgtgtgga	cgaatgggtg	gagcacttta	2340
ctcttccgga	tggagtaaag	atcgggtttac	ccatgaacag	tatttgaacc	tctatctgcc	2400
gctcgtctctg	ctctcgtcct	gaagcttgcc	gaatgacagc	tcccccttcc	ttttttcaaa	2460
tccccctct	aactaagatt	cgatatgacc	gagcgacttt	ccttcttgat	gcttatgctc	2520
tcatctttcg	tgcttattat	gctttcatcg	tagtcccgcg	atcgactcta	ccggctcgta	2580
caccggagct	gtattcgtct	ttgccctgac	cttattggat	atactggaga	aggagtccgc	2640
ggagcaatcg	ccgtggtatt	cgatcctccg	ggaggtagtt	ttcgtcatcg	cgagttgcag	2700
agtacaaggc	tcaacgagag	gaaacgcggg	aaggtattcg	catcccgttc	cgttgattaa	2760
agagatattg	gcagctttcc	gtattcctgc	tgtgaagtgc	cggactttga	agcagacgac	2820
acgataggta	ctttggccaa	acagccgaag	agcaagggct	tgccgtcaga	atgggtaacg	2880
ccgataagga	ttcggccaac	tgggtgcgga	gcgaatcaag	atctatcgac	ccaagtccgg	2940
ggtggctatg	aaacatgggg	gccggcagaa	gtctgcgaaa	agttcggact	tccatccccg	3000
ggcaaatgat	agattacctc	ggcctcgtgg	gagacagccg	gacaatatac	ccggatgtaa	3060
aggcattgga	gcgaaaacag	ctgagaacta	ctggccgagt	atggaagcat	agacggcata	3120
tacgcccacc	aagatgattg	aaaggagctg	tggccaagaa	aattcaggag	ggggaagagc	3180
aaacggcttc	tgcgctact	tggccactat	ccgcacggat	gctcctattg	tcttgattcc	3240
gaagcctatc	gacgtacttc	gcccgatatg	gcagccgttc	gtgatgcttt	gctgcactgg	3300
aatttcgcac	tttgctgaaa	cggttggaga	gtcacctacc	gatgcccctg	cgacagacct	3360
gtttgcccgg	atggtacag	ccaagagcct	ccgacagatt	tgttcggaga	aggcaccgat	3420
gctacaggac	tccgctaaag	aaactgacag	acgtaccaca	cgaatatacg	attctcaaac	3480
cgaggaagag	atagcggatt	gcatccgaat	gttctctgcc	acgccttggt	ctcattcgac	3540
acagagaccg	actcgaaaaga	tgcacttcgg	gccaatacgt	tgccatcacg	ctatgtccg	3600
agtcgggacg	ggctttcttc	ataccgtgcc	ggaagacgaa	gaaatcgga	aacgcgatt	3660
agatctcttg	cgtccctttt	tgccgatata	gctatcggca	aagtcgggtc	gaatatgaag	3720
tatgtatcca	agtactctcc	cgatatggta	tagaagtacg	cggacagcta	ttcatacgat	3780
gatagcacac	tacctctctc	ttcccgatct	ccgccacaat	atgatgagat	ggcggagacg	3840
ttgctgggct	attgcaccgt	ccactactcg	gtcttgctcg	aagcgacaaa	caggaggtgc	3900
acatccgtca	ggtaccattg	agaatctggc	agactatgcc	atggaagacg	ccgatattac	3960
ttggcagctt	atgaacgcct	caatgctatg	ctctccgagg	ccgggatgac	ctccttatcg	4020
aaagtataga	gatgccactc	gtgccgggtc	ttgccaatat	ggaacgcccg	gcgtaaagct	4080
ggacacggag	gtgctccgac	gcacagcttc	cggactggcg	aagagatgca	gcgaatcgaa	4140
gatgaaatct	accgtttggc	cggacctcat	tcaatatcaa	cagtccctct	caagtgggaa	4200
ccgtgctctt	cgagaactgc	aaattaccga	aaagcccaaa	aagacgaagt	ccggcagcta	4260
ctcacaacag	aagaaattct	ggtcaagcta	caggaaaaaac	atccccatcg	gctctcatac	4320
tggactatag	aggaatcaaa	aaactactca	gtacctatgt	aaagctctgc	cggagatgcg	4380
ctacccccgat	ggtaagctgc	atacctcgtt	aatcagaccg	tcgctaccac	gggacgtctc	4440
tccagcagca	atcctaactg	caaaacattc	cgatccggag	cgaagtccgg	agggggctga	4500
gggctgcttc	gtaccggaca	atgacgaatg	tattttcatg	agcgcagact	attctcaatc	4560

gagctgcggc	tgatggcgca	tctgagtga	gacgagagct	tgatacggct	tttctccatg	4620
gggaagacat	ccaccgagcc	acagcctcca	aaataacagg	ctgcctcttg	tagaagtcac	4680
ggatgacatg	cgcgcggag	ctaaacggcc	aacttcggga	tcactctacg	catctctgct	4740
ttcgggctta	gcgacggctc	aatatctccc	gtacagaagc	caaggccttg	atcgaagggt	4800
acttgccctc	tacccggggg	ttaaagcgta	tatggatcgg	agtattgccg	agccaagcga	4860
cagggctacg	tcaccacact	gttcgggtcg	aagcgattcc	ccgggatata	aacagtgcc	4920
atgccgtcgt	ccgcggctat	gcagagcgga	tgccatcaat	gccccatac	aaggctctgc	4980
tgccgacctg	atcaagctgc	gatgatcaga	atacacgagg	aaatcactga	gcgtaagctg	5040
cggagccaat	gacctgcaa	gtgcacgacg	aactcaactt	caacgttctt	cgtcctaagc	5100
tgcaagaagt	cgcgagcttg	tacgctcgtg	tatggagggg	gtgatccctc	tttgctgtgt	5160
cctctgatag	ccgagatcgg	cgaaggagcc	aattgctgga	ggcgactga	cgccattttc	5220
cacctgacat	aatcccgaat	agtccatgga	cagttgtata	aaaacgaaa	tcacagcgaa	5280
ttgaggttcg	gga					5293

(2) INFORMATION FOR SEQ ID NO:262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

gccagttcgt	tttccaactg	attgcgact	tcatttgctt	tccgctgact	tcgtaaacgt	60
ttttgcgtaa	ctcttcctcg	ctttcacggt	gacaggtcga	caggtgcggg	cpatgtgtgc	120
caaaggactc	gtgatgtgat	gatcactaac	ttcactcctc	cttcgcttat	gtatggcata	180
tggaatcgg	cgcacgcaca	cctcgctggg	catggattcc	gtgttgagag	atctcgaagt	240
ccggagctgt	gctttcacia	tgggggcgcg	gctcaggggtg	tgaatataat	cgtatactca	300
gcttcacgt	aatatcggtc	tgcatcctcc	attgtcattc	cttatcccat	gggaaagtag	360
ggtatttgcc	ttctccctta	aagtagtatt	cccatgacat	tgggcgcata	cgagtgaagc	420
catctcctga	tgtgaagcct	tggtatatcc	agcccacgtc	tttgaaaagc	ttcgataagc	480
gcggggcggg	gatgtgcaga	tccatcggtt	ccggatcatg	gcagtctgca	caccctatcg	540
attcactatg	tcactgcccc	gactgctcca	tttggtttta	tagaattctc	tactccaatg	600
gcttgcatca	tgctgtggac	atcgggactc	ttacatacca	gcacgtggca	ggctgcatgt	660
ctcctgcccc	atcgattccc	ggattccggt	tcgcagggta	cgctgcatat	cctgtatagc	720
atgcatatga	ccgcgggaga	tgtataatct	ctggagaagg	catagccggc	ccagaatata	780
accagttggg	acgttggttc	aatacgtcta	ttgc			814

(2) INFORMATION FOR SEQ ID NO:263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

gggcaaaaaa	cggatctttc	tcctacaaca	tcttcgtata	acaagtatac	tgaaagctga	60
tgttatctac	tgaacacttc	ctcctctttg	cttctatttc	ctatttgacg	gtattatggc	120
cggaaaggtg	ggctatcggt	tcggatacct	acccttttga	tctttctctt	caccgggatg	180
ctcttcggag	tggatgattc	ggttttcagt	tttctaaatg	cccgatgtgg	gcacaagtcg	240
gtaggatcat	cgctctctcc	attattctct	tcaccggtgg	tatggatacg	cggacagaaa	300
ggtgcgtccg	gtcattgccc	agggacttac	gctgtctact	ttggtgtctt	gctgacagct	360
cttctatccg	ggttctttat	cttttggtcg	agggttcgga	ctttggccct	taccggttcg	420
ctctttctac	ctcttttgctg	cggtcgccac	gatggccagt	acncgactcg	gcttcgggat	480
tcgccatcct	cgttcgcaaa	agatgcagct	caaagagaat	ctggctcccg	acactggagt	540
ggagagcggg	agtaacgacc	cccatggcgt	atatgctgac	catcgcacca	tcgatttcat	600
caccaccg						608

(2) INFORMATION FOR SEQ ID NO:264

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

gagctggtct	tcgatacggg	catccagcgc	aacatcaaac	taagcgaggc	cccagccacg	60
gtattccggc	actgctctac	gatgccgata	gccgcggacg	gtcaatcata	tgcagctggc	120
ggccgagctg	atcaaaaaagc	acaaacaaaa	ggagcctgac	tctcatatga	agcatacgaa	180
gaaaacgctc	ggtcgtgcct	ggactccctc	ctcgatgcgg	aggctcatagg	gtctttcttc	240
atcaggaagt	ggccatcagc	gatatatacc	ccaatcccg	tcaaccgcgc	cggatttcga	300
ggaggagtcc	ctgaaagaac	tggccgcttc	gctccggttcg	atagattggt	acagcccatc	360
acactactga	agaagtccgn	cggcgactat	atatcatctn	cggagaacgc	cgcttggcgt	420
gcggccccga	tggccgggtat	gccaccctgn	cggcatacat	caagacggaa	gagga	475

(2) INFORMATION FOR SEQ ID NO:265

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

```

cgaagaagat ctgcaagccg gcgaggacta ccaatatgcc gtggagggcg caggctcgtc      60
atggaacggc agcggcagga ttcgctctac agggggatca ggtgcggcag atggaggaga      120
gcctccataa tatgcgtcgc aatctgggat ggtgcgcgcc cgtgtggaag acctgaacgt      180
gaaggcaccg gccgacgtca gttggggctt ttggacgtgg agatagggca gacggtagga      240
gccggagtcg catcggacag atcaacgtcc tgtccgacta caagggtggag gctagataga      300
cgagcactat atcgatcggg tcaaagccgg tctggccgct tcgtcgaacg gcagggcagg      360
gactttctcc ttcgcgttcg gaaggtatac ccgaagttcg ggacaagcag ttccgcaccg      420
acttcatatt cgacggagag caccgcacaa tatccgcaca ggccaaactt actacatcaa      480
tctgcgcctc gacagccgtc cgaagccatc atgatcccg cgcggagcctt ctatcagaaa      540
ccggcggacg atggatatcc gtcgttacgc ccgacggcaa gcgagccgtc gccgggacat      600
cacgattgcc cgtcagaatc ccgagtatta cgaagtccct ccggcctgca ttgccgncga      660
gatggtcacc acctttcgta tgatattccg cgatgcataa gaaattatcc tgaatgaccc      720
acctatagc                                     729

```

(2) INFORMATION FOR SEQ ID NO:266

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

```

gcgtcgggca tttatcaaac ggcttctaaa aacacagact gatatggcgc ggagtagacc      60
gatagcagta ttttttgaga aagcgaccgg aaagggaaga actttttggc cgcttttccg      120
tttttataag caagtagaac aagaataact caaacgaaac aagatgaaaa agaacatttg      180
ctcgaaagcc attctctggc ttctctgctc ctectctcag tcgggacaat gactgcatcc      240
tgtactccaa gaatgacact cgtcaagaag aaaccgtctc tgccgatagc aaggagagaa      300
agatggcaaa atcatccata tcacggctga atacatgcgc gaaacatata tgattacaca      360
gccaatcccc aagaatgggt ctataaagggt gaaagcctgc tattatcgac ttctatgccg      420
actggtgtgg cccgtgcgcg acctttcgcc caaattggaa gaggtggcca agaaatatgc      480
cggtaaactc ccgtctacaa agtcgatgtg gacaaagaaa aagagttggc agggattttg      540
gtgtcagaag tattccgatg gttcttttctg taccggtaaa aggaatacga cgcaaacgat      600
gggcaatctg ccgatggaga acatcgaaga ggcctatcca aatcatgcaa tctgatctat      660
aggtcaaatt gcagactgta atatactaca ggccaataac actacttgag      710

```

(2) INFORMATION FOR SEQ ID NO:267

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 878 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

gccgtgtaag	cgcaataggg	tcaagcgttt	ggtcagggag	gcttatcggt	caacaaacac	60
ctcctgaacg	atgtcctcca	agagagacag	atctatgcac	tattgcattt	atggtagtat	120
cggatgaact	tcctgacttt	cgtacagggg	gagagcgaatg	caaaagagtc	tgatcagaat	180
tgccggaaat	gtacctcatc	ggctttgaaa	aacgagtaaa	tacgatgcga	ctgatcaagg	240
ctttttcgtg	caactcttac	tgctcccat	tttcttctac	aagcggttta	tatcccgtt	300
acaccgcctt	catgccggtt	tacccctca	tgttcgtcct	atgcacgaa	gccttacgta	360
aatatggccc	gggcaaagga	ctattgctga	gctcaagcgt	attctccgct	gtcaccgctg	420
gggtggaagt	ggctatgacc	cgttccgtaa	gaagttttct	tcaacttaatt	cctcttatat	480
ggtattttctc	acattcatac	tcattctgca	gctcgcaacg	atagcgagat	cattcgagtc	540
ggaatctacg	accgaatgaa	accatatctc	cgaatacttt	ttgctccacg	gcattcatcc	600
gtggagtgtg	ccagagaatt	atagcggaga	gttgcttctg	tccgtgaagg	attgaatcac	660
gacgaggttg	ttgctctggg	agaatggggc	tggtataagg	gtgcagtaca	ccgatgaaa	720
agcaacgaaa	agcttcctcg	atcaaattga	tctgagcgaa	gagtttgga	tgccggtgct	780
actgacatag	tacgagcatg	ggatgatctt	ttggcgatca	aaaacaggta	aagcttcaca	840
gcccgtagat	cgttcatggt	ttcggagtag	tgaaaaac			878

(2) INFORMATION FOR SEQ ID NO:268

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

agaagataaa	gacttcggcc	catgccaaag	aattggcaga	gaagtttgca	agaaagaagg	60
ccgtcagccg	cgtatcatga	tcgccaaaat	ggggcaggcg	ggcatgaccg	tggtgccaaa	120
gtggtcgcta	ccggctatgc	cgactgcgat	tcgacgtcga	tatggggcct	ctgttccaaa	180
caccggaaga	agccgcccgc	aagctgtgga	aaacgacgtc	cacgtgatgg	gcgtttcctc	240
tctggagccg	gtcacaagac	gctgatccct	caggtaatag	cagagctgga	gaagtcggcc	300
gtccggatat	tctggtgaca	gccggagggtg	ttataccggc	gcagattacg	acttcctcta	360
tcaggccggg	gtcgttgcca	tcttcggccc	cgtacccccg	tggcctactc	ggcagccaaa	420
gtgcttgaga	ttcttttgga	aaataatctc	tactctcgat	aaggagtatt	tcagcattct	480
ctgtatggcc	ctcatatgat	tcctcgaaaag	ggagtcgtat	gagtggtttt	tttatgttca	540
agtcattagt	gtcctaaaag	tttcttcttg				570

(2) INFORMATION FOR SEQ ID NO:269

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

ccgatgccgc	tacctccggt	tttggtcgta	tagaaaggaa	caaacatatg	tcgaacacct	60
cttgaggaaat	aggagtgccca	ttgtttctcca	catgaagggt	agtctgtgtt	catccaacga	120
atcgagacgt	tctctgacac	gaatacgaaa	agtcgtttct	ccgtatcggc	aggatattcc	180
gcctcggcag	cattttgacg	aggtttatca	gtaccgaagt	caattgccgg	cggtcgggccg	240
ggacatcagc	tccacgggta	tttcttcaat	atccaccttt	atatcgttgg	aggaagaagc	300
tcttcttgca	ggcgcaatat	ccccgaaaga	aaagcatgta	aagaatgtcc	tccttctcgg	360
gaggaggaaac	tgccgtaaac	ttacggtagt	ccgtacaaag	gataacagcc	ccactccggt	420
actacgaatg	gtatccaatc	cgtagacagc	atc			453

(2) INFORMATION FOR SEQ ID NO:270

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...988
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

ggcggccttc	taccaaatag	cacaggcttt	cagagggagc	cgaagcctct	agccattcct	60
tcttttgccg	aatatgagga	tgcttgctcg	atgtacgāca	cgaagtctgc	ttctatcctt	120
ctaatagagga	cataggcgag	gctgattttc	caatatggat	ttctgctggc	tttgtaaccc	180
gaacaatccc	gatggcgact	gctgcagcgg	acagagatcc	tgcgctctgct	caacgatcat	240
cctgaacgac	attcgtcctc	gaccagtcct	atgtatcggt	tacgaccgag	gaaggattcg	300
tccggccgac	atcaaaggac	ggaaaaacct	tgctatggtc	tatctttcag	tcatgcctat	360
gggataccgg	ggcttcgcat	cggctatata	gtgccaatata	agattttatg	aagcgtgtgg	420
cggcttttcag	tacgccgtgg	gggtaaacgc	actggctata	gaggctgccca	aattcatcct	480
tatccatcct	cacaattcac	tctgccgatc	cgcaagtggc	aacgcaatac	ggtagattta	540
tcacagccct	gaatcgccct	gatgggtgtag	aagtacatcc	ctcagggcaca	cgttcttctc	600
ccttcgcctc	aagaaaggaa	cagcggccga	actgaaaaat	atatgctgga	ggaatataat	660

atgctgattc	gggatgcttc	caatttcgtg	gtctcgatga	atcctacgtc	cgaatcacca	720
cgcagcgacc	tgctcgaacc	agcttttcat	caaagctctg	gagacattcc	tcgagaaata	780
ctaaaatagc	agatgctgca	gatcagttct	tgctccttct	ctgtactcta	tcctattaca	840
agacggagca	agaagagtac	acggtgttat	cgtggatata	ttcgtgcccg	taccaccatc	900
acaacggcac	tgatgaacgg	tgccgtagca	tatccgatgc	accgttgaga	gcggaaatct	960
atgccgggaa	cggttcttcg	agagcgag				988

(2) INFORMATION FOR SEQ ID NO:271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

ggccaaatta	ccttccagtt	catccggacg	gggactgatt	tggttaagtc	ctcccctacc	60
gacgatgaaa	tcgacctgct	gaccaaggcc	ctccgacggc	cggttctttc	agcgtggagc	120
ctgtattgga	tgctccgtcag	gactgggggc	cgaattttat	tcgaatggaa	aaggcgagct	180
ttacttcggt	ggatggctcg	tttcgatact	aacagggtggg	gagcctatct	gggcaatcga	240
cttgcaccca	aaccgatttg	gttgccgaac	tgacccaaac	ggtcggggca	caagacatga	300
agaggctatt	gcattctgtga	aagattatct	acgagaacgc	ttccctcact	gtacaccggc	360
tatatcggag	tagacatggc	agtatatgcc	gaagagacag	tctgtttctg	catccttgta	420
tcgagatcaa	tgtacgatac	aaatgggggt	ggcagctatc	ctgctttacg	acctttggat	480
agagaaaggt	gaagagggtg	gttcgaagtt	aagggttttc	gaaccgaagg	cgaanacacg	540
aatgggattc	aatgatgcag	tcgagcca				568

(2) INFORMATION FOR SEQ ID NO:272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

agattaataa	ttgctggtga	ttacttcagg	attatcttgt	tcgttgacga	tcgggaaata	60
ctacagcagg	cttgaacacn	tgggcttcct	ccatcgggat	ccaggcatat	gccatgatga	120

tgatgatgtc	gcccggatga	acgatgcggc	agctgctcca	ttgagacaga	ttacccccga	180
acctcttttg	cccgggttgg	ataggtctcc	aagcgtgctc	cgttgttggt	gtccacgatt	240
tggacttctc	tccggcgatg	atgttggcag	catccatcag	atcttcacg	atgggatgct	300
acccacatag	ttgaggttgg	cctccgtaat	ggttacgcgg	tgtttttggg	ttttaatact	360
tcgacgtaca	tggtgttttc	caattctcta	tattttttacg	attgcaaagt	aacttaaaat	420
cgctgtaata	ttcgcataaa	acggcagttt	aacgcaattg	ggcttgatta	ttaaggacat	480
acggcgcaaa	tgcagaaaaat	ccgccacctg	ccacgaggca	gtaatatgcg	gattattgca	540
cagaaaaggt	ttcaaatcgt	tacccgaaag	caaggtaatc	acctccgtaa	agaggagaaa	600
aacagcgggt	ttccgtgcat	ccgttgctgt	tgctctatgc	tctatatatt	gcatagcagg	660
gttaggctct	ttcatgttta	attttgaacc	aaaaagaaaa	gacaatggca	agaagcacat	720
tcaagggtgt	gttcttgtga	atggcagcaa	ggagaaagaa	ggtatcgctc	ccatcatggg	780
acgggttaca	tcaacggcac	ggtggctcag	ttcagttgca	agcgcaccat	cccaaggagt	840
tgtgggatgt	gaaaggcaac	agggcgaaag	gcaagagcag	ggagccatcg	ccaccaacct	900
ctcgctcgac	aacatcaagg	cgcaaatcat	cagcactatc	agcgtctttc	cgaccgcgag	960
gcgttcgtca	cggcgagat	gtgcgcaatg	cctatcaggg	gctgggcagt	gagtacgata	1020
ccctgctgag	cgttcgacag	ggaatgcgcc	tctctgc			1057

(2) INFORMATION FOR SEQ ID NO:273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

ggcttggaga	gccgtttcga	agagatttcc	acgcttatca	cggatccggc	gtaatcgccg	60
acatgaagcg	tttcacgaag	ttgagcaagg	agtatcgcat	ctggaaaaga	tccatacggc	120
cgggcgcgac	tatcgcaatc	tgctcgcaac	atcgaggaag	caaagcatac	catggccaaa	180
gagagcgacg	aggagtgcgc	gagatggctc	gcgagatgct	ggccgagggt	aacgaacgct	240
tgcccttttg	gaggaggaga	tcaagatgct	actcattccg	gccaatccgg	aggagacaag	300
aatgccatcg	tggaaattcg	cggaggaacg	gggggcgatg	aggtgcactt	tttgccggcg	360
acctctaccg	catgtacgtc	aagtattgcg	aggcaaaggc	tggcaggtgg	aggtcaccga	420
cctgagcgaa	ggagctacgg	gggttacaaa	gagatcgtct	tctcggtaaa	gggggaagga	480
gtgtatggta	cctgaaatat	gagagcgggt	tgcaccgtgt	ccagcgcgta	cctgcgacca	540
gacacagggg	cgcatacata	cctcggcagc	taccgtggct	gtcttgccga	agccgaagaa	600
gtggacgtgg	agatcaatcc	ggcagacatc	gagatgcgac	gtcccgttca	ggcgggtgcg	660
gaggtcagaa	tgtaaacaag	gtggagctaa	ggtgcagctt	acgcacaagc	ctacgggtat	720
ggtggtgggt	tgccacaggc	tcgttcgcag	attgccaaac	gcgaactggc	tatgcaaatg	780
ctgcctccaa	gctctacgac	atagagctgt	ccaagcataa	cgaagctatt	gcacccgacg	840
caagacgatg	gtatcgaccg	gcgaccgttc	ggccaagatt	cgacctacaa	ctatccgcaa	900
ggacgggtga	cggatcaccg	catc				924

(2) INFORMATION FOR SEQ ID NO:274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

attccggnng	actatcacga	gaaagaaggt	aagagtgtct	tcgaagtgg	tngaccgtat	60
tgcattgccg	aggtaagttt	gacaagggtt	catacaaatc	tcgggcggtt	tgcatggagt	120
gggctgttct	tgtgtgaatg	cactttcaca	tatttgcgtg	cagaggtgta	tcgtaatggg	180
aagatccata	tgcaagggtt	agctgtggca	aacccttgca	tgatgtggag	gtgataggct	240
ccacgagcgt	acggggacga	ctattcagtt	caaaccgat	agctctatct	tctcggttacg	300
gaataccaat	actccatact	ggccaagcgt	ctccgcgaac	tttttatctg	aatgcgggga	360
ttacacttac	gctgacggat	aaacgaacgc	tcaggaagac	ggcagtggct	acaagcaaga	420
tgtattccgt	tcggaagaag	gttgaaggag	tttgtccgtc	atcttgaccg	tatgaaagaa	480
ccggctgggtg	acaaacgtta	tccataatcg	tcaccgagaa	gcagggcatt	cccgtgggag	540
tagcatngac	gtataatact	tcctatctgg	agaatgtata	tagctacgca	atgacatcaa	600
tacgatcgag	ggcggtagcg	atttggccgg	attccgtgtg	gacttactcg	aactttgaag	660
aaatatgcc	cagactccaa	actcctgata	agggtgaaggt	ggagatcacc	ggcgacgact	720
tccgcgaggg	attgatgccg	tgatcagcat	caaagtggcc	gaacctcagt	tcgaaggaca	780
gaccagacca	agctcggtaa	caatgaagtg	accggtgctg	tcgatatggc	tgtagcgaag	840
cactcgaata	ctatctggag	gagcatccga	aagaagccaa	acgatcgtgg	acaaagtcgt	900
tttggcgcca	actgctcgtc	aggcagcccg	taggcccgcg	aaatggtgca	gcgcaaatcg	960
cccttgtccg	gtggaggatt	ccgggtaagc	ttgccgactg	ctcgtccaaa	gacccggagc	1020
agtgcgaacc	ttccttgtcg	agggtgattc	ggccggcgga	acggccaagc	aggggcgcac	1080
cgcgagtttc	aggctatcct	gccactgagg	ggaaagatcc	tcaatgtgag	aaagccatgc	1140
aacacaaggt	attcgaaaagc	gaagaaatcc	gcaacaatat	accgctttgg	gtgtgacgat	1200
cggaaacggaa	gaggacagca	aagccttaac	ctttccaaac	ttcgctatca	taaagtgggtg	1260
atcatgaccg	atgcgatgtg	gacggtagcc	atatcgctac	gcttatcctt	acgttcttct	1320
tcagaatatg	cgtacgcttc	atacaaaa				1347

(2) INFORMATION FOR SEQ ID NO:275

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

gagttgatct	cctttggacg	agacgtctcg	gatttccctgc	cggagggggt	gtcctcgatt	60
aagaaaatca	aaacaaaaag	ccttgcagtt	cagacttcgc	aaggcttttt	tgtgtccaaa	120
attcagccgg	tggtacatta	tcgggtctct	atgagaggaa	aaaagagtga	ttccgaaagt	180
agtgaactct	tcaatatcat	acgccccaaa	agttttcaac	aacgaagatg	agttttggaat	240
gattcaata	agcatctgta	gagaggagaa	aagccgaggt	aaaagtgcag	ggaaaggaac	300
tggcatagat	cgaaattcca	cttaaaacca	agccgtacaa	cgactggata	taaa	354

(2) INFORMATION FOR SEQ ID NO:276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

```

tccccggggtt ggattgattt ggtttcgagt atcccgatga taaatttttg cggtttggtc      60
gagtttttag attgattcgt ctattccgaa ttttgagact ttcgcacca caaaggaatt      120
tgttacctat gtttttagaa tcaaagccag ggcgcattta cttcagccac gatttttagcc      180
atcttattga tcatttctct tccatagcga ttcttcaagt cgaaaatgcg tcgaccagca      240
atatccaaca gcggaagatg ctatttggtg gtcttacggt acgatcacia ctgtggctat      300
ggagacaaat accccgtaac aaccgaagga agaatcattg caagtttttg atgactgcag      360
gagtagggct tttcggaact ttacagcct atttgcttcc ttatttgtct cagataacaa      420
aaaagaagaa acagaaacaa agaatgattg tcaatcttat tgctgctggt gcttgatatt      480
gagcagaata cagctgatac cgcttcact taattccact catgaactct attatcaaaa      540
gatggttgta cagcgaaggg ggcaaattgt attcttttcc gattggagag atagattgac      600
accaatgcat tgttttagatt ctaatctggt ttgaaggata agattcccga ttaaatacat      660
tggcagtgct aaaaaaacaa atccct                                     686

```

(2) INFORMATION FOR SEQ ID NO:277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

```

caagttgttg cacgatgcct atgcaaaagc tttagagctt cgnaagttgg ttccggacag      60
gaggtcgaaa atgtcggttaa gactatctat aagcctttac ggccgagaga tttcagccaa      120
gatggttagag ctattgaagc cggaaggggtg cgtgccaaagg tggagatcgt atatcaaagt      180
ttggaaggct tgcacgcgcg ataccgaatc atccgggaga ctggattttc tccggcgatt      240
atccgcaccc ggaggcgctc atttggtaaa tgaagctttt atcagctaca tggagaggac      300
tatggcaaat aattatttcc agaatcgaaa gagtattaag aactatgaga gagcaaagaa      360

```

aagcgacatt	gatattggac	gatggtagcc	gttcgaaggc	tattcttttcg	gttgcgaaacg	420
tgctgtggcc	ggagaggctcg	tttcaatacg	gctatgaccg	gctatgtgga	gagctgacg	480
gatccgagtt	tcgcggaaca	atcatgggta	tgacctatcc	tttgggtggg	aattatggct	540
tccgatgaaa	gcagctgagc	caaacggcgt	atcttgcttt	atggaaagga	cagaatacac	600
atggaaggaa	tcgttgtgtc	cgactattcc	cattcttttag	tcattggaat	gctgtcgaaa	660
gccttggcga	ttggctcaaa	cgtgagaggt	attcgggtctg	acggggatcg	acacgagggc	720
attggccaag	cacctcgca	acacgggttcg	atgaaaggaa	agataattct	cgaaggaggc	780
gaagcattgg	cttcgccgat	ccttacacag	tcaatcaggt	agcggaggct	tctgtcgtga	840
agtaatcgtc	tacggcactg	gaagcaaaaa	ggtgggtactc	gtgattgtgg	agtgaaggac	900
aacattattc	gctcgcttct	cgtgaagat	aaacgctcta	ccgtgtacca	tgggattacg	960
actttcatcg	aatagcatac	acgggtctctt	catcagcaac	ggcccgggcg	accccaatat	1020
gtgcagcgta	cagtggaaaca	tattcgctcg	gctgtggccg	gcgacaaacc	tatctgcgta	1080
tttgcattgg	caatcagctt	ttggcgaaaag	ctgccgggg			1119

(2) INFORMATION FOR SEQ ID NO:278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

tttcccggtt	tgacacttcc	taaaaacccat	ggcgtgggaa	cttttttggg	tggcgcggaa	60
agcaaaaaat	tctcacgcca	caacgaaaaa	aatctcgtcc	attttttcag	aaaattcgaa	120
ctaaaaatcg	tgcatTTTTg	gttcggacga	tgagtcagac	gtgtactgtg	gtcagaaaaa	180
tatcatccat	aaaagatcgg	gaattagcag	agagacaggc	tatggctaata	aggatcatcg	240
aagtgatcat	cgtctcaaca	actacaaaagc	gcaggctaag	gatcggctca	actcgagtaa	300
ggctctgtgc	accgcaagcg	acgatgtatt	gaaccggagg	cgactttggg	caacttaagg	360
cgaacatggg	gtatcgacgt	ttcagacata	tggaccggag	tgggtgaaga	tggactttgc	420
ctttccggct	atggcttttta	accgaaaaaa	ccgggcgtca	aattggccca	aaaggcaaaa	480
aacacctcgg	gaggcatatc	aatcctcaat	cttaacctga	tttgcttcta	cgtcacgaa	540
agctaaaaag	taacgccagt	tcgatctaag	cgaacatacc	ataaaaaatac	aagtagctgt	600
aaatcatact	cttttgtgat	tctccggctg	cataatgtcg	ggaagaaggg	gcggcttcta	660
agtcattggg	cttcagatgt	agataaaaagc	catctgaaag	caatataaag	gcctgaaaaa	720
cactgtgtgg	aaaataaaaca	cactaataaac	caatgtgttg	tgccattcct	ttatatcgag	780
ctcagtaaaa	agtaggggtt	caagatgaag	ccgggttgct	aaccgactgc	aagagcaaaa	840
aaagagggct	gtgacaaaac	tgaattttgt	cacagccctc	tgcatTTTgga	aaattcttca	900
gtaattattc	tgcgctctca	gcagcaggag	ctcttcggca	gcagcttcca	cgggagtttc	960
ttccgTTTTc	gcagcttctt	ggcagcggca	gcagcctctg	cttcagcctt	agctttggcc	1020
tctgcggctt	tttctctgcc	acagcttctg	cacgagcctt	gtttacggcc	ttctctgtct	1080
gagcttaacc	ttatcgctcg	ctacagcggc	ttctttcacc	tttgccctcat	gttggttaaga	1140
gcattctttt	tgcccttcaa	ccaagcctcg	aacttgtttc	tgtgtcagct	tgatcgaaag	1200
cacccttctt	aacaccacca	aggagtgtct	catcatgagc	acaccctcac	gggacaaaaa	1260
attacgtgcc	gtgtggtagg	ctgtgcgcct	acaccgatcc	aatacaaaagc	gcgctcgaaa	1320
ttcaatctat	tgtagcagga	ttcgtgttcg	gattgtatga	accgatcctt	tcataaaactt	1380
gccatctcgt	ggcgccctgc	tgtctgcgac	aacgatctta	taaaggcata	acctttgcga	1440
ccatgtcgtt	gcaattctgat	ttttgttgcc	ttcttttgaa	tttattattt	gcgttcgcta	1500
ttgtatttag	ggctgcaaaa	tagattatta	aaatggaaca	aacaaagtgg	ctttctcttg	1560
gcacatacac	aaaaaacgat	cgggtacaga	taagcgctca	gcctgtctgt	acccgatgga	1620
tggtggagct	ggagggaatt	gaaccctcgt	ccaaacatgg	aatcaaatgc	tttctacatg	1680
tttagtttca	gttggaattt	tcgtgagcga	gcggagctga	aacgacccaa	tgacagatcc	1740
ttatcttccg	ttcgatctga	ccacggcagg	aagcatcctg	tagcggttcc	cgatttgtca	1800

gcaccgcacc	atcagctact	tcgggaaaaa	gctgctcggg	cgatgtctcg	tcgctgccac	1860
ttggcgcgga	tgaagcgtct	aatctactat	tcttcgatta	cgcagcgaga	ggtagttatt	1920
ttcgccaatt	aaacttttga	tgtctgagat	tatagtgcga	ccaccacgc	actacatgct	1980
tacataccgc	ttcatcacgc	tgtcaaagcg	gtcagcccca	ttgtgggtat	cgatagtggg	2040
agcaaatgta	gcattattac	cgaagcgatg	catctttttt	ttcgaaaagt	tttcattgat	2100
catttacgac	gtgtacttgc	cgtttgatgc	ccttcggagg	aaggaagcaa	tccagagggg	2160
aaagagatgg	ttttcgccct	tactccttac	ctttgtccgg	atcagatggt	tctgatcaga	2220
tataatgagg	aacaggacaa	tgcacaactt	tgcctcatcg	gtgtggccgg	ctatattgct	2280
ccgcgccacc	ttcgcgccat	caagatacag	gcaaccgctt	ggtatcggct	atggataagt	2340
tcgacagtgt	ggtatcatgg	acagttactt	cccgaagct	gccttcctta	cggagcaaga	2400
atgttcgacc	gtcacaactc	caagctacga	ggaaccgatc	aggctatcga	cacgtgtccg	2460
tttgtacacc	gaactatctg	cacgatgtct	attgtcgctt	ggcctgcga		2509

(2) INFORMATION FOR SEQ ID NO:279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

ccaaatgaat	tcatatatga	atttctccaa	ctattttctat	ttctcttcag	gttcagtaaa	60
tatcttctat	gcaaaaggcg	tatttttagtt	cgcaaagtac	tcattttataa	taagaaaggc	120
aaataaaaag	gcaagaaaaa	gcctcttcga	gcataaaaaat	gtcgcaagag	gtgtatgtgg	180
taatcagggt	acataaacag	ggcaaaactcc	acctttcgtc	gtttgaagag	acctctgagg	240
actttccctt	gtatcggcag	aaagagacaa	attcacgata	gaaattcctg	tcgccgactc	300
tatcttccgc	aacagtcggc	tcttgggatg	cttgccgtat	ccggcaacct	gcctgtcccg	360
acattgtagg	aaaggacggc	aagcagaaga	acgttccatt	taaaacatct	gaagataggg	420
atttacaata	gcttcctaaa	ttcatctccg	ccaatctgtt	gatttcatcc	ttgtagattt	480
caaggtgatg	aggatgatgt	tctccacata	gataccgatg	gtcatatccc	tgtttctcac	540
gacatgacta	tctccgccaa	cgtgtcttgc	aactcttttg	caatatagtg	gtcttgcgat	600
ttttcaagggt	gttgcgacag	atgaaaagcg	actcatatca	cctttatcag	cctttcgctt	660
ttctcttctt	gggactcttg	aaaaatcttt	gacattgggt	cttcatttgg	acgttccgat	720
tcaacacact	gctctcta	tgagagcggt	ttatttcgct	ctcatttctt	ttcatgggaa	780
tacctgtgaa	acaagttccc	ggatggcaac	aggatctacc	ttgccgtttt	ggtctctgtc	840
atactttctt	aatttttatt	attacacaat	tcattgttca	ttcgttgcc	gtatatttac	900
cgatgaagat	gaatacatcc	gctatcgaag	aatgcccaat	aatcggttg	taccagtagg	960
gctacatcct	ttcattcata	cctttctgtn	ggagatgttc	attagtgtcc	atcaatacaa	1020
tcgttcgatg	tatctgcctt	cgcacattcc	cacgttcgag	tgnaaagaat	caanggactg	1080
ttctttgaca	tacaccctcg	cctatatcgc	tcacgaaac	gtgatgtatc	gaagacacat	1140
accatcaccg	acatattcga	cagtgcacaa	atatggtcgg	tgatgctgta	atcagcgtga	1200
tttcttttag	tgcgtacttg	tggcacgatt	tggataattg	tggcttcgtt	ctacctaata	1260
gctttgggta	caaggatcgt	aactttgcag	taagcgataa	gtcgggtattt	catggcttgg	1320
gaacatacat	ttcgagagaa	t				1341

(2) INFORMATION FOR SEQ ID NO:280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...869
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

ggcaaagctg	gaggagctat	ctgcatctct	cccgatcggt	gaggggctgc	ttcggtgatg	60
cgcaaattca	aggagcaagg	tattcgctct	gccattattc	gggaggattc	cgactttatt	120
cgcacaacat	caaagagcgg	tacggctcga	ctacatctgc	acatcggagg	cagaggtgga	180
aaatggcctg	ctgacagtcg	tctatcggtt	accatagtgg	atgcgaagg	caaagccgaa	240
tttctcgctc	cctggccaag	gagctatccc	tcacccctgc	cgaaataatt	gccgaggcga	300
tggagccaat	gatgtaccca	tgcttgactt	ctcggccggc	agctcatatt	caacagttcg	360
gcacatccgc	cttccatgcc	tcaactacgc	atgaagccat	tctccaattc	atgggttgcc	420
gatagtcgcc	gacccgatcc	gatagaataa	gaacctccgt	gctaagagaa	atztatcgta	480
cggaggtatg	tttttgccg	aaatatattt	actttgggat	agaagagtag	accataaga	540
gcttgaatac	gatgcgatcg	tatccgaagg	gcatgcgaaa	tatagatcgg	aaaggtgccc	600
gtattctttg	gttttgcgag	cttctttttt	gactttccgt	ggagtttttc	ccctgatgta	660
tggccgaaga	ggaagcattc	gtgcctttca	gggcataggg	acaaaatttt	taagaataca	720
attatcagat	ttatccaatg	aaagtaggtt	tgttcatccc	ctgttatgtc	aatgcagtgt	780
atccgaagtg	ggtatcgcca	cgtacaaact	gctgaagagt	ttggacatag	atgcgactac	840
ccgatggatc	agacatgttg	cggccagcc				869

(2) INFORMATION FOR SEQ ID NO:281

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 703 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...703
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

gtcgttactg	tttgaggat	actctcccta	tcgtatctct	ctattgatta	gagtgcgttc	60
cgagaatgag	tttaattctat	ttttcgtggg	gcaagataga	atttttcaat	tccagcagtc	120
tttcccctct	tctttctgcc	tttcagccga	gagcctcgaa	acaggcaaaa	ggataaagga	180
tgcgcgacga	agtatccctac	aaagttccag	aaaatgatca	ccgtcgggac	tgcatatcga	240
atagcgaccc	tgtgcgctta	taacggatca	gacgagcaaa	aagataaagg	gtacgaacaa	300
aggaccgaaa	gcaacgacgt	aggccacagg	gtgcctatcc	cccaataaag	cattgtcata	360
gacaaacagc	aagaggagat	agcacgtcca	taaacgggat	ttgctccata	aaggtgggtga	420
cagccacatt	gcgaacgaca	gcatgaaaga	gcgaatctgc	tcacagcgga	gcacgtgtcg	480
ttgtacccaa	tgaagagatt	gcatcccgtg	cgggagctga	gcagatagcc	aatcatcacg	540
ccaaggaacc	ctcaccggat	ggcataatga	atatgcaaga	gaagaaaaaa	accgtgaatt	600
tgtagtttgt	gactaagaga	cttcccggcc	tttctacttc	gttctgtccg	aatgcccattg	660

aaccactctg ctacagccgg atggcctagg cagggatgaa ttc

703

(2) INFORMATION FOR SEQ ID NO:282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

ccccgggaat aggcggattt tcgccggcta tcgtactgta tctgctgatg ctatcgtagc	60
caagcgtaca ggctgcgagc agaagtgaag ctaaaatctg ctccgctctc ctttctcttc	120
ttcttcatca caaccaaaaa gcaccatata atatggaact aataggcact tttttcttta	180
tcctgctaata ctatttgtaa tccgatttct gattcggatg ttccgccattc gtcagatggt	240
tttcgacaga agaagaactc ttcacgacaa ggaacagaaa cctcaaaaaa cctctccgg	300
gtgaaaaagt cgaactcgac gaacttgaaa agcgaaaatt tgaaaagacc aaggagaata	360
cggtagactt cgaagacata aaggacaaga gcgatgcang aaccggatgg atccatatat	420
tcagcagact cggatccttt tctccgatat caccctgtcc gcttgataac cggatccgac	480
atataa	486

(2) INFORMATION FOR SEQ ID NO:283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283

tctgcatcat cttttctcct ctctgcattt atcctgcctg ctctcggaca aaatccaagc	60
aggtacagcg acttgagaag caacgtaagg aggcctctca gccatcgaaa aaaccgatcg	120
cgaactacga aataccaaga aagacaacaa gacaaacaaa agcatctcaa cctcctgaac	180
aagcaggttg ctcaaccaag cagatggtag aactcttgga caatgaggtc aaagagttgc	240
aatccacatt gattccatga cgggtgtatg tcatcagctc tctgtagaag agaagccgca	300
tcggatgaat atgcccagc tctacagtct atgcaaaagc ggaacgctcg ttggatcgca	360
tccttttcat ttcatcggcc aagagctttg acaaggcatg cgacggatgc gtttcttgga	420
acaatacgct tctgcataca actggcatct gtccggctgc gcgatacacg tagcaagttg	480

gagactgaac	tgcgactgta	gaagacgcca	aaaaggagaa	aggacatctc	ttagtcatcg	540
agaagaggaa	aaaaagaaac	tcgaaggaca	gcaagccgag	caacgtcgca	ggtgcaggct	600
ttgggagcca	aacaaaaaga	cttgggaagcg	cagctgcaaa	gcagaaaaag	caagccgaag	660
ctctgaacag	aaagatcgag	aaacagttgc	caaggaaata	gaagctgccg	aacgtcgtgc	720
tcgagaagaa	cgtgacggtt	ggcacgcgaa	gccaaagcca	agggtaagcc	ggttcctgcc	780
gaacggaacg	gaaggcggag	accaaaggcg	gctatgctat	ggatgcctct	gaggtgctct	840
ctcgggcagc	tttgcacaga	acaaaggctcg	cctgcccggc	ccgttcgcgg	cagataccga	900
atcgtaagcg	actttggcgt	gcatcagcac	atgagctgaa	aaaagtacaa	gttaataatg	960
gaggtatcga	catcgctgta	caacaggatc	cgatgctacc	agcgtattcg	atggtgtagt	1020
gtccagtgtt	tcgtgatacc	cggttataat	tcggccgtaa	tggttcgtca	cggtaactta	1080
tcacggttta	tgcgaatctg	agcaaagtgt	atgtaaattc	cggcactgtg	ttaaaacggg	1140
tcaggctctt	ggtcgtgcct	atacggatcc	ttccaaaacc	agaccattat	tcacttcgaa	1200
atctggaaag	aacgcagcaa	acaaacccaa	gactatgggt	acgatagcca	ttcccaacga	1260
ctataatacc	ccattcgaga	tcttcctgga	ttccgaaagt	ggcttgctac	gatcggacat	1320
tcgtggcata	cacttcgggc	atcgt				1345

(2) INFORMATION FOR SEQ ID NO:284

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

ggctgtgttg	tccggctgtc	ctgtcttttt	gaatttgacc	atgatgaaga	ttccgggtcgc	60
ttctccgggtg	tggagagtgt	ccatttggtta	tagtaagata	gaaatggata	gaattggcag	120
gtgccgactc	tgcaatatca	agatatctga	tgtcttatag	gatgcagcag	ctgggatctc	180
ttgagcttct	gtggtaggaa	ccccttcggt	accgaattgc	gaaactttgc	ctgtatatatt	240
ccgacacttc	atataccttg	acattgatgg	tgggttttat	catgcgaatc	tttgtgccac	300
tcgttttgagt	ttataatccc	ccaacagttt	cccttctgtc	gtaccatatt	gatctgctta	360
ttgccatgag	caagcattac	gaaatcggca	gggctgtcgt	agaagagact	tcaatagatt	420
tctctaccac	aaattgagaa	acgcagcttc	tgtggccgga	gcattgaaat	cgagattggc	480
cactacatag	tgctgaagtt	gttgttgcca	ttgaatagtg	gtcgcatttg	ctctttgacg	540
gaatgatata	ngcccttca	tggatttgat	agtc			574

(2) INFORMATION FOR SEQ ID NO:285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

gggaaggcgt	aatgaagaaa	gaaattcttt	cagcagatta	caaaggcgag	ttgttcgtca	60
ttctgtagct	gattatgtca	aagccgaaga	cttcgctgaa	acattattga	gcgtcatata	120
gaagcaagca	aatccaacct	caaggctcac	ccattgtcgt	tgccggtggc	tacggagtcg	180
gaagcaagga	aaatttgccc	tcttgcatga	tcttgcatct	gtattgggtg	gagaagttgg	240
agctttcgtg	ctgcggtaga	tgctggtttt	gccgatcatg	acatgcaaat	cggaagacag	300
gcattaccgt	tcgtcccaag	ctctatatcg	cttgccgngt	cagggacaaa	tccagcacat	360
cgccggtatg	ccaggganag	ctct				384

(2) INFORMATION FOR SEQ ID NO:286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

cggataagtt	ggcacgggct	acatcgacat	ggataaatat	cttcaggact	cgtacggggac	60
naancgatac	tgggagacta	agcgggtacca	attatccgaa	ggagnaaaaan	cggtcggaaa	120
gggncctgcc	ccgaatatga	atcgcgttgg	agtctatcaa	aaaagaacgc	aaacaaatac	180
tggacgaagc	ccgccacaag	catccgtgat	gctgtcccaa	tcgtctgcac	agatagagaa	240
atcaaccgcg	acatcaaaga	ggcacaagcc	gaaagggaga	aaacgcggag	agcagacagg	300
agctgaacga	cttcagggaa	acgatcaaca	aagaagagat	cgaaaagaag	agcgaatcaa	360
tcgggagata	gagaaaaata	aacggaggaa	aaacggaagc	aggagaaagc	agcaagccgt	420
tcggccgaaa	cacctgtaca	gcaaagctgc	aagaagtgc	ccaacccccct	gtcatacaag	480
tgggcgatac	gtacgaatca	aaggacagac	ggctataggc	agtattatag	atatgaatgt	540
cgggaggcta	ccattgctct	cggaatgatc	aaaacgactg	tgccgatcat	cggttggaac	600
cggccaagcc	cgtcaaggag	cggaagtctg	agcctgttcc	ggggcatctg	cccgaatgat	660
catagaccgg	atccacgaga	agcgttggat	ttcaagcaag	acatcgattt	gcgtggcatg	720
cgtgtgaacg	aagcctccaa	gccgtcatgt	attttatcga	tgatgccatc	caactgggaa	780
taccgcgcta	cggatacttc	atggaacggg	aacaggtgca	ctcagaacgg	tgacaggagg	840
tatttgcca	cagtcaatgg	cgtaaggcat	tttgacagacg	aaacgtccag	ttcggaggag	900
ccggcatcac	tgctggtgaa	ttgggatgat	actttcgata	cgatcccaaa	tggtcgaat	960
catctgc						967

(2) INFORMATION FOR SEQ ID NO:287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

gtgactattc	ggcaaagaga	tatgaagacg	agccactccc	aaagtgtcgc	acgaagactg	60
acatcggcat	gcagttcttt	gagatcgaga	ccggtatttt	ttcgagaaaa	gaaagatggc	120
gcagctgagc	tttcagtcce	gtactgtcgc	ttggaaaaaga	cgtacttttg	cattcaagtc	180
gagcaatccc	aatgtgcgga	ttgggtcttg	tacaatcccc	aagcagagag	ccggcagttc	240
ctgagaagat	ggtattgata	ttgagtcgta	gccggctcgg	ctcttcgga	ttctactttt	300
cagagcatcc	agaaggaaact	gaatgttcag	agccgtatcg	ggagcgaacg	atatacatcg	360
agttcgcctt	tgaacagacg	agcagaggag	aactcagacg	gcctttcaaa	agagggagca	420
gatccagccc	cccgggtcaaa	cttcggctga	caccgcagga	cgacgggcac	gatcgaagat	480
gacaatatcg	cgatctccat	ttgtcgccac	caaccaatgc	tgatgtgccc	gatgcggact	540
gcgttcgag	tgctttggat	agctcgggtc	gcacacgtcc	ggcgacggac	gcttactga	600
cggaatttgc	aaaatcagat	tgggaaggat	caacaggaaa	aagcaacagt	cagcacggcc	660
acgacgatcc	atttgagcgc	acgcatgcct	tgcgataacg	acggataaac	cggatgagac	720
cggctgacag	tttttctttt	gactcacgca	gacaacttta	ctttcaagtg	gcaaagatac	780
ttacttctct	agcttaaaaag	tcgaaaaaga	gatccgccga	agctccccca	aaaaggaatc	840
cogtaaaaaac	cgaaaatctg	taatatactg	tatgaaaagt	ctacaaaatc	cctatcggca	900
ctcccagataa	agaaaaacacg	agcggcaaga	ccaaaaaaaac	ggaactgaaa	aatccgaaat	960
agtcgttcgg	tgatcaaaaa	ttctcgctcg	tctttttttc	gcttttggtt	cgagatttgg	1020
aaaaaagaca	accgtaaatc	cgaaatcatg	gcgcgagttt	ttcccgattt	ttcgttcggt	1080
tttgtctgtt	gcgactgctc	tatcagtagc	cgataacaga	ttttatccaa	atgggtattc	1140
ggagttttgt	atcg					1154

(2) INFORMATION FOR SEQ ID NO:288

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

ggcgcagtgt	tttatacca	tggatagtag	aagcagggat	gattcgggtat	cgtgccagta	60
gaattacaga	tcctttccat	gcgattcttc	atgcttatcg	tatgctgata	ggacacaaag	120
aagatgaagg	ggggcactta	gaggataaag	ggaggggatt	tgtagggcg	gatttcaaaa	180
aaataagggc	tatctccgac	agcccttact	tccttattaa	ccttaaaatc	taataccatg	240
aaaaaactgt	acaaaaataa	ggcgatgtat	ttctcgtagc	actatattag	gccaaaaggc	300
gcatattagt	ccaatcaata	tttgttttcg	gccttatacg	cttttttctc	ccatattcga	360
acggggatca	tacgccagaa	agcgaccagt	aacgatagcg	ccagtcgaaa	gtcagcagtc	420
tttttcgacg	gatgacagcc	ttactattgc	ttgggcaact	atcttggact	ccatcagcat	480
tggatactta	cgtctcgtag	caggggggta	tcgacaaatc	cgggacgaat	ctccgtaacg	540
tcaggtgtag	gctgtctgtc	gtggccaatt	ggcgtatgga	ttggagatgt	gcatttggaa	600



gcgtttggtg	gcgagtagg	caggagcgga	tcccattctc	ttgttgctgc	taccgaactg	660
atggctacta	tttgaccctt	tttccgaggc	gaaaatagcg	gtaggcgcca	ccgatcattc	720
gggtaaatcc	ttctcattgg	tacggagggt	gtccagctct	ttcgtttcgt	ccagttgctg	780
attgtataac	cgataccgga	cgagtggaa	tatacatcca	taccgctcat	ttctcgatga	840
ggtgggacag	ccgttcagga	gcacgcgaat	gcgtgatgtc	tatacggctg	tataaacctg	900
tgagggtattc	tcctgcttca	atgcacgcag	ctttgggtat	tgcggccggc	aacacctacg	960
aaccaaccgc	gagagataaa	aggcgggcta	catcaagccc	gatgccagag	gtggctccta	1020
cgacaacgat	cgtttggctt	ccatgatttc	ctgttatgaa	atgaagtcca	tcccacgaga	1080
attttcgctt	cttctgtcgt	agctcctacg	acagtgaag	ccttcattca	cgtaggtgctg	1140
ggtaggcttt	gcgttgttct	tcgaatgtct	tccgctgccc	cttagcgatc	gatccggtac	1200
gagcggtatcg	aaggtatgca	gcaaaccctt	tcgatacgat	ggtcggggaa	gagcgacaga	1260
tctatgatgg	gatggctcgt	gggggagggg	ctaaagtatg	cagcagggga	aattccagtc	1320
cgatacttcc	gtaattggctt	caaggccat	tctggctcca	ttggcttttc	cgctgcagag	1380
aatcctgcta	tgtaggagt	cgcgatgtct	gccaaatcca	aaggctgagg	tctatatcgg	1440
gttctccttc	ccagcaatct	attacgagg	ttggagccat	ccgcttttga	cagcccgaat	1500
aagagcttgg	gtatccgctc	ggctcctcgg	caggcattga	tcaggatagg	ccttttgtct	1560
gcacagctcg	tagaaaagcc	tcaccgatga	ggtgataggt	ggcgtgagg	tcttcattgt	1620
gaggggaacg	tggaaatgaga	taatgtcgca	ctgctccacc	agtcggttag	aggaagaaag	1680
ctattgtcct	gctctgcctc	cgaccgaggt	ggtaccagag	caggaactcc	atgccatagg	1740
cggaggccaa	acgcttcagc	tcacgcctac	atggcctaca	cccactatac	ccattacctt	1800
ctctttcagg	gaaaaccctc	gcgcaaagcc	agacgacaca	ggcagcacat	tacatactgc	1860
gcacggccgt	agcattgcag	ccgggggaat	tgcgccagag	gataccgtgg	cttcgcagta	1920
ttcgcggtcg	atgtgtgcca	atccggccgt	ggcagtcggt	tcaaccgcac	atcagtagct	1980
tgcagaagag	ccggtgtgca	cttgggtgatc	tgcggacgat	cagcaccggg	gcatgacgta	2040
tcgtatcggg	agagaagcgt	ccgagtgtag	gtaagttaat	tccgcaacag	gatcgacaat	2100
acctctcaat	agggcacgga	tgcttctgcc	actattttga	gaggaccgga	tagagagaaa	2160
gcattttctta	ggcttcgcct	tttatttttg	ttgggaatgt	aaatgggcat	ccgatacgcg	2220
ttgctcgggtg	tggatctcgc	cgtgttccac	ttcgagcgat	ggatattgtc	cgagagagtg	2280
gtcaaaagtc	ttttggcatt	gtcggagtca	ggatgatgcg	attttggact	cgtgcggtgt	2340
cacgattcgg	aacatacgga	tgaagtccaa	gacaaaattcg	ctcggagagt	gcacacgat	2400
aagagattgc	agtagtggcc	ctgagctatt	tcttcgggca	gttcgatgtt	attgttttgc	2460
tttcggtttc	catttggttct	tgaatgtttt	aataagtaga	tgagggaaa	tgccaagctg	2520
aataacgtat	ggcaccgtta	ccccctttga	acaaagttac	tccttttcgtc	taaatgtgaa	2580
taagggttca	cgtgccagag	tgaattatt	gcggttcgaa	ttacggataa	tgctcttttc	2640
ccatccgtac	aaatataccc	tgtacgaaat	acgctctttt	tgccgaggca	tacttgtaca	2700
gggtaagtaa	gcatgtc					2717

(2) INFORMATION FOR SEQ ID NO:289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

ggccaaatcc	tgctgtacga	tcttttccatt	tttcgcagcc	agttcggccg	aagagacgaa	60
atttcgtttt	gctgcttttc	caccagctcc	atcagcttcg	gacgttatac	tccagcttcg	120
aaagatcgag	ttcctcttct	ccggtcaaga	ataatccttt	tccttacaaa	agtaaattat	180
ccgcgccaaa	ctggcactaa	ttttgtgtac	ttgtataaa	agtaaataag	acagtcatta	240
cggagaaaaa	gatttgggta	tttttgcctt	cacagaaaag	ctgctctgca	taatgcttct	300
ctatattcaa	ggagccggta	atgaattgaa	aaagagaaga	ttgatagaat	tgcaaaacat	360
agaaatgcta	ccactcatga	cccaccgcct	caatcaatcg	gaatatcctc	ttcgatcgga	420

tatgctgcag cgatagacct catccccgtc gggattgtag agaacgaatc catcagatat
gcaaatcata atcgaccgat agcatcatag cataggacaa gc

480
522

(2) INFORMATION FOR SEQ ID NO:290

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290

ggcataaacc	tccagcatcc	gtctggcttc	ttcttcggct	tcctcttttt	agcatgagcc	60
gtatgccctt	cttgccaaag	gaattcggct	gtccggagaa	aagacgtgta	cgcatttccc	120
atcgaactac	attggcccac	tgattgcgag	gataggcaga	tcacgggtggc	tttgtatcca	180
gttcttatat	gtattcaaat	gatggctccc	gatgtcggac	gtacgatcag	ctcttcttcc	240
aacttgcttg	cggatccact	actacgccgt	ctccatcggt	attggctttg	agccatagtg	300
agttaccacg	gcgcattcct	tagcaaagcc	ttccacatgt	ntctttcacg	gctcaggang	360
ctcttcggga	taaaaagagg	gaaataggca	ttaccgtgt			399

(2) INFORMATION FOR SEQ ID NO:291

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

tgatgtccgt	gatgatgtgc	ctcatgttca	tgtttgtgct	ccgagcaacg	gcgtgggcgt	60
gagattgttt	tgtttccata	gatttgtctc	ctacacatat	gatctgatgt	ttttgttttg	120
acggcgtgtc	ataatgagca	atttgctcgt	tgccctgcgac	attcggcttc	agtcacgtac	180
ttcagtagct	tccttttagac	tctgttttag	cacctttgtg	ctccaaaaga	atthtgacac	240
tgctcatctt	tattgcaaat	gtcatcattt	tgtcgacatt	tttaccatat	atttgccgtt	300
tcaaaaagta	taacccttga	tttcaggaaa	ttcatcatgc	ggctaaagat	cgagaaatga	360
gccgagaatt	cggtttggag	gtaattaatc	ggcagcctac	ggtgtccttt	ctgtcgtgga	420
ttcggacggt	gcaccctatg	cttgccctctt	ttcatcgtgc	gcgatgggga	gaat	474

(2) INFORMATION FOR SEQ ID NO:292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

```

caaaacagaa aaactatact acctttgtta cctaaacatt gcgataccca tcatgaataa      60
ctttttcaaa atacacgaca acttgctacg caacctatcc cttcgctgcg taggggattg      120
atggacgaga tcgattggaa cgatagatga tcggtatcaa ggggtgcacga ggcattgggaa      180
aaaccacatt cctcctgact atgcacgcga aaacttcggt ataggcaata gaaaatgcct      240
gtatacaatc tgaatcaact ctatttcacc acagaatcct tggatgaact cgccgtgagt      300
ttgtcaagca aggaggagag gtactgctac ttgaccaagt attaaatata ccaattgggtc      360
tatagagctg cgtcagtgtg tggagctata ccggacttac gcattgtctt tacgggggtct      420
acgggtgatgc gcctgaaaga aaaaatcccg agctgaacgg actggttaca tcgtacgttc      480
tgaacggttt tcattccgcg aattttctcaa tctgaaaaca gggctgtcgc ttcagccttc      540
agcttcgatg agattgtatc caaccacgaa cagatagctc cgcgaatctc gagcagggtga      600
accctctcga ctgggttcag gactatcttc accatggtac taccccatat tcctggagga      660
taagaactat tcggagagtc tgctgaaacg ctcaatatga cgcttgaagt agatgtgctt      720
ttcatccgac agatcagcag cgattcctgc acaaaactgc caagctactc tacctactgg      780
gacacgtgct cccggctcgc tcaatatatc gagcattgcg aaggaaagtg acattctcgt      840
acgacgataa ccaactatct gaagtacctg tccgaagcca gatgatcaag gagcttcacc      900
gcgaagagga gacgggtgcc aagaagccgg catgatctat ctggacaata ccaatgtggg      960
atacgtaatc cagccgggaa tctcaactat atagacgtac tcaaaacatt cttcctcaat     1020
caggtcaagg tcgcaacgaa gtatgtttgg gatctcgctc tcaaatcgca ttctgcgtaa     1080
tcgccaatat cagttctgca tcgatgagaa gatgagccgt cgctacaacc cgaccgctac     1140
tatgccatcc agaacatgcy cagcggtagc cgcaactgat cccctctggt ctcttcggat     1200
tcctgtacta aaaaaacagg acaacaactg tgaaagccga tcggggcggt cggcttgtcc     1260
tcactttgct ctgattcctta gtgagcagac aaagaatatg gacaaagccg atgcatccgc     1320
aacaccgact ctgtttcagg gttgctatct cagaatacaa gaccgaaatt atacttttta     1380
taactaaaaa ccaaatggc taaagaaaaa aaattcctaa ctgtgacggg aaccaagccg     1440
ctgcgcataat tgcttatatg ttcagcgaag ggctgccatt tatccgatta caccttcgtc     1500
tacaatggct gagtatgtga cgattgggct gctgccggcc gtaaaaacat tttcggcgaa     1560
acggtaaggt ccaggagatg caaagtgaag ccgggtgcagc cggtgcagtt cacggctgtt     1620
gcaggaggga gcactaacca caacctttac ggcattcacag ggcctatgct catgattccg     1680
aatatgtaca aattgcggga gatttgcta

```

(2) INFORMATION FOR SEQ ID NO:293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

gaaataacat	ttccaaatgg	agaactgatt	aaggacaaaa	agatccggag	gaagattata	60
agatgaaatt	caagaatcta	atctatactg	ttccagaaac	agaaagcacc	tatcttacca	120
aacaaaatct	ttcgatacaa	aaaagaagat	gagcctatgc	aaagatgagg	atcatgattt	180
gtgcgaagat	gatacgacga	acatcgaaag	cggatacacg	gtggcgtaga	ccacagaggc	240
tccgtacctt	tgagctggct	attcacatag	tcgagagcca	tcggattggc	cgtattccgc	300
atatcatacc	ggctgtgcca	tcgtacctgt	tgcggagcaa	cttatagaag	cccaaccgac	360
caatagcgta	ggaagcatcg	taatcaaaaa	gccgctccga	cccaaagcag	accgtcccca	420
tggataatgg	tatcaaagaa	atggctcact	ggccaatcca	gtc		463

(2) INFORMATION FOR SEQ ID NO:294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

gcattacccc	ctttcagaaa	aaagtactcg	ctcggataga	taaccgacca	tcgaaataac	60
ctccgacatt	caattgatag	aacagtgcgc	atgccggtaa	aagacaagcc	gctgctgtat	120
gctcaaatcg	aggtgggtgga	aacgtgctcg	gacttaagcc	ccatcccga	agctccgcga	180
taagagagag	aaaggacgga	gcacgtatgc	cctcaccctc	acgaatgaga	aatccatccg	240
ccgtaaaccg	taataaggac	gcggattgaa	tgcatcttta	gctcgtactt	ccagaatcgg	300
tgatgaggaa	ctatgcgagg	aagatcggga	tcggcattgc	tgaattcaga	atatcggtaa	360
tactgccacc	gaagagactc	cacgtctctc	cagcggcaaa	ggattgcgct	cggccagcat	420
cacgcttgtc	tccacattga	gttgggcaat	aggctcgatac	tattggtcag	acggacaaat	480
ttatcatcgt	gcgagttgtc	gggccttgtc	cgttgagcag	ctccatcatc	agatcggtcg	540
ttggtctatt	ctttcgcgcg	tgctgtacaa	atcgaaagag	cgatgtccgc	ggataattgc	600
aaaagccctc	tttgccgagg	agaatagtac	ag			632

(2) INFORMATION FOR SEQ ID NO:295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 784 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295

tgcgaatatg	aacaaagaaa	tcacttttga	taagctaccc	gaagcggtag	gtatctgacc	60
gaacagggtct	ccgccattaa	agaaatggta	tcagcattca	ccctcctgtg	cctgaagaaa	120
aatctctcat	aggcatagac	gaagcgctcg	aattattcag	aaagctaaac	ctaccatcta	180
tgctttggta	cgcaaggaat	tgccctgca	tataagcgtg	gcaagaaact	ctacttctac	240
aaagagagtt	actacaatgg	gtagagtctg	gacgaaagg	tgcaactaca	gccaatcatn	300
tgaggagcaa	ctggccatga	tgcgtcaaga	ggtgcgtcgt	aaacgaaatc	tatcaagtaa	360
cgatgggcca	tggaagaaga	agctatcggt	ccgaagtcc	tcttgacaaa	gcaatagagt	420
tgggcttgct	gttcacgggt	tgacctttcc	tatcagcata	tttccctctg	agatacgaaa	480
catcattgca	aggtacatga	gtgccaaggt	tttcccatcg	attacatcgc	ctctgccatc	540
ttgtggcaat	tgctgtgggg	ataggaaata	ctcatcttgc	cgaactcaac	gcggctggca	600
ggaaagtacg	atgctctatg	tcgcattgg	cggacgtcag	ggacaaataa	gagtcattccg	660
ctaagctttg	cgatgaagcc	ttttctgatt	ttgactatca	ggaaaacaaa	ctatacgaac	720
gctcctatgc	cgaattgaca	acatcatgcg	tatgaatcgt	aaggagcgaa	tagagggagg	780
cttc						784

(2) INFORMATION FOR SEQ ID NO:296

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 984 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

tgaaaaacgg	gattctatcg	catcgccgta	ggagccggag	tgccatttcg	ctcgctgtga	60
tcgactatag	ctataaagaa	atgagcgtat	tcgagctgtc	acccctacgg	gcaatgaaga	120
agcggatatt	gcctacatca	gaagtcgtac	agggcattcac	aggcacggca	cccccgaaac	180
tttgagaat	cagaaaaatga	tcaaacacga	gagctctcag	ccattgagag	ttgctgtagc	240
tcaatccgga	tagactggga	ggataagcac	gccaatctac	gccgaatgga	gcgttggccg	300
aagaaacagc	cggtagggcg	gatgtcctct	tctttccgga	aatatgacta	cgggcttttc	360
gatgaacgta	caagctctgg	cggagccctt	cgagagggcg	aaactatcat	gaagcctgaa	420
gagagtga	gctcgtcatg	gttggtctctg	tcggctacga	tgcccgtagc	ggagaacggg	480
aaattctata	tcgtgcctat	ttcgtgacac	cgggaaggaga	ggtcttccat	caggacaagg	540
gcacctcttc	cgtgtagggg	gagagcatga	ggtgatgact	ccggcacaga	acgccggatc	600
ttcaactatc	gcgggttgaa	gatcttccat	attccctcta	tgatctgcgt	tttcccgctc	660
ggtgtaccaa	tcaggatctg	gaatacatct	gctcgtctgc	atggccaact	ggcctgagcc	720
gcgtcgccg	gtctgcaaac	gctactccaa	gctcgtgcca	tgagagaacta	tgccatgtg	780
tgccgatcaa	tcgggtgggg	gaggacggta	tcggctctgcg	ctatacgggc	gatcggctat	840
cctttcgcc	cggggcgagt	atcttgccac	ttgtgcccga	agagaggaaa	aggtggctgt	900
accatacgt	cgataagggg	gcgatgcaac	gtttcgcgac	aagtcctgc	gtggatggat	960
atggactctt	cgtcatcaac	atga				984

(2) INFORMATION FOR SEQ ID NO:297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

```

ggaagcagtt ggaggacatg cagggataag ggctgtggaa atgatgaaat ccgctttgac      60
aagcggccttg atgagaacac gatgaagggtg tattgtatga ttatcatatt attgaaaaag      120
tactcatcaa ttcatcagaa atttcatact ccgacttcgg tgggaaacgg cagtggcatt      180
acaggcggaa acggaaaaggc agaacacgct gatataagca gtagaaaagg tagtcacggc      240
aagcctgcat tctgtatttc caagtatgca gggggttcag acattcgggt gcagccaagt      300
atgccttcgg agaaacaagt ccaatcggca gcaccgatgg agagccgtgg ggacttcaga      360
atacaaggga aagaagtggc tggggcaaat gccacgtggt aagcacggta cggatatttt      420
caaaagagaa aataccgtag ccattagggg atttttctca cgcttcactc cgtgtccgnt      480
gaaaatctcc aataagccaa cggggttgca cccctctgga caccctgcc gagcctgttg      540
catgaaggaa cgggcaagct gaaacaagtt tcattttccc tctcaccgta aaatcaggaa      600

```

(2) INFORMATION FOR SEQ ID NO:298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

```

gggaacaagc gagttctcat cacgggagca acgggcttca tcggcgggctt ctggtcgatg      60
aagccctgcg ccgtcaatat gaagtgtggg cggtgtggt cccacacagcg atcgctcacg      120
cctgacagac agccggatcc gatttgtgag atcgactacc gcgaccgctc cgatattgct      180
cgcttggctg ataagaagct cccgaagggtg aatccgcatg gcacttgggt atccacaacg      240
ccggttaacc aaagctcgtg acacctcgtt tttnagagag atcaatgcag agcaaccaag      300
cgttttctga taggattaca aggggcgaag cactgccccg aacctttgtc ctgatgagca      360
gtatgggtag ctatggagct cctcccagcg acgccaacca cttccctcct cttccgtacc      420
caaacctacg actgcctatg ggagagcaag ttgctggcgg agcaatatgt gcaaaccttt      480

```

gtcacaatac	ctataccata	atacaaccca	caggagtcta	tggacctcat	gaccaagaca	540
tctgatggca	atccgcagcg	tgcacaaggg	attcgatttc	tccacgggaa	tacgccgcaa	600
acactgactt	ttattttacgc	agaggatctg	gcctcagagt	tttcatcgca	gccgaacacc	660
ccgatgcagc	agggcagaag	tatatatata	ggatggaaaa	gaatacacccg	atatagagtt	720
cggacgaatg	atccacacct	gctcgacaga	aaaaacgtat	gccattttgcg	tattcctctg	780
ccttagtaaa	agccacctgc	tatatcggcc	aaaaatgggc	agacatcagt	ggccattgac	840
accgcttaac	ctcgataaat	acgccatcat	agcccaacgc	aatggcgggtg	cgactcttct	900
ccgatcaggg	caatcggttt	ttctcctcgc	ttaatctgga	gcaaggtttg	gccgagacca	960
ttcgttgggc	acgtaccacc	gacaaatccg	tcgttaggag	acattccggt	tccttcgcgc	1020
gaccgtatcg	atgttatcgc	tatccggtca	atccaatctt	tcgaggtact	tcttacttct	1080
ggactttaac	attaacgtca	ggtttgaccg	ta			1112

(2) INFORMATION FOR SEQ ID NO:299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

cggccttcgg	gaatcgcctt	actcattccc	cggtaaaacg	ctccgcctga	agaggatgac	60
cggccggtaa	agtggcagtc	gtatcctgcg	caagggcttc	gtcccgatag	tcgtaagcag	120
gacagccgat	aaagtcatt	ttttcatata	gtcgatagat	tgattgtttt	actttgtctg	180
tactaaaaag	agtcggaccc	gcctttgagc	gtcaactttta	cgggtgcggag	tttcttttgc	240
aggagtgact	cgctccctgc	atcaccccg	gggcccgttc	ggaaaggatc	tggttttggc	300
ggaggaagca	aaggtgaacg	aagtcccgac	cgttcctccc	atatggctcc	cacttctttc	360
agcgcggaga	cctcttcgga	tccgggaata	aaactccttc	ctgtccgtcc	gtatcgaagg	420
cggagagctg	aacggaaaacg	accgtccgcc	atactcgata	ctcgtgatat	gaagcttcat	480
ccggttgccg	cgattcgggc	ctgtgccatc	agtcgggtat	gacggggaat	ggaaaggctc	540
gcaggcgagc	ggactccagc	agacggagtt	gtacgaagtc	tccatgctca	gggtgggtgt	600
cctgtccacg	accaccgcga	acgtattacg	ggtgacgacg	atgccggcac	gtcggcgagc	660
cggaaaccga	agtttcgctc	cttatgccgt	actcggcgat	aaaagccgaa	tcgctcatgg	720
gctgatccag	agacgaacga	ttgctttctt	ctccggaaga	agctccacag	cgggtaaagc	780
cgccgttctg	ctgtcacccg	tgtcttgggt	gcgggagcat	cggccggggc	ttctgactcc	840
gggtgtatgc	atcccgggaa	tttgcatcac	cggaggccgg	gagtatttgg	ctgccatccg	900
gtaagatttt	tcgagcagtt	cgagatgata	gtctcctcct	ctttttcttc	cttgagagtt	960
gcgagttcgg	agcgtatcat	tccagctctt	cccgcagggc	ttctttctca	tagtcgtatg	1020
ccggtggctg	tagaatgaat	gtaccatctg	cgacgtttct	tcataccggc	ttaccgacgc	1080
tcgatcggat	gaagcccgtc	cgaagcggcc	tcttccgaga	tttctctgct	cgtgtttcgt	1140
ctttcttctc	gaaatagtcg	tagaggttgc	cgagggtctc	tgccgggtgg	attccttttc	1200
ttcatcgcgc	cccagttcat	agccttcagt	ttatcgtcgg	tcagttcccc	gtcgggtggc	1260
tgcggaacgg	tttcttaaga	cctgctgtcc	tctcttctct	ttgtcgtctc	tcggccgaag	1320
gaggaagatc	agccataagg	aaatcaggaa	gaggatgcct	aatccggcga	agcaagcagt	1380
tttttaagct	gttctttctt	cttttcggac	tgttctcttt	ttctttctct	tctttgtccg	1440
ctccctttcc	cggggtctcc	ggaaaaacgg	atgcggatgt	ttcggatgtt	tttcattgtt	1500
catattcgat	cgtattaagt	aatttttggc	gtaatgcttt	tgcggaagtc	gtcccgcccg	1560
aaggctgtcg	tgcgaaacgg	actgtcgatc	agctcgcgga	atcttttttc	ttccaccgtc	1620
tgtaatcggg	cggagcaaa	aaccggacaa	tcataccgag	cgaacacaca	gataaatcag	1680
gtcagcccg	aataccgcga	tttttcggtg	caggggctta	aacggtcaca	ttgccgcttt	1740
aggccgaggt	gtattttcag	atagaccgtt	tcantcgttt	cacggtttga	atgtcctgat	1800
tttgacgac	ggtaaacgtt	ccaacaggaa	accctgcgga	ttgttgctcg	aacgaacgga	1860
atgatcaggc	tgcattcggg	gataagcgac	cgctccgtga	tggttgcctg	gggacgataa	1920

```

actgccgggc gtaagtcctg acccgataag gataggcctc aaatcgcacc ggatggagtc 1980
gagctcgtga cgctgggtga tattgcctga atcatccggc tgtaatatcc tttttccatc 2040
aggctcttgt agtaattgag gccgttttgt cggccagcat caaagcgctt ttgacattcc 2100
cttcgatgcc gccttggtccg gcgcaatcgt aaagaagagt tcgtgaaaac gcctgagtgc 2160
tcgcggtctt ccacgggacg gttggctttg gcatcctggc tgagacgagc ataagcgact 2220
ttccgtttgt cagcacatag actttctccc gctgttttct gcaaaggaat aggatgaaaa 2280
aacggcatag cccgtgataa tgagcagagt acgacaaagg caatggcata aagccggatc 2340
tgccggaacg attttcgata tttttcaatg atttgaattc cataaagtaa ggtgttagct 2400
gtcgttggtt taggttggtt cgtcaatgct ccgttggtgt ttccaccgcc gaatcgctt 2460
cggaggaacc tttccggaat cgcttcctga aacgtnccaa gcattaccgc acaactgcgc
2520

```

(2) INFORMATION FOR SEQ ID NO:300

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300

```

cttcagcag caaatcgaag ttcggagcag agaaaagcac cttgccggca tcgcatcgtc 60
aaagttttcc aatgccgact ttacatccgc ttcggaatgt tgatccctc tttgactttg 120
aagatctgaa tcgggaagat ggggtactcac catgccccaa accttcctcc gtggcacgta 180
acaactcctc catcacattc gaccttcggg cgaagtatca gtgccgtaat tgatggaact 240
gaataaacct gattgcctcc acgagagtgc atcgtattca agttgtggat gaagcttcca 300
tagcctgatg cgtatcctta cgcgtctttc ggaaaactgt ggcagagcga tctccacctc 360
tgtactcgaa aaaggggaaag acgccgcaca tcgtccctca tata 404

```

(2) INFORMATION FOR SEQ ID NO:301

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301

gacaacaatc	cgtacgaaga	gagattcgaa	gttgatgtag	atggagccag	ctcaccgtat	60
tcccggccaa	aaaaggtcag	gaaatagtg	gttacgctta	gaaagctata	cagacaaggg	120
ctttagcgg	aagttcactg	tgatgtagga	ttcgatatgg	atggcaaaat	ccacgacttc	180
tccgtgtca	gccacacgaa	acacccggtc	tgggagccaa	gatgcaagag	tggttccgaa	240
cgccgccaaa	aaagaaggac	tgatccaaga	tgtacgtgg	gtacagatga	gtgaactcct	300
ctgactgttt	ccaaagacgg	cggatcaagt	gatgctatca	cagcgcgacg	atcagtagcc	360
cgagcctttt	tggatgcaat	ggatcggtgc	taagagggtt	caaagccgct	caaggcagtg	420
cccggacagg	ctcaggagtc	ttcagggcag	c			451

(2) INFORMATION FOR SEQ ID NO:302

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

taaaaggact	cttaagggac	gactaaatat	gcttttcaat	acgcccattgt	ctttctctat	60
tgtttcccaa	gaatgaagct	tatatctccc	tgaaaacgat	cttggacatc	ttcaaacaaa	120
tacttctgat	tagctttgag	gctaagatat	agtcggcctc	tgattgaata	atcacttcag	180
caatagctgt	ttgtatccca	ttgcatcaat	actaacaact	gatccactta	aatcaagact	240
atccgtactt	cggaatagc	ttgtaattca	ttgtgtttgt	ctgtaactgt	ctctgacaag	300
acttaagctc	acttgatcaa	tccatgccga	gagtatatat	gtaaccaggt	cttctttggg	360
agctacgcaa	acgcttgcca	tctatggcaa	tagtttaccc	tctaaatcgc	taatcaagtc	420
ttttccataa	acactgagac	agcgtaaaga	gcaatgan			458

(2) INFORMATION FOR SEQ ID NO:303

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

agagttttatc	atcaacctgc	aaacctgaca	ctctccatta	tactttgcgc	aataatgaga	60
tagccattct	tgccactacc	gaaatatcat	ttgagaaaca	catatcgctt	gacaaaactt	120

atccatattg	ccagttgatt	ctcaatatat	agctctcagt	gtccgagagc	atattgtagaa	180
gttccttttt	cggtatat	atctctat	atcttcattc	gtatcggata	atatttgctc	240
ataaatcaac	accctaattg	caaacatata	atacattcag	aaaactttgt	gtttacttac	300
aaactaaatt	ggttttgaca	aggagggtta	tatctccttg	tgaagacagt	tatattat	360
ctttgtat	atcatactta	ttcccagtg	ttatacacat	tctctaaaca	ttgacgaaca	420
aaattgaggt	tctcatgcga	gagtttaact	ctgagaagag	cagctgttga	aaaccttgaa	480
taatctcatt	cttaaagggc	catttttgaa	tatattaatg	aataatattt	ttatctcaac	540
tctttttgat	tagtatcaag	ttgtgtttgt	acaatcatat	ccactaattt	acacatggca	600
tagcagaaac	catactggat	atcttctaag	caattagata	ataattatct		650

(2) INFORMATION FOR SEQ ID NO:304

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2664 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

gcagatcggg	ttttgagccg	atgattttca	gcgtgtcgtc	gggagtgaac	cataccatcg	60
ggagtaaaaa	atcacaggaa	taccacagc	cgacccttca	acctctccaa	aatccggggg	120
tctccacggc	ttttcggtcg	ggaaaattca	ttgttcggcg	tgcaaacctg	caaactcggac	180
acgaaattca	ctgctcaact	tggaggagca	caaatccgcg	cggaaaaatgc	ttcctccggc	240
ttggacgact	tttttcggcc	cgcaatgcag	atttcctgtc	ggacattccc	tctttgccga	300
aagtaccogt	atatcccttg	cagagagtga	aactgtcgca	cggcttttcg	tcgaatcctt	360
ttgccgcaga	gtcgatccct	ttattcgttg	caatccgggc	ttcggcaaat	acggcttcct	420
tactccgtta	atgctctcat	tatttagaga	atgggatcgg	gaaaaataag	agacacgaac	480
ggaatcttac	tatcttcgtc	ctgaaattat	ggcagatcgt	agaagaaccg	atgacaatag	540
ggtgcgagag	aggtgggtatt	gctgctgaat	atcggctcgc	cggacagcct	gaggagaagg	600
acgtggcgcg	ctacctcaat	tctttttctg	ccgacagagg	atcatcacct	tgcctttttc	660
cctgagacag	ttactcgtga	gaggtacatc	actcctttca	gaaagaaaaa	ttcggcacaa	720
aaatatcgga	ccgttggggc	gaaagacccc	ggtctttccc	cctcatatcg	catacgaaaag	780
ccatgcccg	gcactggcac	atacgggcag	agaagtcct	gtagccatgc	gctcggcaag	840
ccggctgtgg	ccgatgtgct	gaaggagctg	ccacacggcc	gagcctcgtc	gtcctcccgc	900
tcttcccaca	ctacgccatg	agcagctacg	aacggccgtg	gagcattgca	aggccgaaat	960
ccgccgcctt	tgtccgaatc	ttccttcgcg	gtcgtgcagc	ctttctacgc	acacgaagcc	1020
tatatccggt	ccttgccgat	aacatcagac	cctatctgac	gaagcctttc	gacaagctat	1080
tctttcctat	cacggcatto	cccgcgatca	tttggaacaag	accacccaca	ggctttgaat	1140
ctccggcatc	ccgaaggatg	ctgcacggag	gaggatctac	ggcaaacgtc	tgctaccgct	1200
atcagactta	caggacgacg	gctctatccg	cgaggcactt	ggcttggccg	aggagcaggt	1260
ggagcagggtg	ttccgtcacg	tgtaggccat	accgaatggc	tgcgccctat	ttgatcgaac	1320
gacgtccgct	tggccgcaag	aggaaacaaa	acgtatcctc	atagcctgcc	ccccttcgtg	1380
tgcgactgtc	tggagagcct	cgaagaagta	gccgatcagc	gcaaagcatt	ttcaaaaaag	1440
caggagggtgc	ggatttcact	tacatccctt	tctcaatagc	ggggcgaatt	ggatcgatgc	1500
tctccgaaac	attttagaga	ataatacagc	atgctcagtt	atcataccga	tataccgaca	1560
gacctgccct	cctgaggcaa	gccgtcgaag	ccatccggcc	ggaagaatcc	ggcgggtgct	1620
acccgactcc	gatcggccga	gggtgatata	cgaggcgcg	aaccggttta	cgccatccgt	1680
accgcacagg	gagagcaggt	ggtgaagagc	ttccgatccc	tattgccatt	cagcgcgtgg	1740
tctactcatt	cttcgcctcc	tgcaggctgc	tcgctcttat	cgcaacgcca	tacggctggg	1800
gcgatgcggc	atcgactcc	gcgaccgtgc	ggctatgcc	tcgaacgcga	aaaagggtct	1860
cttgaggag	ctactacgtc	tgcgaaagca	tgcacgactg	tcgggatatt	ctctctccat	1920
gcaggaggtg	gaaggaggcg	aggccttgct	ccgtgcgctg	ccggattcat	cgcccgaatg	1980
caccgagcag	gcattcatca	cattgatatt	cgccgggcaa	cgtactgtat	cggacagacg	2040

agaaaggcga	gtattcgtct	acctcataga	cctgaaccgg	atgaagttct	acgacaagcc	2100
gattgtgggc	ggaaagccta	tgccaacttt	gcacgtctga	gcttttgtcc	ggcagtagca	2160
agcagcttgc	cgaatattat	gcagaggcac	agggcttgaa	tacggcggag	tggtccaagg	2220
ggtacaaaagc	gaatcggatc	ggttcttccg	cagcaagtcc	gcaagtatgc	tcgcaaggca	2280
ttggtgcgcg	aacaaaagcg	aatagccgct	ccgctttccg	tcgggcatat	atccgctatc	2340
gctcggtagc	cctatccgaa	aactcacggg	ctgcacccgt	ctcttccgta	tcgagaacga	2400
ttgtacacat	cctatcttga	agtgggcgac	ctgcgccata	caactgaaaag	gccgaaggat	2460
attcctcgcc	gaaaaacggt	caataagaaa	aaaggaaaacg	aatgaatcgt	atagcttttg	2520
atgccaaagag	aatcacatcc	aacgccacgg	gctgggcaat	tacagccgct	tcgtgggtcga	2580
agccttggcc	gcctttcctc	cgaacaccgc	tactacctct	gttctcccgg	gaagggcaat	2640
ccggcttgta	ctccgccttg	cagc				2664

(2) INFORMATION FOR SEQ ID NO:305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

tgctcaacaa	agcagccaaa	gctcgtatcg	accagtatac	caaaactgcg	gtatcggtta	60
cgaattgcta	tataccgagc	taaccattta	tttctcagtg	gacgtgtctg	ctcattcaac	120
gacaagcaag	tgcatagcgt	actggagggt	caggcgctcaa	acgcaagtct	tttgcaggag	180
ctaccgagtg	gtattctgcg	acttagcaac	cgtcaagcgt	gccatctcag	ccatcaagga	240
gggcaggata	gcttgggggc	aagcgaagtg	acgctatctg	acaaccccat	tatttgcgtc	300
ctgagcagaa	agaagccatc	gagcgcacgc	tcaagcagtt	ccgaaaggaa	ataagatgct	360
gtggaatgcc	aagatgcgtt	ttggcaaaa	gcctgtgccc	tgctgtgtgc	caaagagatg	420
gaagctgtgc	gtacgattat	ctcacgcac	gcccggtggt	agatgccagc	tggtttgagg	480
actttggtaa	accttctacg	accgtcctga	gtggcaactat	ggctcccgtg	gcaaagggtg	540
agcttcgctt	ctctcgaaaa	gcttgcttcc	caagggaaaa	agtgtgtcat	tttgctctta	600
tgcaagatat	gcgtggttcg	aaggacgtag	gaggtaattt	gacaaaaaca	acgaagtctt	660
ctctacttca	tgggatttag	tgattgggac	gaggcacacg	aagggaacaca	gaccgagctg	720
gggaaaagcc	gtattgggtca	gttgatgggt	aaggatacaa	aggcatttac	atctatcggg	780
aacacttata	acctcttcga	tcagcacaaa	gaggaggaaa	gtctttacgt	gggctatgtc	840
atgggaacaa	caagccaaaa	tcgattgggg	aantcaatca	tctggcgaca	cttacccect	900
atgcctta						908

(2) INFORMATION FOR SEQ ID NO:306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

```

cgggtgccggt atcggttggg ccatggcaca gctgtgcaag atgatacagt gcctcagatg      60
gtggccttgc ttaacgggtg cggaggggct gcttccgcct cgtggggatt ttgtctctcg      120
cagctatagg aatcaatccg aataatacac ggctgccgac tatccgatct tttcgcaagc      180
taccggtatg ctggcatgac tgctgggtatg attaccctca taggtagcct tatcgccgcc      240
ggtaactaca caaactactg cctcagagac cgggtgatatg gcctaaccac tcgagtttac      300
ctcttttgcta ctgatcctga ccgtgggatt cgtgggtgctc ggtctgtttc tatcgaaggg      360
tttccctctt tctgggctat catcgaggga cttttttctc ctctctcttc ggtttgttct      420
tctctatccg tgctgggtgga gggatatgcc tattaccatt tcgctactga actcccttag      480
cgggtgtggcc gagccattgc cggtatggct gtgggcgata ttctactcgt agccgtaggg      540
gtattgtcgg tgccagtggg ctgttgctga cgcagattat gtgccgcgca tgaaccgcaa      600
gctcatgtcc attctgatgg cttcgggagc aaaagcacac ctgccgctac aacgccgact      660
actgcttcaa aacaagaaaa aggagagttg ccgctcctgc tcctgccaaa gcagagaaga      720
cagccggtag cgtacgcgcg atgccaaagg agtcatcatc gtaccgggtt acggtatggc      780
attgctcagg cacagcacca agtaagacag ctggccgata aacttacggc taaggtaagg      840
aagttcgcta tgccatccat ccgggtggcg gtctgtatgcc cgacacatga acgtgttctt      900
gtgcgaagcc gatgtgccct atgaccaact ctcgagatgg atgccatcaa cggagacttc      960
gctcagacgg atgccgtggg gtaatcgggt ccaacgacgt aatgaaccct gctgctcgca      1020
atgctgaggt acgcctatat acggtatgcc cgtgctgaac gtggacgatg ctcccgaata      1080
atcatttgca acttcgacct gaaacccggg tacgcagggt tggacaaccg ctctatacac      1140
gagcaacggg tgtattcttc aaactcggag atgccaggaa tctctggcag agatcatgaa      1200
ggaaatggat gccacaggcg ataccagct actgctgctc ctgccaaagc agagaagaca      1260
gccggtagcg tactcgcgat gccaaaggag tcatcatcgt acccggttac ggtatggcat      1320
tgg                                     1323

```

(2) INFORMATION FOR SEQ ID NO:307

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

```

agaggctcta ccttttcatg ctacagactt ttctgccact cctgctgata cttttgccat      60
ctggttggtt gtggttttga tgcagtttct gtggaaattg tggacgacat ggtcggcaaa      120
ggactgagtg ccatcatctt gtccaagtgc ttttctacgc agccatgacc ttggttccca      180
tggcactccc gctgggggtc ttgttggcctc attgatgacc ttcgaaattt tgggcgaacg      240
cttggattgc tcgccaatgaa gtccggccgga gtaccgctct accgcatcat gaaactcttt      300
tcttctctgt ggttagccatt gcttgcgggc ttttcatctt tcaaacgac tcgatgatcca      360
gtcccaagtg aaattctaca ccatcctgtt tttgcgagaa gggcgactcc ggaactggaa      420
attcccgaag gttcttttcta catggtattc cgtgggtaca atctctttgt agccaagaaa      480
gatcgccgca ggaatgctc cagcacatga tgatctatga ccactcttc      529

```

(2) INFORMATION FOR SEQ ID NO:308

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308

```

ggatgccatc gacgaaagta ttatcggtag cgggtatcatt cgatacgaat aagcgcacgc      60
ttcatattatc cctcgccggt ggatggagtg gaatctttaa ggatacggac aagacttctg      120
ccgaccttgc cataggagac attcagacaa gctgaagccg gacgtaacac ctctccccgg      180
aggaggagta tcattagctg gaaagtccct ttcttaagcc agttgggttc ccgattcgga      240
gaaagcccaa tcctgtgttc aaaacccttg gaagtgccct atgtttctgc cgcaccgcac      300
aaaccccaa tcctcccggt ggcgtagtca ttgcagacaa gttatggccg gtacatatcc      360
cgaaaaggct gctatcgctg ccgtttatgt aagccatccg ctccggactc tactttccac      420
ctctttctcaa gagcaacaca acagaagatt gcagaagggt acaactccct ccgattggca      480
ggccggaaca ggttgaggat caatttggat aagccgttcc cgggtgaataa tgaccatata      540
tttttgccgg tatcagaatg cctaataagt acaagctcaa tcgtgctacc gttatgtaag      600
aaatccggat aaccttttct ccattaccgg taagaagttt catataacaa cggagtctct      660
ttcgaaggct acggaatacc ctgcctttgg gctatatggc tatcaaata ctggtggtaa      720
ataccgatgc tccgagatcg atatgtcgct tgtacaggag cttatgcta agggaaacgaa      780
tgtgtcccat tccccgaatt ggtcggcata tatgtctata agaacggaac attatcgga      840
cacaggatcc atccgtcaca acttattcgg tttcagacng aaagagagcg atgaatacga      900
aataaaactg ggtatataag gggatccggg ctttcgaatg ggcgttgctc aagattgaga      960
ataacaatgc tgtccgttgc tatccgtctg tt                                992

```

(2) INFORMATION FOR SEQ ID NO:309

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

```

agtgtaaaat gaaaggataa aggggataaa gggcctgctt attgcgaaag tcttcatacg      60
acaaaagcaa atcctgaaga tcgatctgcg gcgaatggga aggaagagga agggaggggc      120
ttatttgggc tgttgcccc ttgccttcga agttgtaggg gtgtattgcc gagcatcttg      180

```

cgacagaaaag	cacagagtag	ctgacagagg	agaagagatt	cttttccgct	attgccttga	240
gagacgagac	ggatcggcc	agtctgtgta	gacatgcttg	gccctttctt	catgatccat	300
ttgagtggcg	gacaaactga	ttcctgattg	aagtgcgctt	tgaagaactg	agcgacagat	360
tcattttggc	tgcaagctct	tctgccgac	ggactccaaa	tgggtgcgga	atacgaaaagc	420
acgaaaagccc	ttgttctgac	atggaatgag	gagagaaaagt	tgtctaaaaag	cggcttttctg	480
tagcgtgagc	gaagatgcag	aagagttcgc	gcagtttcag	ctcgaatatc	tcggacgaat	540
gggcattttct	gacaaatatc	ccatcacaga	gtggagccag	gagttcacat	tgtctctcgt	600
tgcaaggagg	agatgtgaac	gatttcggtt	cgtctccgca	ttctttctta	ttgcccgaag	660
agggacaaat	gccgagggcat	aaatgggcgt	gggatggaaa	taaaagcaaa	tgagcgtagc	720
cgggcctttt	tcagcctaag	tcttatacga	agattggcag	ccaaaaggac	aacattatct	780
cccgcgaattg	cgaattaccg	gattccggcc	cgacaaatac	ggccggctct	ccttgagcag	840
gaagagcaaa	gcatggctgt	ctttgggtcca	gatttccaaa	tcgctccttg	tcctaccgtg	900
tggagtccgg	gcaatccgga	cagagcagtg	gcggtcggct	gttgttcagg	atgccattcg	960
gattttcttt	gggagagaca	gctgacagat	atgaatactc	ataaggagga	tggtcggggcg	1020
ttatcttttg	aaagcgagct	attatgtgac	gagctgcctt	gtccgaggta	ttgtccgtcc	1080
gatgcttttg	cggatggagt	cgtatccgga	caactgtgct	tgtcgcttgc	ggacgaagca	1140
tcaaggagcg	gagacaaaact	tgccggccaac	cttttccgct	gaacaaggct	ccgaaaagtt	1200
cgggcactac	agccctgccc	gcaataggtt	ggtcagcgaa	ataaaaaggcg	taccaaagca	1260
atacttgaaa	atcaattggt	cagtcgacct	cctcgaatat	agtagcatac	gacctgtggc	1320
gtacgatcag	tgcggtttcg	agcgtagccg	ttcctgaagt	tacgagggct	gcttgctctc	1380
tcggagtatt	tcatacgtgc	gtccgaatac	aacgggaatg	cgtcgtcggg	caaaaatgga	1440
gtatagtcct	gtatcgtcag	tccgggtgca	cggctatgac	agggcggtag	tccgggaatt	1500
gcttcatcac	acgcagcata	caggcaaat	ctccttcaact	tcgagcaagc	gacttccaca	1560
gagaagggtta	cttgacgaga	atctttggct	gaccgctctt	gctcttcgat	cgtaggcgca	1620
tgtgttgctt	gacggcatca	tagcacggat	tycctacata	gatgacggaa	aatcgtgtcc	1680
ggcaaaaaaa	tctttctcga	aaggcaagat	gcagacatga	gatcgacgta	tttcttcaac	1740
gtccttgattc	gccaggattt	ccatcccaga	ccttaggaga	gatataatag	actatcggct	1800
tgccaagctc	ttccgtacaa	acggaagtac	gtagcgcata	ttgaagcccg	ggtagtccac	1860
tggatgacaa	cgtcgggggt	aaatgctcgc	atctgctcct	gcacatgttc	gccgcgcggc	1920
ggatgacacc	gaggtgcgtg	agtaccggaa	tgaagcccat	aaggctactt	ccctgtaatg	1980
aaagatcggg	cgtctccggg	tagcctcggc	aagaaatccc	cccccatgaa	tgcaaacacg	2040
gcttccgggt	catgctcttc	aaggcacgaa	ccagattgga	tgcattgcagg	tcgcccagag	2100
cttcgcgcgt	acgatgaaat	agcgcatacg	caataaaagaa	aatcaggga	aggggaagga	2160
gatcagacgc	tctctcttgc	aagttcctcc	aagacaggta	gataagtctc	gaagtcatat	2220
tcagtttgat	gggagatagt	gtaacgtagc	ccgctgcac	agttccaaat	caccctctat	2280
ggtgccttta	ttgatctgac	gtctgtcac	caatacacag	cattgccccg	tgcatcttcg	2340
gaagccatgt	atcgctcgaca	aaacgaccgt	ccgtaacggc	gcaaggcttt	agccccaaaag	2400
gtttcccttc	ggaacattca	tgcttagcat	cgtgtcctga	ggcaagccat	cttcaggatc	2460
atacgactga	catgcacggc	ataggccgtg	gcattgactct	atcgcaaatc	tcgctatggg	2520
cgtccagcga	aacggccaga	gccggcactc	acacacacat	ccttccatcg	cagcaccac	2580
cgtgc						2585

(2) INFORMATION FOR SEQ ID NO:310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

cagctcctcc	tgtcgtctaa	aaaaaacctg	cagcagcaca	gtatcatcac	gaaaccacga	60.
acacgaacta	ccggcaagag	ttcgtccaac	ttggcacgag	atgagtggta	agctttcctt	120

cgaagaatgg	aaagaactgt	accgccgatc	gtattctggg	agatagaact	ggaacaagcc	180
gacagacaga	tgggcgactc	ctcgaaatgc	agaaacagga	agccaaccgt	ctctttgccc	240
gattctcaca	caaaactatc	gggaatggat	tgccaagccg	gatacacgtt	cgacatgagc	300
ccggatcttt	tcaaacaaaa	ggtattcccc	ctactcgaca	atgcgaaaag	gtattcttca	360
tccttcatag	acaacttttc	ggcaggatca	gtggagagcg	tgaaatccat	gctcagcgag	420
ttttacacct	tcgaagaaga					440

(2) INFORMATION FOR SEQ ID NO:311

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

ggtgaagatg	tagtcaataa	gaacttcgcc	gcagtggatc	gaggtggcgt	gtggtagaga	60
taacggtgaa	acccgaatgg	gctgacctgc	ccgacgatcc	gtggtacgcc	acgagggaga	120
cacggacttt	gtccacaacg	tggtacgcgc	atcaacgcac	aagccggaga	cgacctcccc	180
gtatccgcctt	tcctcgacgc	gaagacggta	catgggattc	aggaacggcc	gcttccgaaa	240
aacgcgtgtg	gcagctttcg	ttcctgtatg	ggaagctgac	aactgtgtac	agtgaaccag	300
tgtgcctacg	tttgtcctca	cgctacgatt	cgctccgttcg	tcccaccaag	gaagaagagg	360
agaaaaccgg	cgtcaagggtg	ctcaaggctg	tcgaaaacag	ttcccagaca	tgggcttccg	420
cattcagggtg	aacgtaatgg	atgtctcggc	tgtagcaact	gtgtggatgt	atgtccgggc	480
aataagaatg	caaggctctg	accatgcagc	ctatcgagga	gcagtacgaa	gaacccaaaa	540
actgggataa	gatgatctcc	ggtgtgaccg	gcaaggctca	cttgggtggca	tcgcagccaa	600
tgtgaagaac	tcgcagtttg	cgacgcgcgt	ctttgagtct	cgggtgcatg	ttccggttgc	660
ggtgagactc	cctatgtgaa	gctgataccc	agctctatgg	agaccgccag	acagtggcca	720
acgctacagg	ttgttttcca	tctactctgc	ttcggctcct	tctacacctt	acacgaagaa	780
cgaggcggcg	aaggcccggc	atgggccaat	tcattgttcg	aggacaatgc	agattcggtc	840
tcggtatgca	cttggcatat	aagaagatgc	gtcgcgcgct	tggaatcttg	cagaagaagc	900
tcagcagtct	ccctgtctgtt	cggacgagct	gaagctctct	tgagagaatg	ggtagaaaag	960
cgtcaggatg	ctgtcgccag	aaagttcttg	ccgataagat	caaacctctt	gtcgtctgct	1020
gcgattgtgc	atctgcaaga	gaatcgcccg	tgctcgattcg	ttcttcatca	agcgtgcaag	1080
tggtatcatag	gtggagacgg	ttgggcatac	gatatcggtt	tcggtgggtt	gaccatgtga	1140
ttgcatccgg	tatgaatgtg	aatatcctcg	ttctcgtaca	gaggtttatt	ccaatacgga	1200
ggacagtcgt	ccaagagtac	tccgacggag	ctatagccaa	gtttgccgca	gccggtaagc	1260
gtatcaggaa	gaaaacctcg	gtatgattgc	ttgctacgta	tggctatgtc	tatgtggcac	1320
aagatctatc	ggagccaatc	cggcacagac	gctcaaagct	atccgcgaag	cgaagcctac	1380
gacgggcctt	ctatcgttat	cgcctactcg	ccctgtatct	ccacggtatc	aagagcggta	1440
tgggcaagac	tcaggccgaa	ggcaagagag	cgcttgagtgt	ggctactggc	acctctggcg	1500
ctacaatccc	gaactggaga	agagggttaag	aatccgttcc	agatggatag	caaagagccg	1560
aactggagga	attcaagaac	ttcctcaaag	gcgaagtccg	ctatgcatac	ctgtacagga	1620
attccccgag	gatgccgagc	aactcttcga	cgtctgcgtc	gaaaatccca	atggcgctat	1680
cgtaactaca	tgcgtatgag	tgcggcagac	tggctcttgc	tcttgggtatt	caggacatca	1740
aggaagaaaa	agactgcgat	cactagcgta	tctacgcctt	tataacaaaa	tcgaggctgt	1800
gcagctaagg	atattattctt	agtggcacag	cctcgattgt	ttctattcct	acccgatttc	1860
gtcctgctca	aa					1872

(2) INFORMATION FOR SEQ ID NO:312

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

ggtcttgctg	gtggatttgt	tttttaagac	tatacaagac	gtaaaataaa	aagcaccttt	60
cctcccgag	aagtgtcttt	tttcggtatt	tctatgaatc	ctaccgactg	cgatcgattt	120
atcactttta	taatggttac	atcattagac	caaattggctt	tggctaaaca	aatgtgttac	180
tattacattg	gcaaagtata	gccagccatg	catctccaca	ataccgatta	ataagtaaaa	240
ttattttag	gctacctaac	catatggcta	aatggatatg	actttcaaga	tcttccgatg	300
tgaactaaat	aagctgacag	tcaaaaaagt	taattcagct	tt		342

(2) INFORMATION FOR SEQ ID NO:313

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

aggatccccg	cttgaagcta	ttgttcgtac	atgtcgttcg	agtagtcggg	catcaagctt	60
aatccttgcg	ctttggggcgt	aaagaccaac	tcccaaaagg	acgccgcgat	cagcaataat	120
aatttctctca	tacttttaaaa	caatttaggt	cgtgattcag	agaaccacgg	ccgggttaaa	180
aaaacaaaaa	aaatcccaaa	taagattcat	ttcaagaaca	atccaagaaa	agaaaaggaa	240
tttaaggcaa	aatgctacct	tctatttcta	ttggtacttt	tctcaaggag	ttttttgcgg	300
cgcaatttag	agaaaaaatt	cgatttaaga	agagtatcgg	atttaaagaa	catgttttca	360
atataagcga	caaggggatta	acccttataa	aagctgtcaa	ttagcctttt	gccaaaatat	420
tgactgtaat	ctgaaggaga	aatgaaagag	gaaaagggtc	atgctccacc	tcattaaaag	480
tcagagtctt	taaaagtgtt	gtctaacaac	acttaaagtt	attgtgttgc	atgtatttaa	540
accgaaaagt	agagcagacc	aaggtttaag	cagtcacaga	tgaggaagga	gcggaggggga	600
aaggggaaaa	aagatcccttg	actaaggagt	cgggggttga	tgtggaagta	aagagttctc	660
gggctgtaca	ttgttcgaaa	agacaaacgc	cccttactga	tatgataggt	accattatgc	720
tgagagaaaa	gagggcacta	tatgcgaaag	agtaacc			757

(2) INFORMATION FOR SEQ ID NO:314

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

```

gactctagag gatccacg atgacatccg ctacatgcgg atcgcgctca agaggcacga      60
gcggctgctg acgaaggaga gattcctatc ggagccggtat cgtctgcaaa ggcagatcg      120
ttgcgcgtgc tcacaacaga gtggaaagct aaacgaccct acggctcatg ccgagatgct      180
tgccatcacg atggcctaga tgccataggg gggaaatacc tccgcgactg cacgctgtac      240
gtgacgtcga accctgcctg atgtgtgctg gcgcacttcg ctggacacaa atacgcgagt      300
agtgtacgga gcatccgaac ccaaagtggg ctacaggctg ttcccgatca tgcactccat      360
cccaaagtcc acgtagaagg cggatatattg gcgacgaatc ggagaatctg atgcgtagtt      420
tctttgccga acggcggtag cgagcaacac attatatatc tttgtgcaat atggcagcat      480
tcagtgtaca atattgggct gcggatctgc cctgcccaacc acacaccacc atccctcttg      540
caagtaatcg acctgcgcga caaactctac atgatcgatt gcggagaagt gtccagcgac      600
aattcagaca cgaaaagctc catttcggac gtctcatcat atcttcatca gccatctcca      660
tggcgatcac tgttttcggt ctgcccgtatt tatctccacg ctccggtctgc tggggcgtag      720
cgccaccctg catgtcatgg gccggaggga atagagcggt tcctcagccc catattggag      780
cagtctgtca ccgaatgccc tatcagggtg agatacatat gatcgatgcc tccgacatgc      840
gcttgtacat gaggacaaat ccgtcaaagt ctatagcata ccctcagcca ccgcatecct      900
gcgggtgggt acctcttcga agagaaatgc ctgcaaggca tctgaacaaa gcgggtgccg      960
agttctacaa tattccgctt ccgaatatcc cctcatcata gaaggatccg attacacgac      1020
accgatggc ggatcatccc caaccgacac ctcacgaccc cgggtacacc acccagacat      1080
atgcttactg ctcgacacg gagttttgtc cctccatcgt cctatttttc aggtgtgga      1140
tttgctctac catgaagcta cttttatgga ggaggacggg caagagccaa agagactttc      1200
cacagtacag ccaaagaagc cgccgaatag cagcacaggc aggagcaaaa cgcctcctca      1260
tcgggcatta ctccgcagat acaaggacgt ccaaggtttg ctggaagaag ctcaaagcgt      1320
atta

```

(2) INFORMATION FOR SEQ ID NO:315

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1803 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

```

aatgcatcca gatttagcgt aaaaatctca ttcttacctt gtattcatta accgcttctt      60
aggctcctat agaaatagtt gatctttcta agtgcttctc tagtgttttc gcaggatatat      120
aaaaagaata tccataacaa gcacagctgt atcaaaaataa tcctcctctt cttttccatc      180
tctcagggat atgataaaga gccaaacccc ttggattgtc tcgcacccaaa gttatggagc      240
ataaaaagtt ggtgatgaga ttgttcacct cttctcttag tccagcattc tgaagcgtat      300
taccctttca actggagtat tgacaaatgt tgctaattgt acctctgcca gttttcttca      360
aatattcttt ttttattttt tatttgggtc ggggtgtcacc atgctttata ttaggttctg      420
athtagcctt gtcctcatta gaaagtaaga agtcaagggt agcatctcaa cctcttgcac      480
tcctaacttc cttgtgagag gctttttaat ttatctattt ctttcgggtt actactcatg      540
gcaagaaata ctgcactttc gcatcagggc ttagctttaa agagagttgt agttcaaggc      600
tccttcttgt ccgggggatga gacaaagctc caattttcac cttattccc tttctttttc      660
tcttctcat acactctgag agcctctcat ctttattttg aaagtattct atcccccttt      720
cgataaagtt ttttttggtg tcgaagcagt ttctcttaca aacctcttgc ctatctgtgt      780
caagtaaaact tgctgagctt cggtttgacc tcggaggcgc gcagcgttgc cccgcatccc      840
tggcctggaa gtggatgatg ggcgtatgct gttccaattc aattccaact tatacatcgt      900
gggtctatgct ttttggtttg tattgtcctt aaatagactt ccatgagtc cttattgggtc      960
tcaagcaacg attcggagaa ctctgccatt tattcaaalc ctttgttctt tctcgttcta     1020
attcgaacat gttttgtctc gtaattcctc ctttttgatt tttaatttgt agctccatta     1080
atggctacga caataattgt ggcagtggtc actaccacaa aacagagaag attaaagttt     1140
ctattttccat gctattttct gtatttgaaa taatgtttat tgggaagtag aggcagatgg     1200
caaatactat aagcgtaata atatcccacc caatagcccc catgtcgagg gacaagggtc     1260
cccgatattg aagagcgagt gatgcacact ttttcaacaa aagtgttgat gcctaaaaag     1320
ccacaagtaa cgtgataggc aggtagaggt tggcagtttt gttgagtaca cctgttcttc     1380
aagggtctgt tagttaaaga gttcgcccat ctcttcgtcg aggccttagc atctttctcg     1440
atgtttatct tgctttgaag catatcgtag tttctatgcc ctgtatttga ggggtaacct     1500
ctcgaaagta ggtctcatta gaaagcggat atagttgccg tacagctctt tgacctgctt     1560
ttcggttttc tctttgtctt cttgtccaat atcagttgtg tgatagaggc tatttcgtgc     1620
tgaagcgtag tatggtggag cgttgacaaa ggctcaatgt tgccattggt agtacatagt     1680
tgtaatatgg tctcccataa gttcccaacc tgaaaaccta cgagagagtc tttggttaga     1740
cgaagagag taccttctcc cgacatcttg cataggttgt tctcctgaca tctccctttt     1800
gta

```

(2) INFORMATION FOR SEQ ID NO:316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

```

gatagagata ctcttgagaa ggattgattt ggaagagggt ggccgaagct ttccggctat      60
tttgccggag ctgaacggta ccacatagtt gatacctctc gatctgcata gcgtgatata      120
gccgctatct ggtcattgga ggctcctcga taataagggt acagtcattg agctcaccac      180
tgtggatcac atcctcgcat cagacgtatt cgatacatcg taaacgcgca aagtcaccga      240
cactctctct tcttcagacg attcagcccc atcagcatak cctcgtagaa ttcccatatc      300
gctgggtatt gcccgataga gggagcatca gtccgacctc tatgcctccg actgcgatgt      360
cgtaggggag gaagccatag ccgtggaatc gcgcccggga tgcgtagttt gtggcctgca      420
gggaagttgg tagcagatat accgatttgg ctttcatcag ttctcttctg ctcaatccat      480
attttctgct atggagtaga gcgtttcctg tggccggata atgtgttcgc tcggatgaca      540
gcggcggata ttttgctatt ggcccggacc ggtttggacg gaatgagcga gtctgccctt      600
ccttgatccc ttgtctggcc gaagggttga gcgtataata tcatcctccg acagaccgta      660

```


ttggcgcgcc	agtccataaa	cgggtcttttg	gcttgcaacta	cgtgtacttt	tgteectgcta	720
cgcgctctgac	cggatccgat	actacggaca	tcagcacaca	cgtaatcagc	aggatataaa	780
gacctttatc	cggaatacat	gatctgtcat	ggtttccccc	tttctttttt	agtctattta	840
ttattaggtg	agatggggca	aaggttaacaa	taacgactct	gcggcaaatg	gttatcctct	900
ttgcaatctc	catataagag	aactacgtgg	gttaatgtct	tcgttataaa	tcaagccatt	960
tcaatatcga	aagacatggt	gcttaaggtt	atcccggatt	ggtcattgga	aaagtaaggc	1020
ctaacgacaa	ttccccgggt	ttatcgactt	cagtcgggtg	ctattgattt	gggttggtgag	1080
cattcttgcg	cgtgagcatc	ttcgagtcgg	tgtagatgtc	cgtacttctg	cgagctgcag	1140
tattgcaaag	gtgtgatgga	agcagcaata	agcaattgct	tctgaatgcc	cgaagctgca	1200
atcgaatacc	ttagaaggcg	atgcgcataa	cgaggccgga	aactccgtat	ataaggcgat	1260
aaattttccgt	atatagaaaa	tttattttcg	tatatacaca	aattttatttc	cgtatatacg	1320
aaaaaatattt	ccgcataatgc	ggaaatctcg	ctaccttctg	ggtgcgataa	aaagcaatca	1380
aatcgagata	gtaaagtgtt	taataaccag	ataattaagt	tattatgatt	aagattaaag	1440
caatcgaaag	aaaggccgga	ttcggcaaga	cagcaaacgc	ttggtaccct	gcaatcactg	1500
cattcgatgt	gaag					1514

(2) INFORMATION FOR SEQ ID NO:317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

ggatccccgg	gaaaaccgct	gtcattgtag	taggagcagg	tccggcaggc	ttttcgcagc	60
actccggctc	atcgagcttg	gtctgaggcc	tattattcgg	agcgaggtaa	gtccgtacac	120
gaaagaagag	cagacatcgc	tcgcattcca	aagaggggca	cgtagacccc	gaatccaatt	180
acggatttgg	cgaaggggtg	ccggagcttt	ttctgacggt	aaattatata	cacgtagtaa	240
gaagccggag	atataaccaa	aatactacgt	attctctgca	aacacggagc	acagcttcta	300
tcctgatcga	tgcgcatcca	catatcggca	ccgatcggct	accaaagtga	tagaaaacat	360
tcggcaccaa	atattggcag	ccggaggaga	agtcacttca	gttgccgaat	ggaaagcctg	420
atcatacata	acggtcaagt	ctgggagcaa	gagacaacaa	ggggcgtgaa	tactgcggtc	480
ctgttatcct	gcaacgggac	attccgcacg	cgacatctat	cgctatcttc	accgaaacgc	540
attcgaatgg	aagcaaaagg	aacagctgtc	ggtgtccggc	tggagcatcg	cagcntctga	600
tcgaccaact	gcgctaccac	aacccc				626

(2) INFORMATION FOR SEQ ID NO:318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

```

gccacatagt tgtgaaaagc ccggacaaag agcaccagcg aaagcacgta accaccattc      60
ccgcaagaaa ccatgcgcta ccgaacttga acgggacgaa acggaaagca ccaatatggc      120
aatttgcagg attgtactga cagaggcttc gccttgtctt tggctcgtga ccacgaggta      180
tccaccgcgc gctttctccc tcacggaaga ttgccatata tataaactgt atcagcacca      240
tgccgacgaa ggtatccatg cgttcagcca tccggcttgc aacgtggtga aaaagaaaaa      300
tactcatag tcatcgggaa tgatattgtt tttttaatgt gatagcgata cggcaaaaat      360
cagggtatac accagattgt tccatccgcc cgtatcaaca gaagaaacgg ttgcggcagc      420
gttttccaaa ggaaattgag cagatggtga tcaacggtgt tgcgaaaact atccaacgag      480
gaaaagaagt tgcttttgca gcaccaatac agaaaagagc aaccatccga ttcccattag      540
aaaaaagaaa aaccgcocaa ccagccggca taggagagaa aatggtcgtg atttcgggat      600
gtccctgcga cgatacgatg ccgaaagccg ggaagaagca tgataagcac ctccataaat      660
tatacttacg gatagggaag caagcaccag caggctgttt ttctgcgcgc tttcttaacc      720
ctgagaaaca aatggagaat ccgatgatgt acagaaccgc cgccaacggg cctattatcc      780
ctccgcaatg agacgctcca agggcactgt gcccatagaa agcagcagat cttttcccgga      840
tcgggaatgg gttgtgtcgt aaaatacagc aacatgtcgc cgtatacatc agcaggctac      900
ctgccactcc cacataccct gtcaatctga gttcttatcc ataccctttt cttattattt      960
gagttcgcaa aatatataaa tagaatatcg tttgcaatcg ccaatagtgg ctattttcac      1020
agcccggaac cctattttctt agggtttgtc gattcgtcaa tcagtaactc atatcctcaa      1080
attcaacctt taataatctg tttggcattg gctctctgcc ggattgca      1128

```

(2) INFORMATION FOR SEQ ID NO:319

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

```

aactccttta tagcggcatg atccggtgtc tgaccagatt gcgccggaac gcggtatcct      60
cattggaaga gtcccgtaag ataggtgatt ttttggtcag cagataagcc tctatctcat      120
cccgtgtggc atccagcagg gggcgagat accatcgctc cgcttatagg gcatcccgca      180
caggccgctg attcccttcc tcgacagaga ttcagcacca tggtttcggc attatcgctg      240
gcatgtgcgc caccgccacg tatcagatag ccagttcttt ccgcaactgt ccgaccattc      300
gtaacgcagt tctcgagcag ccatctcgat cgaaatcgac cgccgcgagc ataacgaacc      360
gtgtcgaagt cgatccgatg gagcggaaca tcagatctcg gcataggcgc tccacgaaaag      420
ctgcatactc atcgctctct accctcggag gtgaaaattg cagtgtgccg ccaccgtctc      480
ataccccaat cgcgcaatac cgagagcaga gccaccgagt cggcacctcc gctgagagca      540
ccagtacgag gcggtctcct tctcggaaga gtttcgctc tctgatcgcg ttcggacacg      600
gtttgtcagg gaaatcttca tcttgttgtg aatatatagg gggaaaatat cggcccggcc      660
atcctgccga tggaaaaaat ttcttgaaat gaagaggctc tttatccgaa taagccgaat      720
gctgccataa aacaagagag aactctcgtc ctctctcatc agtctcgccg gcatctccga      780
agaggccgaa cttatctctg gaaaacttat gcacctgtga acccgaaagca tcgccggaag      840
cgaaaaccgc cttacaccgc ctctactctt tggggagctt tagttcccat ttcgggatcg      900
accatgattc gtccgcagta ttcgcagacg agattttttt ccgaagcttg acgtccagct      960

```

gcttctgagg	aggaatcttg	tgaagcaacc	gccgcaagca	tcacgctcta	cgggcaccac	1020
ggccaagcct	tgtgcgcagc	ctttctgatg	cgcttgaaag	ccgtcagcag	gcgcggttga	1080
tcttggcttc	gagcttcttc	gcctttttcg	gcagttttct	ttcctctgct	tagtctcggc	1140
aatgatggta	tccagttcgc	cgcgtttttc	ggccaaacct	cgctatgctc	ttccagcacc	1200
tctttcagag	tagctatata	ggtctgcgct	gttggatttc	gacgttgtat	tccttgatct	1260
tcttttcaga	cagtggatct	ccagctcctg	aaattcgatc	tctttggaga	gattgtcgaa	1320
ctccgattgt	tgcgcacctc	gtcgcagctgt	tttttatatt	tctccagcag	cgcttggctg	1380
tactgatctt	ttccttttcg	gtggttacag	cctgattgag	cgcttggatc	cggctgtgaa	1440
gttctccaaa	cgagtctgca	ttccggcgat	tcgtcttcca	gacctgttac	ttccagcggc	1500
aattcgccac	ggagagtctg	atcttatcta	tttcagagag	ggtattttgc	agcttgtctc	1560
gtgctgccat	ttttcctcta	cgctctgttc	gttctcaacg	atgatctttt	ctttagcatg	1620
atgctcaatt	aactaactac	aaatagttaa	ccggattggg	tgcaacgatg	atgtgtgggt	1680
ggcaaaggta	gggaatttct	gcgatattat	gcgcaaaata	gtcattagc	cacctcttcg	1740
ctctcgtaat	gaccgatcgt	aaccgcagca	gatgctcccc	tgcatcgaag	aagtcgttgt	1800
acttcgcctc	cccgtcagga	agaggtctgc	accctcctgt	gtgcacgcc	gccacatgaa	1860
agaccgctac	cgccgcatac	agccatccgc	ctcaacggcc	gttccctcca	accgaatggg	1920
acaggacctt	cagaccgaat	acctccttga	tgtgcagcag	atctcccgtc	cgcttatggg	1980
cgaaggcaga	tccccacta	ttccgctcgc	gccgagggat	gatcgttggc	cagcgggatc	2040
aggctgacag	ccggcagccg	tacggatgag	ccgcgtgcaa	agcctgcagc	acagtaccct	2100
gcctgtagcc	ggcagtacga	ggctgatccg	ctctccgcc	tcatggtgca	attcgctatc	2160
gctcccacaa	agggattggc	accctcggca	gctctgaaag	ttccttgccg	gcatggctga	2220
acgaacagca	atcgtaattg	cccaaacggc	ctgcccggcc	tgccacaaag	cctgcctcac	2280
ggcatcgcca	tactccgtgg	ggagaagggt	accagttcta	agagcttgcc	ttgcagcggc	2340
tccagcggtc	gctattcagc	aagccgaagc	gttcggccag	cagcgcattc	agtccttgcg	2400
ggcgttgctc	gcattgggat	gagccgcata	tagcaccaga	ccgtgccgta	ggccagctcc	2460
acgcacgcgt	ccacgtagga	gctgccggtc	aatcgcttgg	cggtttgaaa	agaatcggat	2520
ggtgggcaat	gacgagattg	catcccagcg	aatggcctcc	tccaataacc	cttcggtaac	2580
atccacacag	aggaggggac	cgttgcctcc	cgcttggtgt	cgccacctg	cacgccacta	2640
ttgtcaagct	ctcttgataa	gccctcgggc	agaccgcctc	gatagcctct	ataattcctg	2700
aatgatcatc	ttcgagtgcg	agccaagagg	ctctgtttgg	tttcttgctc		2750

(2) INFORMATION FOR SEQ ID NO:320 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

ccgatcgaat	gcctcttcac	gatggacgaa	agagacgggt	atgaccggtc	gatgaaccta	60
aagcccggat	ttttcaatgn	aaagatcctg	ctcaacctga	tcagcgaagac	gaaggagagc	120
tcttcatcgg	gtgcgcggga	ggtatggaac	catggtcgaa	tttgcttacg	aaaagcgcgga	180
agcgacagac	gactattcta	tttcaaggta	aaggctcagc	gtctcaaagg	cggtcactcc	240
ggagggagat	tcacatcggt	ctcggaatg	ccaacaagat	cctgactcgc	tatcctatgc	300
tcttgagcac	gaattggatt	ggaagctctg	ctctttccag	ggagaaacct	gcacaatgcc	360
attccgcgcg	aagctcatgc	cgttatcggc	ctaaggctga	tcagaaagaa	cgtgcacgag	420
ttatcttgaa	cgaactcgct	gtgcagtggg	ggacgaactc	aagcgagtag	atccgggtgt	480
gaagctcgaa	tgaaatcggt	aggaaagcct	gcatatcgta	tcgattgtga	cacgaagcgc	540
gtcttgttgc	cgccctgtat	gcttgccctc	acggcgtcta	cggtatgacc	atgacatcga	600
aggtttgggt	gaaacgtctt	caaacttggc	ttccgtgaga	tgaaagaaga	tgataagatc	660
tacgtggaga	ccagccaaag	aagctcacat	cgtctcttat	cagcgatata	gccaataacag	720
tggcatccgt	attcggcttg	ccgatgctaa	aatcagcttc	cgcgatccgt	accccggtatg	780

gaaaccaatc	ccgattcgcc	gattttgaaa	gcggcatctg	agtcgtatga	gcgattttcg	840
gtcgtaaacc	tgctataaaa	gcaatccacg	cagggtttgga	gttggctctc	tcttgataa	900
atacccctat	ctcgatatgg	tttcattcgg	cctaccctcc	gagatgtgca	ctctcccgt	960
gagaagatcg	aatcaagac	gttc				984

(2) INFORMATION FOR SEQ ID NO:321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

gtagcctctc	tcattcaatt	tatgagctaa	atccaaaatc	aaatcacaac	tttatcaggc	60
atgatacgag	agaaaaagac	aagacgcaac	accttgagg	agtatagga	gtatgacaat	120
gcaagggaga	aaacagagat	atgtcctgaa	gttaggcata	acttttacat	tctctacacc	180
ttgccacac	aaagcacttt	cattgcttgc	ccttcgacca	aaagatattg	caaacttttc	240
aaaactcaac	tgggtatctt	cccttctcaa	cttctaaatg	aagatcccc	cctataccca	300
aagaacaatc	ttacgcttag	gaaagacaac	tttcaaaata	cgggcaacca	atacacattg	360
ccataactag	ttgagaaaat	tatgggagta	ttggatttat	taataagata	aaaggcaatt	420
tccacaatcg	ccaaggctta	gacgactccg	ataggtatca	actataatta	gtttgncaac	480
aaagtcctta	gccttttcgt	taggaa				506

(2) INFORMATION FOR SEQ ID NO:322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

aaacgggttg	ccaagtgact	gattgcccgt	ctatggtata	ggaatagcga	gttctcccgt	60
ggctttgatg	aactgagaga	aggggacgcc	gacgaaatct	tggtgtcgct	gtacttcttg	120
ccggctgcca	gatagatcag	attcagggat	tgctgcctc	ggatagtcgg	aattgcatcc	180
aaagatgatg	aggactttct	ctgaaacgga	tttggtgaac	gtaatagatat	accccatattg	240
agcaagaact	gactctgaag	gctgagcagc	aggggcggat	tgttcgccgt	aatgcctgga	300

aagtttctgt	ctgatgcccc	aggaggttgt	agttgagctt	gaggggaaaa	tagcatgccg	360
gtgttccttg	gagggctgaa	attcgtaggt	ggcgaaaagc	cgaaagagta	catgctaaag	420
tagtgtgccc	tgttcagcgc	gtggcagaag	cctgaaaagt	cgtagtcgtg	gggtagtaat	480
agtatttatc	agcagaccgg	gaaatacaat	cgagggaaac	gagaggttca	cggccgtatc	540
atgttgtacg	aatttatatc	gatcagccga	ttgctgctat	tttcgggaga	ttgccggtct	600
cccactcata	cgatccaccg	atattccaag	aaagattttct	cctccgccga	atacattgcg	660
ccgagcaaga	gcaaaattca	gtccggaccg	atgaagtcac	tgcttttgct	cgtgaacaag	720
gtctctaata	atgcacccaa	ggtttgcga	gggtgggttag	cagtcgcaca	tccaaaaggc	780
cggaatggaa	tcgcgttgca	aaaaattgag	atcgataacg	gagaaggctc	ccaacgagcc	840
aaggatttgc	gtgtcgtctc	atcgtctttc	tgccgataca	gatgccggag	aaagaaacga	900
aagcgtttg						909

(2) INFORMATION FOR SEQ ID NO:323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

aggcagctcc	ggctgattct	acgataatac	taacncagat	aataccgaac	gcaatgagta	60
agaatttgag	tgttattata	aacggcatta	tcaaggagac	ccgacattcg	tcctcctcct	120
cggtatgtgt	cctacgttgg	ccacgacacg	tcggccatca	acggtatgag	tatgggactg	180
gccaccatgt	ttgtatgac	tgctccaaca	tggtagtatc	cttgggtcaag	aatctcatcc	240
ccgattgggt	cgatcccg	cttttattgt	catcattgca	ggtttcgtga	cgatttgag	300
atgcttatca	aggcttatat	gccggatttg	gacaagagtc	tcgtatcttc	atccactga	360
tcgtggtgaa	ctgtatcgta	ctcggtcgtg	ctaagccgtt	gcacgaaaa	aaggtctgct	420
acactccatg	ttcgacggta	tggtatcgga	ttgggcttta	ccctcagttt	gactgttctc	480
ggtattgtcc	tgagcttttg	ggtagcggta	agcttttcga	ctttgcagtt	ttcaatgaac	540
ctatggagca	ttgatcttcg	tattggcacc	cggagctttc	atcgctttgg	ctacctgatt	600
gccttgggtg	acaaaatgaa	gaaaaaagca	taactcatta	agtaattggc	atcattatgg	660
aatttttcat	gttattcata	gcggcggttt	cgtaataaac	gtcgtgctgt	cgcagttcct	720
cggatatatg	ccatttttagg	cgtatcgaa	aaggtagaca	cctcaatcgg	tatgggtgca	780
gccggacatt	cggtattgca	ctggctacgt	tggttacctt	cctgattcag	aagtcgtttt	840
ggatcggttc	ggattgggct	ttatgcagac	cattgcattt	atttgggtcat	tgccgccttg	900
gtgcagatgg	tgagatcat	actcaagaaa	gatctcctcc	cctctatcag	gcactgggtg	960
tattcttgcc	cttgattacg	cgaactgctg	tgtgctcgtt	gtggctatct	tggttatcca	1020
gaaggattaa	ccctgtccca	gagcttcgtc	tatgcaatat	ccacggctat	cggtttccact	1080
tggaattggg	tactttcgca	ggtattcgag	agcaactcga	tatgaccatc	tcccaaaagc	1140
tatgaaggga	ataccttcgg	cactcttggc	tgccgatat	tggctatggc	tttcatgggc	1200
ttcagcggta	tcgcctaacg	agtaagaaca	ataaataagag	agaggggtatg	cccatcgcg	1260
tgcataccct	ctctgttttt	tattgtgact	tagccgtatg	gaaaatcttc	ccgaactatc	1320
tgcaaatctt	tttcgttcag	ttacgacaga	tgcatcccg	ttctaaaaga	tttaccgatc	1380
cgaagagaaa	aagacagagg	cttggaggat	tacagacgag	gtcgattact	tggtactctg	1440
tttcgggaag	ccttcgttca	tcacagtcct	taagaaccgt	ctccatcgga	caaaaataagc	1500
atatagtcca	caccggggat	tcggcggcaa	tagcaggcac	acgctccgaa	ccgaccacca	1560
taaaagtata	gccaaggcat	cagccgtcat	acaatcggga	gcaatgactg	tggcactagc	1620
acatccgtct	gcacaggata	gccgctaagc	ggatcgatcg	tatgtgatac	ttcttcccat	1680
cccgaacata	gaaattccgg	tagttgccc	atgtcccaag	ccccctttcc	cactaagctc	1740
tacgacgagt	tcgaactcct	gcacgccaag	cccagactgt	catcctgcgg	tttacttaca	1800
cctatgcgcc	aagcttgctt	tgaggattga	ggccattgaa	agcaacctct	ccaccgatct	1860
ctccatatag	tcccgatcc	catgagcagc	caaggcttcg	cccaccagat	cgaagcatat	1920

cctttggcga	tggaagaggt	gttcagcgta	gtgcgcggat	atccttaaca	accgtctcgc	1980
catccaatcg	taccctccgg	taaccgacaa	ggccctgatg	ctgtcgatca	actgtgcagt	2040
cacgtcctct	ttatgttcaa	accgaaaccc	caagcattga	tcagcggaga	gcaagtaata	2100
tcgtaaggcc	gccggaacg	gctgcaatct	cctgcgcccg	acgaaatacc	cggcggacat	2160
actgtcagtc	ctgaccggaa	gattccgatt	cactccggca	atgatctggt	actgtcgaac	2220
ggattaaggg	aatgattgaa	agctctgaat	acgcatccac	tcgctgcgaa	tgatctgcct	2280
ctcccttata	tttgatatga	taaaggatatg	gaatatctcc	ccctgcaata	ccgtataggc	2340
aggtgctttc	cgcaagaaaa	aaaggccgca	ccgagaatga	tcatccccgg	aacggccgct	2400
aacctgacca	acgtttcata	atttctcgaa	gctgactacc	tcttcaatgg	tttgcgattg	2460
aaagcctcac	gcggagggtac	ggtcggatcg	ccatagccgg	agccaatatg	gaaacagggtg	2520
tcatgtgcga	agggatgtcg	aagatctcga	acaaagagct	tgatcgaaaag	cacagaccca	2580
cgtacatcca	agtcccaact	atgtgcttcc	agcatcatat	aagtcatggc	gatagaggta	2640
tcgatgtctac	caaategcgg	gtaccga				2667

(2) INFORMATION FOR SEQ ID NO:324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

ggggaaaaacg	actctgacgg	aaaaattctt	gctcttcgga	ggcgccatta	tgtggcagga	60
gcggtcaaaa	gcaacaagat	aaagaaaaacg	gctaccanga	ctggatggag	atagagcgtc	120
agcgtggtat	atcgggtggca	acttcgcgat	gggattcaac	tacaaggact	ataaaatcaa	180
catcctcgat	acgcccgtca	ccaagatttt	gcggaagata	ctttccgtac	gcttactgct	240
gtggaagtgt	gatcatcgtn	atcgactgcg	ccaagggggt	cgagacgcag	acnccaagct	300
gatggaagtt	tgctgatatgc	gcaagactcc	cgttatcgtc	ttctcaataa	gctggaccgt	360
nagggacagg	atcccttcga	tctgctggac	gagtggagga	agagcttcag	atncgngtgc	420
nggcactc						428

(2) INFORMATION FOR SEQ ID NO:325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

gcgaataggc	ctgacaacac	cgtagccata	taggctatca	gcacggtgaa	agaagcatcc	60
tgccggcacc	tttcccgatg	tcggcaatag	ccaccgtccc	aatccgagga	taatcagcgg	120
aatggagaag	ccgagcagtt	cgctgaaaga	gcattgaacg	tgacgaagat	ccgaataaac	180
gggaagctga	agaggtgccg	aagccgatac	cgaggacaat	ggccaatatg	atcttgggca	240
agaggcgatc	cgtagttttac	gcataatggtt	gggggttgct	tgatcaagaa	gattttttgtt	300
ggaaatatag	cggaagttag	catccagcag	acgacgggca	gcgcgaaact	cctggcacga	360
tcttccaaca	cgtctcttcg	actccggtat	gactctg			397

(2) INFORMATION FOR SEQ ID NO:326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

ggtttctgta	ccaaaagtag	tccattctta	tcgaatagag	ccatcggcac	gcgaaaggcg	60
aatcaagaaa	caggaaaagg	gtacaccccg	gattcttccg	cattataatc	caaggtaata	120
caggatgcac	gtctatacgc	ccatatactt	gccatcgaca	ttgcggatgg	aattatgtac	180
ttgtttctca	taagccttca	ttcttttagg	atagatttaa	caatatgcta	taaagacata	240
aaagtgtgtg	cctattcata	atttacgaac	ggcaattcgt	caaaattccc	caccttgccc	300
tgactatca	gggaaagaac	gatatgaaa	gactgataac	aacggagcag	cctttctact	360
ggctgctaca	ctctctgcct	gcaacggcaa	tacacaagtg	aaacccaagg	cgatcggact	420
gaacaggccg	aaacggtaca	accgatctct	tctcgccga	ctcggttac	accttcgtgc	480
agcgtcaggt	aacttttggc	cctcgcatcc	ccggcacagc	tccgcatcgt	gcctgtggaa	540
ttggtcgtg	gccacgcttc	gcagctttgg	tgccgcggtg	caagagcaac	agccgaaatc	600
aaagcgcatg	atggcaccat	gctgcccattg	cgcaatacat	agcctcatac	cgccccgaag	660
ccaccgggcg	tatgctactg	atggctactg	ggatacgcgg	ccggtctgcg	atcaggatgc	720
caaccccgct	atgcaacaga	gaccttcgac	ggtgcggacg	atggcggcag	cggaattagg	780
cgttttattg	gagatagcgc	gctatctggg	acaacagaaa	gattttgggca	tggcatcgat	840
attg						844

(2) INFORMATION FOR SEQ ID NO:327

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

```

gccgagaaaag agcaaatgat tttttcgagc gtaaaacgga cgaattgcct tcgtgttttc      60
cggaaaaaatg gaaccataaa tttttcggtt tggtttgaaa cttttttctt ccggcgcggg      120
aagtgaaaaaa ttctcgcgcc acgtttttcg ttccgtctga aacaattttt tggaacgtaa      180
aaactcgaag agggcggggc ggatcaaaaag aaaataagtc cgaatcggag gaaaaaagca      240
gcaagcaatg caggttcaaa ggcaagtgtg gtcgtttttc aggttctcc atttctgtat      300
aacttcogtc taatcccgat cttggcagca gtatcggtgg agtgggactt tcggacaatt      360
atcaacggtg ctcaattcat tatctttgca gcatttagat acgaaaaaat aatctgaaca      420
ataatggata gacaattcaa ggaactotta ttaactacggc cctcccgtat gccaacgggc      480
ctgtacatat ggacacttgg ccggtgtcta cgttcgggcc gatatatatg caccgtatcg      540
cgattgcgtg gcagagactg cctgctgatc ggcggttcgg acgaacacgt gtacccatcg      600
ccctgaaagc caaagccgag ggatgcactc cgcaggagtg gtagaccgat accacgaact      660
gatcaagccg ttcgttcgaa gggctgggtat ctcttcgaca tatacttaac gtaccacaag      720
cga                                              723

```

(2) INFORMATION FOR SEQ ID NO:328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...3294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

```

ggcacatcta tctcttccag caaatcctca gctacgggta aaaggagttt tttccttcgg      60
gcgtagttat agacaaaagg acattgagcg tactctcgcc acatcatcga ttgtccctac      120
gaaacaacct tctcggtcga ataccgtaag ccgatgaaat gttcccagggt gaattcgata      180
gaatcagtat cgaagtctgt cgttccataa agagagacac accggtgtac tgctccatct      240
cctcctgctt tcaataaccgg caaagcggaa ncaaagtaat atcatcggtt ttctacggta      300
gccataaaga cggaacggaa ccggcaatgc atccagctcg aaaagagaaa caaccgctct      360
tcttctcaa agagcgctact caaatcggct gtagacgagc gttgcactct ccctgaacgc      420
catgcggctt acccagcaca cgatatgctc caatgaatcc aaatcgatca taaagcatca      480
aaggcgagag tacgtgcgcc gatagcgttg aggcgagtat ctatggattg gtaacccctt      540
cgatctgttc tacgttgttg atgatacttg ttccttctgc actcatagtg caataaggag      600
ggctataccg gcacgaatat cgggtgaaac catagttcag ctcgcaaggg aacacgtttg      660
tccaaaccga tgatcgtagc acgatggggt cgcaaaggat aatctgtgct cccatatcga      720
ttagcttatc gacaagaaga gacggcttcc aaacatcttc tggtgaaatca gtacactgcc      780
tttccttgag ttgccaccac gagaaagacg ctgagcaagt ccggagtaag accggccaag      840
gagcatctgc aatagtcagt atggatccgt ccataaacgt cttatctcat aatgttcttg      900
cttaggaata aacagatcgt cgccttgctg cccacagcaa tccccaaacg gcggaaagat      960
gcaagggatg ataccagat aggcacgctg acatccttga tcaaaagctc ggaagcggtc      1020
atcgcagcct tccgatgaag ctaccactt cgatcatatc gggcaacatc ttatgctcca      1080
gccatgtaag ctctgtactc cttcgatagc aagcagatta gagccgaacc ctctatatgc      1140
gccccatac taagcagcat cttgcaaagt tgctgcgata tggctcacag gcagcattat      1200
aaatagtggg aataccatca gcaagacagc tgccattagg atattggcag taccggtcac      1260
agaagcttcg tccacagcat ataagtgcg gaaagccggc ttgagtcgaa ttcataggct      1320
tgctatcgga atggtagtgc cagtgggcac ntaatgcctg aatacctaca agtgagtatc      1380

```


taacctgtg	cgccgatct	tatctcccc	tggtttcggg	aaatggcgta	accgaagcga	1440
ctgatcagtg	gcccacaag	caagaccgaa	cgcgcaaggc	gcgactcttt	tcgagaaaact	1500
gctcgctttt	gatatagtca	gattcacatt	atcagcttgg	aaaacacaag	tatcgcggtt	1560
gggtctttta	ccttaacccc	catgtttcga	agcagggtcg	tcagggttgt	cacatccata	1620
tatcggggat	gttacgcacc	acaacctctt	gatcggtcaa	tagcggtcag	agatgatctg	1680
caaagcttcg	ttttttgcac	cctggacgag	aatctaccct	tgagactgtt	gcccccttct	1740
attacgttaag	atgccataga	gatatgtgtt	ttatatgtct	gtatgattat	ttccgcccga	1800
ataccttggt	ccgttggtgt	tgttattgtc	cttccgatcc	gaagcattcg	gtatcgtcag	1860
atacaactct	cctccgtcag	ctctatgcgc	ccttcggaca	gttcgtacaa	accttgaata	1920
tcttgtagtc	atccaccgta	tctttgttcc	atgtcagata	gaacgcttca	tctggttggc	1980
gatgagcagc	tccagcgcac	aacgctcttt	ccctgctcca	tggcacaagc	cttgaggatc	2040
atttctctga	tgagatggcg	tagtgccgat	atacgaatgt	gttgcccgag	tagcttacag	2100
cttttaggttc	cgttcgagca	gctccggact	gatgatctcc	atcggataat	cgatatcaac	2160
ttgaatccgg	acataatagc	cagatgatcc	caaagaatat	gcttgtctca	ctgttttccc	2220
gccgttcggg	aaacatgttt	cccatgattg	taatatcggt	tgtgcacagc	gattccgttc	2280
gtcacgatca	ccgattgtca	tgcataaatt	accatgtttt	ggatattcct	gccatattcc	2340
ggaatagcca	aagttccatt	ttactattat	aattcatcct	ctgatgtttg	taatttctaa	2400
cctcttttcag	tcggcctgcc	attgctgctg	attctgtttc	atagccgggc	tgttcagcaa	2460
agcaaacata	ttgttcttat	aaccttcgac	ccccggttgt	cgaaaggatt	cacaccagc	2520
atatagccac	tgacgcctac	cgttttctaa	agaaatagaa	caactgccct	atataataag	2580
catccaattg	cggcaaatga	tgcgatatatt	aggtaactcc	ccatctacat	gagccagccg	2640
ggtaccaatt	cagccatctt	atttacttcg	tctacacgct	ttccggccag	aaagtaagcc	2700
catccaaatc	cgccgagtcg	gaaggaatcg	tcaagcatgt	atctgatttt	ctacggaaat	2760
cactgtctcg	aatatcgtac	gttcgccttc	ctgatccatt	gtcccatgga	atggaggctg	2820
gtagtcagat	ccacagttgc	cggaagatcc	ccttctcctc	tttgccctcg	ctctcaccga	2880
aaagctgctt	caccactctc	cgatatagtg	cattttggga	tggaaattgg	ccagtatctc	2940
atcttctttc	cttcggcata	caaagcattg	cgagctgccg	cgtatcgtaa	gccggattgt	3000
ccgaaaaagg	aatgtctgaa	gccgtcatgg	cttgcatacg	gctgcacctc	gtaccaactg	3060
acgaatatcg	aagccggcta	ctgccacggg	agcaacccca	caggagttag	gacggaaaaa	3120
cgctctccca	cattgtcggg	atgacgaaag	aacgatagcc	ctcttcatca	gccatacgtc	3180
ttaaacacct	ttggccgaat	cggtaacggc	cacaatcctc	tcccagagcat	cttccgtccg	3240
acctgcgatt	ccagcaatcc	tttcaacaga	cgaaaggcaa	tagcggttcg	gtag	3294

(2) INFORMATION FOR SEQ ID NO:329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 902 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

tggcgcttac	aaaacgaaca	ggatccggcc	aaacgtcagc	agatcatcgt	aaaattctca	60
agctgtatga	tgaccgtgtc	aaatacttcg	gagaagaccc	aagtatggaa	cggactatat	120
catggccagc	aaaatatcgg	actacatcag	tatatgggcg	ataaaacgga	ttatgacaag	180
gtttatgaat	ggatcagccg	accatcgatc	agcatggaga	gaatgctacg	cctcgagctc	240
tattcattat	gcttactcct	ctctgaacaa	agctatcaga	aatgaggcat	ggcagaaacc	300
tatattaagg	attatacggt	tgcatcccag	gccatggaga	agcgttggaa	gtggccgatg	360
agaaaggcaa	agagtttatc	caaccgctga	aactcagatc	gacgaactct	tcgcccagag	420
tggtcttgca	gactgcaata	cttggtgaaa	atgatggcg	ataagctgga	ggaaaacaag	480
acggatacga	tttccctgaag	aatatgctcg	gcatgttcca	cgcttccgac	tgcgagacaa	540
tccgctttat	ttccaagcca	ataaatacct	ctttgccgta	cagccctcgc	tatagctgct	600
atgggccttg	ccaaagaggc	gatggaagga	aatcgatcaa	tgaagccagc	gactatctcc	660

```

aaaaggctat cgaactaagc aagagtcscac agaccgtgca gcectgcaact atacgttggg 720
tctgtttggct atgaacaggg tagttactct acggcacgct cttactgcaa taaagcactg 780
gccgagatcc tgcgatgggc gatgctctta tctgtattgc ccaaattgat gcacaacggc 840
caatactgtc ttcccgggtga tgctatcagg cagcgtgngt attttctctgc cgtggacaaa 900
ct 902

```

(2) INFORMATION FOR SEQ ID NO:330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

```

cactattgtc cgggtttag ccacggagtt gtgcacaaac tcatcgaga gtaatcgaag 60
aaatgggctt gacgaagaa actatcgga tgcacctta ggatgctcag tattcgcta 120
tcgctacatc gatatcgact ggcaagagct gccacgggc gtgcacggc tctggctaca 180
gcagtaaagc gtctgatccc tctaagctgg tatttacata tcaggggcag ggagacttgg 240
ctgcttcgga acagccgaga ccacccacgc agccaaccga ggagaaaaca tngcattata 300
ttcatcaaca acggtatcta cggatgacc ggaggtcaga tggtcggact acccttgaag 360
gtatgggtac cggntacttg ccttcagga agaacgtaga gctgaaccgg tattccgctg 420
aagattgccg atatgcttgc ttgctcgac ggtacttggc tcgtaacggc ccaagaaccg 480
tgcacaatgc gc 492

```

(2) INFORMATION FOR SEQ ID NO:331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...4074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

```

gatttctttg aaagcatatg atgactttct accatcgga cgcaccaaca cagctctccg 60
gaaggcaata catcggaat tatggcatcg aaacgcctc cttatttttg aagggatgg 120
accctaccct cctgtaaaga cactgcaata acgagtgtga agctggctcg cagtatgctc 180
ttctatgtgt ctgtagggtga acgcatctcc tgcataaaag agcggaatat ctctatacga 240

```

tctacgaatg	ccccagaatg	atccggaccg	atgtaggatt	ggggagatag	ctcgatagtc	300
gctttcgttg	atattgagac	cgacacccag	aatgctgtag	tcgggttgct	gcccgtcagg	360
ctgtgctcga	tcagtatgcc	tgtatatttc	cttctccata	gtatatatcg	ttcggccatt	420
tgatgctgag	catctcggca	gaggaagaag	gtcgtagagt	gtatggagca	cggagagtgc	480
acacaatcgg	agagatcgaa	ttgctgctgt	gcaggaagca	tggtcggcct	cagcagaacg	540
aaaaggctcag	gttcaagccc	ggagacgcga	accagctatt	gccctgcttc	ctcgtcccg	600
agtctgattg	tctgtcatga	ccacgggtcca	cgcagggtgt	cgggatccctg	catcaaaaga	660
tcggacagat	aggagtgggt	gctggcggtt	cgggcagatg	gatcagatac	ccttcagacc	720
aactgttctt	cttggctcca	tcgaaaggcg	gttgtgtacg	gatgtattta	gggagtttgg	780
atacacgaga	gcgtacgaat	gtcggatgag	ccgtgcaatc	agatcggcag	gggatccgag	840
tccaaagcta	cgctgttcca	atgtcgtttg	ttcatatgaa	aacccccgtg	ataccctcgt	900
agtgcatect	taaatgttcg	gacgatccgg	gtcgcatttg	agtgcgatga	ctttcttttc	960
ggaatcaagg	ggtatcagag	aaacattttg	ccggctactt	tcataaccaa	cgtaacatca	1020
tcgaacggga	actctcctcc	acctgtggca	gtgacaagca	tagctctcga	gcttgctcat	1080
gtccatatat	tattttattt	ttgctacgtt	atgaattttc	ctccactttg	cttggggcac	1140
ggtctaacaa	aaatacggg	aaaactcatt	tttgcccaaa	caatccacat	aagctcaacg	1200
agattcgtca	tattcttgag	ggaaagtggg	gattgtcggg	ctggacgaaa	taggttgctc	1260
ggaggatatt	cccgaacggc	cgacacacta	cagggaatg	ctttgctcaa	agcagaattt	1320
gttacaacag	atatggttta	ccttgctttg	ctgacgacac	aggcttgga	gtgaagctct	1380
tgacagagca	ccggcgctcc	actctgcacg	gtacgcagga	gaccgaccaa	tgccgatgcc	1440
aatgtacgga	aactactcga	agcattgagc	gtgtaccaca	tcccagaaaa	gcatgcttcc	1500
gtaccgtgat	cgccctgatg	atgatcatgt	aaaacacttc	ttcgaaggga	agatcgaagg	1560
taccatagat	ctgaatgcag	aggatcgggc	ggcttcggct	atgaccccg	tttcatccgg	1620
agggacacac	gctcagcttt	gcagaaatgg	gagaagaaac	caaaaacaaa	tcagtcatcg	1680
tgctttggcg	gtggcacagc	tccgcgattt	tttatatgtg	caaaaataaga	ttcagcctct	1740
tgaggctct	tgtcgtctgc	ttatgtttac	ctctttttct	ctccaagctc	aagagggaagg	1800
tattttgaa	acctcttggc	tatccacaag	acggaaaaag	ccgtagaaac	gcccagaata	1860
gttttgccgt	agccaacgga	gtactttact	cggtgggcaa	agaagctccc	ctgagggcaa	1920
gatcttcgac	cgtatcagcg	gactcagcga	tacatcggta	gcagcatagc	ctactccgag	1980
caactaaaat	ccttggtcat	atactatgct	caggcaatat	cgacatcttg	gacgaagcag	2040
gccgtgtgac	caacgtactg	cattgaaaga	caatatcgat	ctgatagaca	aaacgctcaa	2100
tcgcctttga	tcgtaggcaa	cagggttat	ttggcaggag	gattcggcct	ctccgtctgg	2160
atgtcgcga	agctcgcata	ccggctacct	acgcacaagg	aactagggtga	ccgatgtggc	2220
taagttggac	aatgatcgct	tgctgatgct	gaaaaaggcg	agctcttcac	cggaaaagag	2280
accgataacc	tgcaagatcc	ggcgcatgga	cagccttgct	tttgaatttg	ccgatgggct	2340
cggtcaccgg	tcgggcattg	tcggggaaga	catctgtttc	ctgctcgccg	atggccgtgt	2400
aatgtcgcgt	caaaccaatc	gtttgagccg	gagctattgc	tctcttctcc	gccgattcac	2460
gactgtatgt	gacggatcgt	ggtctgttca	tctgtgcccg	aatcgaattt	atttcataga	2520
aaaaggctcg	aaaacgcac	aatttcccta	gccgacgtcc	ttggtgtcgg	tgccatgaac	2580
gaaagcaata	cggcataata	gcattgggag	aagaagggtt	ggcttcactt	cttctcgacg	2640
agggaatacg	gccgaagcca	tgctgttagc	attcgacgga	ccgggggaca	atgattctac	2700
gagatgcggt	ttagtcacgg	acgtctgtat	gcagccagcg	gacttgggga	acaaacctga	2760
tgggacatgc	cggatagggt	aagctatacg	acgcaaccga	tggactaact	tcgacaagaa	2820
gaccgtacag	gaacagttgg	gcgcggattc	agtttcaatg	atgctatcga	tatagctggt	2880
tccaacggag	acccgatcac	ttttttgtcg	gtacatgggg	aaacggtctg	ttcgaattca	2940
ggaatggcaa	gcgtatgctc	gctattcggg	aacgacaaat	gctatcgcaa	atgtaatccc	3000
ggagatgccc	gtgtgaaagc	gattgccttt	gacaataagg	caacctctgg	gggacgctcg	3060
gtgccgtagg	caagaacatc	ttcatgtcga	tcgcagaggt	agcacatggc	attctttcag	3120
ctatccggat	gtagccatct	ggcctccttc	ggcaatatga	ttatcctacc	caacggagac	3180
aaatggtaaa	tatccttcac	cgtagtggcg	gatccacgcg	caaagggtgt	ttgacttcaa	3240
cgatcggggg	acaccggaaa	cgacttcgga	cgacagccat	cttacgtcga	gcagtttgtc	3300
aatcgctcgt	gggcagccat	aggacataag	acatctatgc	aatggccgtc	gatcataacg	3360
gctctgtctg	gatgggatcg	gtataggcat	tttcggcgct	tacaatgcag	ccggagtatt	3420
gtcctcgact	ctacccttat	cgctgttcgg	ccggtcggag	gagaagaacc	caatttgtat	3480
atgtgctgga	caagggtgac	gtgacagaca	tcgtcgtgga	caaactcatc	acaaatgggt	3540
tgccacccaa	gggacaggac	tctatctcct	ttcggaat	gcagtaagat	cctcgcgcaa	3600
tttaccgtag	aaaacagccc	tttgcttcta	acaacatact	atccctggcc	ttaaatgacg	3660
ataacggagt	ctgtcatcgc	gtacggcgga	cggatgtagt	acgttccaaa	cgggtacggg	3720
gagtgatcag	cttccgaact	ggacggcgct	tatgtatacc	ccaatccgct	aagccggaat	3780
atcccgatgg	cgtcaccatt	gccggactgc	aagccggctg	tatgtcaaaa	tcaccgatac	3840
caccggcaga	ctgctatacc	agactgagag	ctaaccaccg	aagtcaaatg	gaatgctcga	3900
ggtgccgatg	gcaatagggt	gcttcggggc	tatatgccgt	tgcatgttac	gatccgggat	3960
cgaaaaagtc	aaactaattc	gcttcgcagt	gattcgcgtg	cacacggcct	ttttctctgt	4020
aaacaacatt	ttaactcaaa	ctaattaggta	atgaacaaaa	agattttggt	gcat	4074

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

```

ggctgcatg tctataccac tctcgacatg gatatgcaga gcatagtcga gtggagttgc      60
gcagcaagct cgaagagggtg cagggagaaa gtggaacccc atcctcatgg aggtagctac      120
agggcaggta aaggctatca ccaatctcag cgcacgccct ccggcggata tatcgaatcc      180
aagaactacg cagtagcgat atgtcagaac ccggttctac gttcaagacc gtgtcgatga      240
tggtacactc gatgccggca ttgtgcatcc ggaggacatc atcgaaacgg gcaagggtctc      300
ttctccgtag gcaagcgtag tgtaagagac cataatgcac acaaggaggg tatggccccc      360
ttacggcagc tcagacgatt tggtactcaa gcacgtaggc gtagccaaaa tcattctcaa      420
aggctttgcc cacgatcccg aaaatacgtg gaggcggtca ggcgaaccgg tatcacggac      480
aagtccgctc ggaaataccc ggagaagctc cggccgtagt gcgcaagcgt gccgacaatc      540
tgaccgctgg tatggcacga cccttgcatg gatgtcattc ggatacgaac ccaaatcccg      600
ccgatccata cattggcttt ctacaatgcc gttgccacgg tggtagaatg atgcgtccct      660
acttcgtaac gaaagtgatg gatagaggga ggtcgtacag gagcaccggc cggtagtatt      720
acgcgattcc atctgaagca ctctacgctt atcgccatac aggatatgct ctcgaaacgta      780
gtggcaaagg gaccggctcg ccggtcaaaa gctctacggt aaacatcagc ggcttgaccg      840
gtacagcgca gatctcacag ggcaaaagcg gttatcgtgc agtggcacca tgcacttggt      900
attctttctg tggttat                                     917

```

(2) INFORMATION FOR SEQ ID NO:333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

```

cggactggca cccgaacgac aagggtgtctt tcttcttcgg acgtcagtag cgcgtttcgg      60
agggatagaa tacgacatga accccgtaga gatctaccgt acagcgacct tgtggattac      120
atgacctgct atacttcggg cgtgaactcg catggaactt ccaccccgaa cagcagctgc      180
agctacaggt actcaagctt acaacaaccg cttcgccgac cgctaccacg tgacacccga      240
tgtcgtaccg ccacgagcta cccgctcctc tactcggcac agtggaaacgg tacctcctcg      300
gaggagcact gcatatgcgt tacgccgtgt cgatggctca tcagcccaag agcgtaatat      360

```

gtgggtacttc	actgcggggca	acctgtttcaa	tcgggcaaac	ggatcaacgg	atacctcgac	420
ctcacctact	cgatcgaggg	atggacgaca	aaggcattat	gactgctcgc	tacggcaagg	480
gcaagaccct	acggacgtca	agtactatgc	tctgggtatcg	aagtggaaact	tccgcatttc	540
gatcaggtca	atctcttctt	caaaggcatg	tacgagaacg	gctatgcgct	gccccaatag	600
gcgagagcag	ccacacgcgc	caactcctac	ggctataggg	aagggtggaa	tattaccctt	660
acggagacca	actttccgtc					680

(2) INFORMATION FOR SEQ ID NO:334

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

ctgggttata	acgggtgtttt	tttggctttc	actcgccaca	atggtaatcc	cttgtcgttc	60
ttggccagct	ctttgatcaa	ttccatcggg	ataccgaagg	gtagcgtacc	aaaacggctg	120
cagagcggtc	gtactcagcg	atagcaccac	aggacctgca	gggggattcg	tttcctggaa	180
tgctcgttgc	atctctctgt	tgcaaattga	ccgtttgttc	ggtctgcttg	catttgcgtt	240
tgggcattgc	gggcagttgg	aagagtccca	atgccagaat	caaggcttta	gccttaaaaag	300
ctttttcatt	gtttgatatg	ttttatgatg	ttatgaatat	gttctgaaca	tatgataaga	360
tctcggggaa	ataataaaga	gggacatggg	ccatcttttt	gcgaaatata	catggaggga	420
tttaccttcg	gttttttcacc	tcaaccgat	aaccgcccgt	aaaattagaa	gaaatcatca	480
atatgaaata	aataaacctg	ttttcttgc	ttttgagccc	tttgcaaaaa	gagaaggtct	540
caagaagtat	cttttcggta	tcgtttttgc	tcacctatag	agtgtatcca	cagtcattgg	600
aggaggcttt	agagggtatt	atatctataa	tgacactaaa	aatcagtc	ttgacaatga	660
aatctcccgg	aaaatgccgt	gcgacatctt	atctatcggg	ttcacagctc	gcacggaacc	720
tccacttccc	gatccgccat	ccgacacaga	gcagatagca	tcttccatca	atagaccata	780
gtatctctca	taggagacca	taatatcctc	tcataggaga	ccatagtatc	ctccatgtga	840
gaccatagta	tcctc					855

(2) INFORMATION FOR SEQ ID NO:335

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

gtcgttgatc	agtcccaacta	cgcgacaacc	tttaggcgta	tgtttacgga	gaacttactg	60
cttggctgga	agattatagt	cttggagaaa	tttgggagaa	aatatcattg	gtggacaacc	120
ttgggctaag	tagtgagatg	gggaatagaa	aaaacggctt	gtttttattg	tcgagggaga	180
tacagagggt	gccttttcca	tgaacgtgtg	atcccatacc	taatgagcaa	aggctaccgc	240
aatgcatgaa	tgcccagaag	atcaccacca	ataaatcgct	tcataaaaag	ggtgtatagc	300
ccgcttcgaa	tacttggaag	atgaagtctg	aagcgtagca	gccaaggaga	tatcttgatt	360
actactttgt	tagacttctt	caggctacca	acaattttcc	taactatact	gcggatagcc	420
ataagatttc	ggatatagag	caggggttag	acaagggtatt	gatgggggta	atgtttcgct	480
tttctatcca	atattcagcg	ccacgaacta	gaggcactca	tgtacacgag	tatggatggt	540
ttgagatcgt	ttgtgacgaa	aaaagagagt	tagatcagct	gagagcaatg	tagagggtta	600
cgataatccc	gaagatatca	attctggggc	tgaaacccgc	catctaagcg	ccttatcaag	660
attttccccc	aatatgagaa	ggttcttatg	gagaactgat	atgttgaggct	ttggagattg	720
atgctatacg	agctcatgcc	cccgtttcaa	cgattggata	caaatccttg	aggacggatt	780
aaagaaggat	acttttaagc	cagatTTTTT	attatacttt	tttaagggac	tttagctctt	840
gtactctttt	cgataaagaa	tatcgctcaa	tctatgcttg	cacgcccgc	aatgcgtaga	900
cttt						904

(2) INFORMATION FOR SEQ ID NO:336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

gcgctcatgaa	tgctgcgaaa	gcttttagccg	agatcgggtct	ggaatcgggg	aacgaatcgg	60
tatctattcc	cccaatatgg	tacactgtct	gtataccggg	tgggggcctt	cgccatgcgg	120
ggtgtagtag	tgcttttgta	tgccacagct	caccggaaca	gttacgggtc	atcgtggagg	180
attcatccat	ggagacttgt	ttgtcggaga	gcagttccaa	tacaacaatg	cttatcgggt	240
acagaagaat	atggtacgct	aaagcgcata	gtcgtattcg	atgagcgcgt	ggtgtcaatc	300
cggaggataa	gacttcgaaa	tacttttccg	aatttgttcg	tttggtgatt	ccatgccgaa	360
cgagacgaag	gtcaaagtct	cttctcgcga	agcattcctt	ccgatccggc	actgatcatc	420
tatacatcgg	gcacttccgg	tggagcaagg	gcgtcctcct	cctgcacagc	aatctgatgt	480
atcagatgaa	gtccatagcg	agcatatccc	cgtctatggg	ccgggcgagc	tgtcgatagt	540
ttcctgccga	tgagtcatat	tttcgaaaag	gcattggacac	tcttttgctg	acgacgggaa	600
cgaggattgc	catcttgaga	gatccgaaga	aagtatttag	gcactacctc	agatacgccc	660
atcgctcatg	tgcaacgtgc	cacgctttgg	gagaaagtgt	atcagggcgt	gaatgagaag	720
atggcctcct	ctccccgcac	ctgaaagggtg	tctacaggcg	tgctatggcc	gtaggccaac	780
gctacgtctc	gactattgga	atgaggggaa	gcgtgcgcga	ctgcttctga	gtagcaatat	840
gccttttaca	actgcactat	ttttaccctg	ctcaagcgcg	tatgggacta	cagcgagggc	900
gttattttccc	cacggncgga	gcaccgctat	cgatgagatc	aacatcttcc	ttcagtcctg	960
aaacattccc	atcattgtcg	atatggtctg	tccgaaacga	ctgccacggg	atctttctat	1020
ccgcagcgag	attcaagatc	ggctncatgg	gcaaagtgat	gccgggctgg	a	1071

(2) INFORMATION FOR SEQ ID NO:337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

accaagacat	ggcgcagctc	tgtcgggtgga	tgggatatct	atatggcacg	aaaggctatg	60
ccgtctttac	ggtggatagt	cgcggatctg	ccaatagagg	gctgctttcg	agcaggttat	120
tcatcgctcg	ttggggcaga	ccgagatgcc	gatcagatgt	gcgggtgtgga	tttccctcaag	180
agccaatcat	gggtggtgcc	gatagaatag	gagtacatgg	ctggagctat	ggtggcttta	240
tgactcgaat	ctgatgctta	cgcacggcga	tgtcttcaaa	gtcggagtag	ccgggggcct	300
gtcatagact	ggaatcgata	tgagattatg	tacggtgagc	gtttttcgat	gcgccacagg	360
aaaatcccga	aggatacgat	gctgccaaac	tgtcaaacga	gccgggtgatc	tgaaaggacg	420
acttatgctg	attcatggag	catcgatccg	gtcgtggtat	ggcagcattc	actccttttc	480
cttgatgctt	cgtgaaggca	cgcacctatc	ctgactctta	cgtctatccg	ag	532

(2) INFORMATION FOR SEQ ID NO:338

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 902 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

ggaaaactat	catcaagact	atttggatca	taaccctcgc	ggttattgta	tatcgatcct	60
tctttattcg	aattggcgag	gaaagccaat	ccggccagtt	ctacaagaag	gccgatgatg	120
cagagcttcg	tgcccggctt	acccccggca	gtatgccgtc	acacgcaaca	atgccaccga	180
accggctttt	gacaacagta	ttggaatgaa	tttcgagaag	gtatttatgt	cgatgttact	240
acagggaacc	gctatttctt	tctactgata	agttcgactc	cggctgtgga	tggcgagttt	300
cagcaagccg	atagggaaag	agctgatttc	cgagcgtatc	gatgttcttt	cggaatgact	360
cgtacagaag	tgcgtagtac	gaccggcgat	gccatttggg	acacttgttc	aatgacgggc	420
cactggaaga	aaggcggact	cgttattgca	tcaatagtgc	ctcccttcgg	tttattccca	480
aagaggatat	aagaaagaag	gctatggcag	tcttcttctt	cttttgaaca	aacgatgaga	540
tgctcttgta	gcataataatg	attcccaatc	gtctcagata	agactaactc	caatggcata	600
tctcggaacc	aaagccaagt	ggctgttact	actctcccca	tcgtgcttct	tgcaatagtc	660
ggagtctgga	tttttcaata	ttccgggatg	gggagcgatt	cgaaattgtc	gacgaattgg	720
gtggcaatat	ctttcgctcg	ccatactgtc	ggtggccacg	accgatgctg	aagtaatcaa	780
accgtcgaag	gcctgtacgt	gggcaatccg	aagtccgtta	taagtattcg	cctaaaacgc	840
gaagggccaa	tagccgtgtg	cgtgtggaag	tagccgaaac	gcttttttct	cccaggggga	900

(2) INFORMATION FOR SEQ ID NO:339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

```

agtacccgga gcgggcaaga gttcttcgat cgatgctttc ggtatgcatt catcaagcan    60
gggcggaagc ttgccgtgct ggccatagac cccagcagga gagatccaaa gggagtattc    120
tgggcgataa gaccggtatg gagcagcctc tcgagagaag aatgccttta ttcgtcccag    180
tctgtctgcc ggttcgtggg tggcgtggca cgcaagacgc gtgagaccat cgtgctgtgt    240
gaagcgccgg attcgacacg atctttgtag agacggtagg angtgggaca gagcaaaactg    300
ctgttcattc gatggtggac ttcttctcgc tgatccaact ggcggtacgg gggatgaact    360
tcagggtatc aagcgcgga ttatggagat tgcccgatgg gtattcatcg tcaataaaaag    420
cgga                                         424

```

(2) INFORMATION FOR SEQ ID NO:340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...3153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

```

cacataggag ttattcgtac atttgtccga cgagggatga gccgaaaaaa atgaatccaa    60
caacagtgac tcagcaatta caaaaaacat atcaggcttc ggggatggac tgctgagcga    120
ggcgttcggc ctgctccgtg catcggtccc tcgcagcaat cgcatttcct cacacgcac    180
gacgatctgg agaacgctat cggcagctct tgtcatactt cgcccaagggt gtgaaagacg    240
aaaaacaggc cgagatgctc ctctacctca agcgcaaaact cataggtctg gcagtgaagt    300
gcatcgcgaa tccgtggtgg cacagggcac ggggcttttc tacatcgccct tcgttaccgc    360
cgcagcatcg gtttcgaaa ccttgtcacc ttctggagca ggctgagaca agcactgtcc    420
gcaagcagtg cgacgaattg gacggctcat attcgatagc ttgtggacgg ccgatgctct    480
gacggacgaa aggctgctgc cctctcgcat gccggcgaat acattcgccct cgtggcggct    540

```


cggccttgac	aatggctctg	caacaacagt	ggcactcgaa	aaagctctct	tcctgctcga	600
agagctggct	cgccccgaca	ttacagccga	ctatcgcccc	gcctgctggg	cggagtcggt	660
ctcacccttc	gttccctatcc	ccaccaaccc	gactctatta	taatgagatc	gcattgcgac	720
tggaagccgt	caatgacata	tccctttgga	accgaccctt	gagatgcttt	cgatccggtt	780
cctcttgcc	gcgaaacaga	gtccatcacc	aagcatttgc	aaaccgagag	ctttaagcga	840
tatacagaag	atagcccccg	acctgcgcaa	attcggtatg	gggataccga	gtccatacag	900
gagacaggca	atccggagtg	gatggaggag	cggagaagag	cgggtctggga	gacaaaatca	960
gggagttctc	ggagttgcag	tcgaaggagc	cgatgtaatg	cactcttcgt	tcatagaact	1020
gaagggaaga	gctttttccg	cgagatgcac	aactggtttc	tgcctttcga	tgccgcccc	1080
gcccgatagc	tcactgctc	gaagagaatg	ctgtgctcaa	gcagctttgg	aggcgatagg	1140
cccacagctt	tgcaactcgg	accgctactc	tttcatgttt	cgatggaaag	cctccctgct	1200
gcacttcgag	gttcggccat	gggagcgtag	gcggtgaact	ggatgcactc	aaagagcaga	1260
taaagcagga	tgtacggtcg	gcgaaaccgg	caaattggac	acggccatca	agagctatct	1320
gcagatctgt	acagattcta	taaggtatgc	gaacggaaga	acgaatttga	cgatattttc	1380
tctcgcccc	cccaccggat	ctgcctgtgc	tcgatcgcta	ttctacaagc	gtgatacgct	1440
gctgcatacg	gccgaatttc	tcttccgccc	aagcattacg	atcgggcagc	gaagcttgct	1500
ggccgatttg	gctgaaggga	agaaagtgcc	acggatacca	ctctgcacca	aaagctgggt	1560
ttctccctca	gcagcagggc	cttttcgccc	aagctttggc	tgcatattcg	cgtgccgact	1620
gatcgatacg	gagaacgaat	ggctgctcaa	gcgtatggct	cactgtaccg	ccagctgtgc	1680
cgtccggccg	aagcggccga	aatatatgaa	cgactttcga	gcgcaatccg	cacgaagcga	1740
ctctactcct	gcagcgagga	aatggctcgt	cgaggacagc	cgatacgatg	aagctctaca	1800
atgcttcttc	cgaatgagtt	cagtgtggac	gatgcttcca	aggctcgtcg	tcccatcgct	1860
tgtgcctctt	cctcaccggc	cagtacgaac	gtgcggcgga	ttactatcgc	acatactgga	1920
atccgacgat	ctctcgactt	tcaccgatcg	gctcaatgcc	ggcatacgtc	tttggctatg	1980
gggcagatcc	ctgttgcgat	cgaccattac	ttgcgggatt	gaagctcact	ccgacgggaa	2040
agatgaattt	ctcgcagcta	tacggcagac	ataccggttc	ttctcaaagc	cggtatcgag	2100
gatgccgat	caggctcatt	ccggaagtac	tgaggctaca	cccgactaag	ggaattctaa	2160
tgtttcatct	cacaaacctc	catcaatgag	taaaaaattt	gttttgcaat	cagtattatg	2220
gcaatgctca	cagcatgtaa	cggcagccgt	aaagagatgc	caacctctcc	gacaatcctc	2280
tgctgcaatc	gagtgtcttc	ttctggaagc	acccgaattc	gacaaaatca	aaaccgaaca	2340
cttctgcct	gcttcgaagc	cggcatggag	cagcagttgg	ccgagatcga	ttcgatcgtg	2400
acaactccga	agctcccaat	ttcgagaata	cgctcgtagc	catggaacgt	cgggacagac	2460
actcaaactg	gtttccaatg	tcttcttcgg	gtctcacgga	gccaatacga	acgatgaact	2520
acagaaaatc	gaagaaaaag	tatcgccctt	ttggctgcac	acagcgatgc	catctacctt	2580
aacgacaaac	ttttccacgc	gtaaaagccg	tttacgaaag	tgaccaatcc	gccatcgaa	2640
ccgaggacaa	aagttgatcc	aagagtatta	cgatgccttt	gtccgtgccg	gtgccatctg	2700
agtgcggagg	acaaggccaa	gctcatggaa	ctgaacaagg	aagagcttcg	ctgacgaccg	2760
aattcggcaa	caagctgatc	gcagccacca	atgcgcagcg	gtaatcgtag	ggagcaaaga	2820
ctcgctcgat	ggtcttagcg	aacggagata	gccaaagctg	caagcgatgc	caaagctgcc	2880
ggccacgaag	gaaataacctg	ttgaatatca	ccaataccac	tcagcaggat	tatctctcgg	2940
actgaacgac	cgtaccattc	gtcagcgtgt	attggaggcc	tctatccatg	cacggacaaa	3000
ggcgatgcca	acgacacgca	gtccatcgta	cttcgtctgc	caggctccgc	gcacagaagg	3060
ctcgcttct	cggcttccct	aattatgcgc	atggaagctt	cagaatcaga	tggctaataa	3120
tccggagaca	gtgctgcttt	tgtccagtcg	ata			3153

(2) INFORMATION FOR SEQ ID NO:341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

ggaggttttg	gctcttgaag	catttggagc	ttcgcatatc	ttgcaagaat	tcttactgtg	60
aaatctgacg	atgttgttgg	acgttcaaa	gcatacgagc	gatagtcaaa	ggagatccga	120
tgcctacacc	gggtattccg	gagtcgctaa	cgtgctattg	catgaattga	aaggccttgg	180
tttaagtttt	tctttgacta	acttctaacc	gagagtctgt	acaattat	ttgccttcac	240
ccattctatt	caagcaaagt	gaactatggc	ttttagaaaa	gaaaataaga	taaaaacaac	300
ttctcgaaga	ttcgtatcac	cttggcttct	cctgaagaga	ttctgagaac	tcattcggag	360
aagtattgaa	gccggagacg	atcaattatc	gtcctacaag	ccggaacgaa	gatggcctat	420
tctgtgaacg	catcttcggg	tcggttnaag	gatttttgaa	tggtcactgt	ggcaaataca	480
agcgtattcg	taccgtggta	tcgtatgtga	tcgctgtgga	gtcgaggtaa	cggaaaagaa	540
gttcgccgtg	agcgtatggg	gcacatccat	ttggctcgta	ctgttgctat	atttgggtatt	600
tccgttctct	tccgaataag	atcggctatt	tattaggcta	cctaccaaga	agttggatgc	660
catcattttac	tatgaacgct	acgttgtatt	caaccgggtg	ttgccgaagg	gttgagtcaa	720
cttgatctat	tgtcaaggaa	gaatacctcg	acaagcttga	tgaaatagag	cgcactcaca	780
agggaaaccaa	aatttggagg	ataccaatcc	ggacaaat	attgccaaaa	ttgggcagag	840
gctattttatg	atcttctatg	tcgtgtggat	ctggattcta	ttcctacgaa	ttgcgagatc	900
gtgccaatac	agatggttcg	cagcaacgta	aacagaagca	cttaaacgtc	ttcaagtcgt	960
tgaaggtttc	cgtgcaccca	aggtgtgaat	cgtcctgagt	ggatggttat	gaaagtgtatt	1020
ccggttatcc	gccggatctt	cgtcctttag	ttccttttga	tggtggacgt	ttcgctactc	1080
cgatctgaac	gacttgtacc	gtcgcgttat	tatccgtaac	aaccgtccaa	acgattgatc	1140
gagatcaaa	ctcctgaagt	tatcttacgc	aatgaaagcg	catgctacag	gaagcggttg	1200
actccctttt	cgacaactcg	cggaaatcaag	tgcggttaag	tctgacaaca	atcgtccttt	1260
gaaatccctt	tctgtagtct	caaagycaaa	caaggtcgtt	tccgtcagaa	cttgcttggg	1320
aaggtgtcga	ttattctgct	cgttcctgta	tcgttgttgg	tccggagctt	aaatgcatga	1380
gtgcggactt	ccgaaagaca	tggcagcccg	aactctacaa	accttcatca	ttcgcaagtt	1440
gattgagcgt	ggcatagtga	agaccagtca	gagtgccaag	aagattgtag	accgtaaaga	1500
gcctgtttatc	tgggatattt	ggagtagctg	atgaaaggga	catccggtcc	t	1551

(2) INFORMATION FOR SEQ ID NO:342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

gatccccgtg	tgccaattag	tcaatagaaa	agcttccccg	aaacatccaa	gtcggccacc	60
gggttgaata	tggccaaata	gagtgtaagc	ggagtcatac	agccataaag	agaaagatga	120
agcgagctgc	catgcgtctg	tagataccat	caagagaaat	gctccacaga	tgaactcact	180
acagcaaagc	aaaatgtaag	aataagggat	aagccctcgg	acttaggcaa	agcaaaaaca	240
gtaaatactc	actgattttg	atcgctcctc	cctgcgggac	gatagccttc	agaagcccga	300
aacaacgaag	gtcagaccta	atatgattcg	agaaaagctc	gcaggaaacg	tttcatccgt	360
tcaactgtat	caatgcgaag	atggcatagt	tgtcataacc	atgtagttgg	catccaccoc	420
ttcggatata	tatgtatcac	cccagatctc	tctatctctt	tagtgcgaaa	taccttagtc	480
agaatcaagt	ggcaaaggat	gacacacgca	tctgtctcca	cgcctctcca	tagtcatgat	540
cttatcaagc	atcagcgaca	tggcttcacg	aatcttgagg	tcatacagcg	cagagcttcc	600
tctgtctcca	tcttaggtgt	gtcagctact	cccagctcaa	ttggatgaga	gctattactc	660
cataattgac	gacacctata	aactcaactc	cactccttca	tccaccttac	tcaaaccctt	720
catctgaata	tttcgatcgc	gttggccttg	atataaagct	gatcggtcag	agacgacgga	780
cgcacactcg	ccacgaggct	ccatagtcgt	gcagtttttt	ctgaaaaacc	tcagacaaat	840
atcaatcacg	tgctcgaact	gctctactgt	atttggcttg	gcgtagtcat	ttctttcttt	900
gcttcttctc	cgttttttcc	actttttcgg	tttctctctc	tcggtcttct	tgccaaagga	960

atatatatcg	gtggtatcga	gactttctct	tcgagcaaa	cttctttcaa	cacctcgtta	1020
atgttggaac	atagtggaac	ttcaagccct	tcagatagat	atcgtttatc	tcctctattc	1080
cttgcgattc	tcttcgcaca	ggattatttc	cgtgataccg	gaacggtggc	agccaatatc	1140
ttctccttga	ttccacctac	aggaagcacc	tttccttttag	agtgatttct	cctgtcatgg	1200
caataccggc	ccgcactttt	cgacggtaa	agccgacacc	agcgaagtca	ccatcgtaat	1260
acctgcactc	ggacgtcttt	cgggatagca	ccttcgggaa	catgtacgtg	tacctgccaa	1320
ttatgaaaa	ttcctgagag	atgcccaact	catcactatg	ggcacgaata	tatccaaggc	1380
tattacggcc	gactctttca	tcacatcgcc	cagattaccc	gaagcgtgag	cttcgggttcg	1440
cgtccgcggt	gcagactcgt	ctcgatgaac	ggatctcccc	tcccaccgaa	gtccaagcca	1500
atccgatcac	aacgcctgct	cgccattgcc	ttgatagcga	tcgcgcgtat	agcgggggtgc	1560
tccaagaag	taaccaagtc	ggacggttcc	accttggtag	tatgtaccac	attcgtgcgg	1620
cctcctttgt	tatcttacgg	atcacagctg	cgatctgctt	ctccaagtac	gcactccact	1680
ctctctgggt	tagtcgtcga	tcagcttttc	tatggttttt	tggagaactt	gatgtcgttc	1740
tttctgaatc	catgctccac	aagtgtcttg	gaatcagatg	gcgggcagcg	atctccactt	1800
tttcttctat	gattaaccgc	tcacatcgat	cagctccatt	ctgtccaaaa	gaggacgaga	1860
gaactgctca	aactgttggc	cgtagcgata	aaaagaacat	gactgaggtc	gagtctatat	1920
ccagataatt	gtcatgaaaa	gcattgttct	gtcccggtac	aggacttcga	gcaaagcaga	1980
agaaggatcg	cccttgtagt	cgctgtcgac	ttggctattt	cgtcgaggac	aaagacggga	2040
ttagatgtac	ctgctcgccg	aaactctgaa	tgatccgtcc	gcacatagca	ccgatgtagg	2100
tacgtcgtgt	ccacgaatct	cagcttcgtc	atgcaagccc	cctaaagaaa	tgcgtagtat	2160
ttacgacca	agctctcggc	aatgtctctg	ccaagagagg	tcttaccact	cccggagggc	2220
cgtacagaca	gatgatgggc	gacttccat	cgccttcac	ttgaggacag	ccagatgctc	2280
tatgattctc	tcttttactt	tctaagaccg	aaatgatctc	tatccaaaac	ggattgggca	2340
cgcttcagg	tgaattatct	ttactgaata	cgccccacgg	cagactgatg	atggtctgta	2400
ctactgcatc	tgtacggagt	agtcggggca	ttgaggatgt	agccgttcca	cttgcgaggt	2460
tctttttcga	aagtttctgc	tacctcgctg	ctccacttct	cgtagcagct	ttggtacgca	2520
gctcctgcac	ctcgatgtcg	tttatattcc	accaggttcc	tcttgaatcg	tcttgatttg	2580
ctgctgcagg	aagtactttt	ctgctgcttg	tccatctcct	cgcgctctt	catctgaata	2640
gaagcttcag	ttccattacc	tgaagctcct	tgtgcaacag	gtagagaaga	cgataccacg	2700
atccttcac	ttgctgattt	ccagcaattc	ttgcttgacg	gctagctcgt	ggatatattg	2760
gccgatgcaa	agttgatctg	atcacatcga	ttctgttccg	tctcatcgag	aggataagct	2820
cccgaagggg	tctctcgacc	atagctccat	catcttcaga	ctcatatcct	gtatggtgga	2880
gacgagtgtc	tgaactcgtg	atctttgttc	ttcccgggga	gaatgtctgg	gagcagcttc	2940
cgcgaccctt	cataaaagg	tccgtagccg	ttatctcctg	cagtgcacac	gctggcgggc	3000
ttgtacgata	gccgtggtag	taccatcggg	catctccaca	ccctgatgat	ttcagccacg	3060
accccgacat	catacaaate	ggcacgaccg	gttcctccac	atccatatcg	cgctgtgaaa	3120
cggcaccgaa	atagaccctt	tcttctccac	gtagcggatc	agcttgagtg	atctttctcg	3180
tccgacatga	taggcattgc	cacacggggg	aagagaatca	tattgcggag	agccaaatcg	3240
gcattctctc	ctgcatatga	tcttctttca	cctgaaatcc	tcacttcttc	acaaacggaa	3300
agcaccggaa	agaatacggg	gaaccatcat	cccgtcgtcc	tctccaggcg	tatatatttc	3360
tatcatcatc	tttagtcttc					3380

(2) INFORMATION FOR SEQ ID NO:343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

ctgctcccga	ctcttgagga	tccccggggc	tgtgtcaaaa	tccaatttca	cacaaccggc	60
attgttattt	gtaggacttt	gtgacccggg	cgggattcaa	cccgcgacct	tcagaaccgg	120

aatctgacgc	tctattcagc	taagctacag	gccttttttg	aaaacaaaag	tacgaaattc	180
tttctgtttg	agattgtttt	tctcaaaaca	gcttagcgct	tgcggcggaa	aaagaagctc	240
agatgttcat	aatcgacttc	ctgctcccgt	agtaatgctt	catgatcaaa	aatcctcttt	300
gagagaagcc	ttatgatttt	tgtaagttat	ccccccccta	tcaccaaaga	gtgcaccaga	360
atcatttctg	tattgacgat	attgcgagca	gctgaagaat	acgaatacac	caatcgaaat	420
cagctgaaaa	tcggtatttc	agttgtacgg	cggtgctatc	aatcgctttg	caataaaaagc	480
ctgatggcat	ccaacatacc	atccgcaaaa	cttctccatt	ggagttcgaa	aggaggacga	540
gccgtcgtaa	acccttctcc	ttaccgggtg	catcaatcag	catgggtatg	cgtaaaggac	600
atccggtaat	cccattggag	agctttttaa	gccgttgcta	tcgcctcgac	aagatcatcg	660
gatggcagaa	ggtcgccggc	attcagaacc	aaacatagtc	gccccaaagc	atacgcaggc	720
ccttattcat	agcatgtata	gccctttgtc	cggttcgctg	atcagtcatg	atatcagaag	780
a						781

(2) INFORMATION FOR SEQ ID NO:344

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

cagcaagctg	agatcgtttg	gcgcgcgaagc	gtgcgatacg	cttcgtcttg	gtataatggt	60
agcaatagct	caagagacgc	gctccaagca	gagaagcata	aagaccgtat	cgttgccatc	120
caaggggcta	tacgaaaaca	ggaagcctct	ctataagcag	tacgatgtag	atccttaatc	180
acaaattgag	cgcgcggaga	gcaacatcaa	gatactcctg	ttggcgtgta	acctcatatc	240
cctcctcaga	gccgtagcgc	agaaattcgt	agccacaacc	gtcggcgtat	atttgggaaa	300
aggaaaagtc	tgcgcgcttg	ccaatcaaaa	ttgtaccccc	agcagcccca	ctatagtcac	360
cagg						364

(2) INFORMATION FOR SEQ ID NO:345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

aaacacatac	caccatgaaa	gttaaatac	ccggcgcatc	ggcacggnag	atgtattccc	60
attccgagtc	catcgcgta	aagaagtagc	cgtgcgctct	ttccgcacct	tactccgaat	120
tccggtacac	gtgctctg	aagaatctct	atggggatca	agatctcctc	aattcgatga	180
gagaacatgg	ttatgcctgg	gacagagatc	cttgacaccg	gctatgctca	acgtcccttac	240
agccttcttg	gttcgcccga	agatttttgt	ccttgacgga	caatagctga	aagttgctta	300
tagggggtat	gtcgaagtcg	tgatttgctg	ctttcggcat	acccctttca	gtatatgcaa	360
agaggatggt	tagatgtgag	aggtggaaa	gtttcggcaa	aggcggctac	attctccgat	420
ggagtagccc	atgaagtgc	cgacgaatgg	ctgagctgtc	gggtgatacg	gcttgccaca	480
cgtagaagtc	aatacggttt	tcagtctttc	gatcagatcg	ttggggagga	tcgggaagac	540
tggttggttt	gcggagggtg	gaggaaggaa	taaccgcaga	aggagatact	gtcgccagat	600
ctgctgccat	tctgttgga	tgagctgcaa	gccggtataa	agcccatcgc	ggaaaagcgt	660
ggcaaa						666

(2) INFORMATION FOR SEQ ID NO:346

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

aagaagcatt	tccatctgac	gctgcatg	gctgcttctc	cggcaagctt	agcagcaaac	60
ccctccgtat	tatccgcata	gatgatactg	cgcgaagctt	gacgagcaga	ccgcaatgag	120
cattcatgcc	gtactcggcc	acatcttcag	acttccaccc	tgagcaccta	cgccggggac	180
aagcaagaaa	gcgtccgcac	gatctcgca	atatctttca	gcatggaggc	ctgcgtagcc	240
cccacacata	catcagttga	ccggcattat	cccacgtctg	gctgatacga	ataagcgttc	300
gaaaagggtat	tctccatcgg	catcgcgcat	catttgaaag	tctgcgaacc	tttgttcgag	360
gtcagtgcca	gaagcacccg	gaacttgcc	gctaactcag	gaaagggctg	atgctgtcct	420
ctcccatata	aggagaaacg	ggagggcac	caccttgaga	tgctcgaaga	acgaacgggc	480
atacatatca	tcgtattgcc	gatattctca	cgcttgccat	cggctatgat	aaattgatcg	540
ggtatcgctc	tcgaatgtat	tcgatcggtt	tttcaaaaga	gtgagct		587

(2) INFORMATION FOR SEQ ID NO:347

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

ggtgtctgtc	taatttggtc	tcttcctctc	ggatcaacac	tttcaccaa	ttgatctgaa	60
gcaatggctg	aatgagcctt	ttactcctcc	accggagacg	aaaatcagct	ctttgaatag	120
gcagggggga	ttcccctaaa	atcaaaaatg	atagtcccg	agttattcca	ctccgggact	180
aagaactcgc	atcccctaaa	aaacatttag	gatactattg	gtctataggt	caaattgcag	240
gctgtatgat	tgagttgtgg	ttctatagat	caaaatctca	aaccaaatac	tccaaaaatg	300
gcgcgagaa	cttttcgttc	cggcgcgaga	ttttttcaac	tccgaaccaa	aataaaaaatc	360
ttctcagacc	acgtttttca	gaaccgaaat	accgtcaagc	tattttcaga	agcgatacga	420
cattgtcatt	gctaactctga	attagagcga	gtgagttttg	ccggtgcagg	agattccact	480
tccaacacat	ggccggattc	gggtcgtccg	ataccattcg	gccaaaagta	tagtagtaat	540
cttctcatta	cgatagatca	cagccaaatc	gcccgaaga	ttacgcgtaa	acggtaaccc	600
aagcctcctg	tcacgggtata	ggaattgccc	ggaagttgta	atgaggcata	gcccccatag	660
ggaagacggt	cacctgtgcc	gagccgcgaa	agctttcaat	ttttcatttt	taatgggatt	720
ggaagtgtgt	gaataccggc	acgcagactc	agacgcgata	tgggacgcag	ttctcctccc	780
aaacgatggg	gtggcgtgaa	ccaaaatcct	ctgaaatgaa	cttattatca	acgatgccgt	840
accgtttctc	tcctttaatt	tgatctggcc	gnaagattcc	aatcataatc	catactgaga	900
aggccgattt	tgccagcaac	gactgccaaa	cagccacaaa	tcgtcccga	ctactcattt	960
gataagtatt	atacgattcg	gagtctggct	actcatgaag			1000

(2) INFORMATION FOR SEQ ID NO:348

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 940 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

acgcaccccg	tcccatcagc	atacagaggc	gtatgtacac	ccctcgtgag	ggaacttcca	60
aggctgtcta	tgtagccaac	ggaancagag	gagggaagat	aactacggag	tcgctgtaga	120
tcttaccatc	gtggatcgtg	atggaaaccg	ttggatatgg	gcactcctgt	cgatcacttt	180
ggccgagcgg	cacatggggg	caggaagaac	gcttggccgc	agacggcctg	atcagccgag	240
aggcttccgg	aaccgcgggt	tgctacgtcg	cataatgaag	tcggtcgggc	tggtccctat	300
cgcagggagt	ggtggcatta	cgaactgccg	gagagcatga	gcccaccgcg	tcacattatc	360
gcttgtctga	cttttaatcc	ttgttcttgt	ttccgagagg	tctgcaatgc	ggacatcatg	420
gaaatacgaa	ccaaaaatcc	tcgattgcgg	ctcgtgtttc	ctgaaaaagt	ggcgtgagat	480
ttttttcggt	tggcgtgtaa	attctttaat	tgccgtgcc	aaacaaaaaa	attctcgcgc	540
atgtttttgt	ggggaacaaa	tgcgaaaatt	ccggnacgca	aacctaccga	tatgaaatga	600
tgtattccgt	tgtacttgag	accggagtgt	gcaggatcct	ctctccaaaa	tgtacttcgt	660
aagtgtaaat	tagcttactt	tgtaatatata	aacaaagtag	tacagtcgga	aaaataaagt	720
atcacaaatc	tcacttaagt	taaaattatg	gcaaaagaaa	aagaaaagct	cttttccgaa	780
ttcctccggg	ttcgagagaa	gcctggatcg	ataagataac	ggccgatctc	aaggggttcc	840
ctttgagaag	aagcttgtct	ggcggacgaa	cgagggtctt	aagtcaatcc	gttttatcgc	900
agagaggaca	tcgaggatct	gaagacaacg	attctcttcc			940

(2) INFORMATION FOR SEQ ID NO:349

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

ttggaaaatg	aaaggggaata	agtttgcgct	cataaaccta	acgattgctc	gttcggttat	60
caaacaagta	cgaattaatg	ggacctttgc	acaatgagag	gcacttttgt	ttattcttct	120
tattgtgtgt	cagggcacta	tttggtaacg	cgaattttcc	acaagtggaa	agctatcttt	180
ccaccagtgg	aaagtttggt	tccaccagtg	gaaaaagaat	ttccacttg	tggttttggc	240
gaaaattcca	taagtataga	atgagagcta	tattgtcttc	actttcccaa	tctctgggtc	300
gaactcacat	tcgtgaataa	accgttttct	aacagatact	atcggtctgt	attgcgtact	360
tttggggcaa	atcagtacaa	acagcatgga	tagaaatctt	ttcaggaata	ttatgccacc	420
ggcttttagcc	attgctatgg	tgtggcacat	cgaacgagca	cggctctgcac	gtaaagagtt	480
attgggcgga	gagcatccgg	atgagacggt	agcgtatttc	cgccccgatt	cacatcatag	540
ggaggattcc	ccggctttgt	ctatggaggg	ctgattgccc	ctatccttac	tgccatggca	600
atggtaccgc	agccgctgca	ggttatcggt	ttcaaagcgc	ccgatggatt	cggagccgaa	660
tctgagatac	gtgacagcta	atctgatctc	aactatcgcc	gtcctacccc	gatgggagta	720
gacttggagc	tacgccccat	atcaaagagg	taacggaccg	gaaagtactg	atggagctat	780
cgctatttga	gaagggcagg	taacggtgga	agggagcatg	ctatccgtcc	tgccccgaa	840
aagaagtatg	ccaagcaaac	ggagagggga	ggatataaaa	cggctttgcg	actcaagcat	900
agacg						905

(2) INFORMATION FOR SEQ ID NO:350

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 745 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

tggagggatc	ccccttgatg	atactaccca	tcattcgctc	cataagcaca	agttgtcgcg	60
atcagcccat	tcgccccgat	agagatccat	ggctcgccat	agttgccctc	tgccaaatgc	120
gctatgcgga	tgatgtcggc	cgtgtttcct	gattgttacg	agacaaggct	tccactattt	180
cgatctcgtg	cagcaacgca	cgttgatcag	ctgtgtacgg	ctcctgatcg	ttcccaacac	240
cttgtcggct	cgctgctgat	cataaagaag	agcgtatgct	cgggggggctc	ctcttcagct	300
tcagcagttt	gtttgccatg	gcttcattca	tccgctccgg	ttgcaaatca	tcaccacacg	360
atacgaggct	tcatagatgc	ggaagctgag	ttctgtctca	cggcttcggc	ttccttgctg	420

taaatgatgg	gttggtgtt	gcggctttga	tgtattcgag	ccagtcggca	ggggtaaagt
aggattccga	ccgagcatct	cgcgccactg	acggatgtag	tcatcgctcg	gtgcaggcga
gaggacgcgt	ttacgacagg	atagacgaaa	aacagatcgg	ggtgtgccgc	gcatcgtatt
tcacacacga	cggacaatga	ccacaagcat	ccgtatcgtc	ggcatctggc	agttgagata
gcgtgcgtag	gccaaaagcca	aagggaagcc	cctccccct	cttctcgggc	aaagagctgt
gcattggccta	tctgctcgtc	tgagc			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- ```
(A) NAME/KEY: misc_feature
(B) LOCATION 1...534
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| cagaaataac  | ttatcaaaaag | caaactcctt | gattatcatt  | ggatatgggt | taaagataaa | 60  |
| ggaataaatg  | aatgataaaa  | ggacaatttc | gattacaaaa  | taaaccttca | ttcattatcg | 120 |
| acaagtatgc  | aggtgcctcc  | gttgaaaatt | cgctcaaaaa  | attaatgcta | aaattattaa | 180 |
| ggaatctata  | gagagataga  | taaaacatgg | tttgtttaat  | gcaaagaggt | aagagtgtgt | 240 |
| gtcaaatgac  | acacactcct  | taaaaataaa | ttattgctaa  | atactatttc | aaattcaag  | 300 |
| gtcaattttt  | ctatcgtgtc  | agtgtagcac | acattttgtcc | actctccatt | ttgaatacaa | 360 |
| atggtcagtc  | cgtaatcttc  | cccattgaaa | tcattccaacc | aaaaggcgac | attgcctgaa | 420 |
| cagggatatac | cccttaaaac  | atcttatcta | ctgattggct  | gacaattttc | gcattggcct | 480 |
| gggagacatc  | gcacattggg  | ttggccaaac | tgggtgcatt  | ccatcccaaa | ttat       | 534 |

## (2) INFORMATION FOR SEQ ID NO:352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

|            |            |            |            |                         |            |     |
|------------|------------|------------|------------|-------------------------|------------|-----|
| gatttgagca | agttagactc | ttatctcacg | gctgaaaaca | tctcttttca              | gaggtttcgt | 60  |
| atgaaaatct | tcaacatttc | gtagccgaat | tgtatgactc | ggc <sup>a</sup> tcagtg | cgcgctcgat | 120 |
| agcgcgtatc | atcagcggtg | tcaagagttc | ttccgcttcc | tcgttttgga              | agagtatatc | 180 |



|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| gaagcggatc  | ctaccggttg  | ctcgaaggcc | ctcgcacg   | tgtccatctg | cctacgggat  | 240 |
| tgacctcgaa  | gaagttgatc  | gactgatcgg | atcgatcgat | ccggcagctc | aggggccccaa | 300 |
| cgcaatcgcg  | ccattctgga  | aatactctat | agctgtggtc | tgctgtcagc | gaactgactt  | 360 |
| ctttgaaatt  | cagcaatctc  | ttcctcaacg | aacatttttg | cgatcggatg | gcaaagggcg  | 420 |
| caaacagcgt  | cttgtagccca | tagcgagact | gctatcaccg | agctgaagcg | gtatctgtcc  | 480 |
| gatccccgaac | cccgaaccct  | gttcttggac | aagaggagta | tgtgtttctg | agcaatcgcg  |     |

## (2) INFORMATION FOR SEQ ID NO:353

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...843

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| tcttcagcac  | acgggtcatag | acatcttgat | gaagaaaactt | cgccaagcgc | caaagatcat  | 60  |
| agcatcaaac  | aagtggcctt  | ggccggcggt | gtatcggcaa  | taccggactg | cgcgatgctt  | 120 |
| ttcatgacca  | tgcccagcgt  | tatggctgac | tgtattcatt  | cccaaattcg | cctatacaac  | 180 |
| ggacaatgct  | gctatgtagc  | catttccgga | tactataagt  | acttgcaggg | cgattttctgc | 240 |
| cccatgatgc  | tgttccattc  | tcgcgcacga | cggtctgatg  | gataatcccg | ttattccgaa  | 300 |
| ctggcgaaagc | tcttgactga  | gcgaggcctt | acattggcta  | ctgcgagagt | tgccaccggag | 360 |
| gaactattgc  | ttcggctcta  | actcattgcc | cggaacctcg  | acttttttca | gagggttcggt | 420 |
| cgtggcatat  | cagaacgaca  | taaaatacgc | cttttgggag  | tgtcccaagc | cgatattgaa  | 480 |
| agccatacag  | agtcagcgag  | cctgtggcac | gcagtatggc  | tgtgggtggt | tgccgtctgt  | 540 |
| tgatgccaat  | ataggaattg  | cgactacggg | aatagccgga  | ccttcggggg | ttcggatctg  | 600 |
| gtgccggctg  | gcacagtttg  | gategctctt | gtcatcgtga  | ggacactttc | gcgcactgtc  | 660 |
| tgcattcttag | cggtactcgt  | gaggagttat | cgctcaggcc  | accgatcagg | cacttttgac  | 720 |
| tatatttgac  | ctctgaaaaa  | caaattgtga | ccggtataaa  | tccaataaaa | atatcagcag  | 780 |
| aaataagatg  | aaatcggtta  | tttgctatag | caatcgctac  | attgcttttc | agcacagcga  | 840 |
| cct         |             |            |             |            |             | 843 |

## (2) INFORMATION FOR SEQ ID NO:354

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature

(B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| tcctgcgcaa | agaggggttat | ccgcgccatg  | cactgggtttg | cgaacgccaa | cgggttcagg | 60  |
| attgacttcg | gaagacattg  | cagccagaca  | gattgcactc  | ctccgggtat | ttataccct  | 120 |
| cagagtattg | aggagaaaat  | tgtttgatg   | ccgataagtt  | ttctccaag  | acaaaactcc | 180 |
| atcgtcagaa | aaagctgaag  | acgtcaggcg  | cagtatgctc  | tcctacggag | ccgatagcct | 240 |
| ccgcctttcg | acgagatgca  | cgccttattc  | aaaatcccat  | taggataaaa | gtcaaggaat | 300 |
| atcaggaggg | tggcccgaat  | aatctaaagg  | attctcttcc  | tgcgaaaatc | tgctttttga | 360 |
| aatagtagag | aagcctcata  | atcaatggat  | cgtgaccgac  | aaattacctt | ttgctctcta | 420 |
| ttcgcggtgc | gtcaaagccg  | gaaacgtttc  | tactacattg  | atgccaaacg | cgattctaaa | 480 |
| ggaaatgact | tctggtgata  | acggaaaagta | acagtgccga  | agaaggttct | gcaatgacgg | 540 |
| gcataaggtt | ttcctctatc  | gcgaagattt  | tgccaaattc  | acagaagctt | tttggaagtg | 600 |
| ctaaagtctt | tcgaaaagag  | gagcggagta  | tccggatcga  | acaggcgatc | ggtttgtctg | 660 |
| aattggagca | gagcctttcc  | gatatgcaac  | gggagtggag  | ggtttagcag | agtcctccga | 720 |
| ttctattttg | gaggagatga  | accgctgaaa  | atagatttcg  | atttttgatc | ttcctcccat | 780 |
| ttcccccttc | caaggaggga  | ctctctctcc  |             |            |            | 810 |

(2) INFORMATION FOR SEQ ID NO:355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| gaagcattac  | agtactattc  | cgtaccggcg | actaacacgg  | tcataactat  | gccgatggta  | 60  |
| aacgttatcg  | ttttgtcgaa  | gtcccaggct | ccacgccgat  | ccggggccaaa | tcggatatcag | 120 |
| ttggaaaaaa  | ccggcaggaa  | acgtttattc | gcttacaagc  | tcctcaatta  | ttggatggga  | 180 |
| ggaacaacag  | accaacgagt  | gaatgggatg | tgacgtccaa  | ttggacagga  | gcccgaagtac | 240 |
| cgctccagga  | gaagatgtag  | agtttgcaac | gacagaaaaat | ttcggttctc  | cggcgtagcc  | 300 |
| gatttgcatt  | tcccgcacaac | caacccccaa | attatcggtg  | acatatcaat  | aattcccagc  | 360 |
| aagggaattta | gtttgtttac  | cacaaggcag | tcatttggac  | gaatcaaccg  | ggcg        | 414 |

(2) INFORMATION FOR SEQ ID NO:356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...590

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| tgctttatgt  | tgaatttggg | caatttgtgt | taaagcgtat | atatcgaatc  | ctcgacttct  | 60  |
| ttaaaaagaa  | tggcaggaaa | atcccctgaa | aaataaactt | atctgcacca  | atttttccca  | 120 |
| actcctggta  | ttcaggatta | gaggctgtat | tcctgaacat | ctcactaaat  | gctcatagcc  | 180 |
| taattttctta | tagaaaaatt | tgtactcatc | tatttgacac | tacatcagaa  | agctcaaggg  | 240 |
| agcactccta  | tatccggcaa | agatacgaaa | aagagattat | atcacaaatgt | ctaagtggat  | 300 |
| ttattttcagg | attgaagttg | tatttttctg | ttatgtaatt | taggtaaaca  | caaagtctga  | 360 |
| gcattatgta  | atacagagat | gagaaagacg | atgttaaaca | aataaggggtg | tttcggaagt  | 420 |
| gcttgctgag  | cagagaggac | aacagcagaa | agtcctgcat | gattgcagat  | tgataataga  | 480 |
| tggaggaata  | atagcacggt | acccgatgaa | gaaaatcaac | ccgtgcattc  | gatattctata | 540 |
| tgaaaagcgg  | ataggcgaga | ttggtacagt | ctttttggtc | ggtgagccgg  |             | 590 |

## (2) INFORMATION FOR SEQ ID NO:357

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...421

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ggacgaggtg | caaattcgggt | ggcacttttt | tatatctttg | tcccgagaca | tttgctcgaa | 60  |
| tctcagcaaa | cgaagtcttt  | caatcactta | aaaacagaag | ttatgacagt | aaagcgcgca | 120 |
| gtgcgaatag | cacttctcac  | gctgatatga | ttcttttttc | ctcaccttct | cttggtcggg | 180 |
| cgcaaagtct | tttcagaccg  | aacatgtctt | gcaactatac | aacaagatac | tctatggaga | 240 |
| gtcggggcgg | ataccgtcgc  | agagaaaacg | gcaggtgagt | cggcatttcc | tttttagaca | 300 |
| aactcatcaa | tctnggcgc   | actttcctcg | gcaaaccata | tcgtatcgcg | gtccttcccc | 360 |
| atggccgatn | gactgctcgg  | gctatgtgtc | ttacctntac | tccaaaattc | gacatcaaac | 420 |
| t          |             |            |            |            |            | 421 |

## (2) INFORMATION FOR SEQ ID NO:358

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| gaattcttta | tctgtctaacc | atttcgggca | caagatcaat  | acttcccaaa | tagcttatga | 60  |
| gcaagatcag | cttcaaaaac  | gactattctg | aagggtcgat  | cctgacatac | tgcatgcgct | 120 |
| gacagatacc | aacttcgttc  | cacaagagga | tacggctatg  | actcctattg | cgaggaagcg | 180 |
| cgtgcgatga | tccgcctgaa  | tgcaataagc | ccgatgccga  | gggccatttc | gtatcgggtg | 240 |
| ggacaagacc | aatctcttgg  | caatcagtca | cctgctccgt  | ccgcacgaag | ctgtatagca | 300 |
| gcacagtcag | ggcatatcaa  | cgtacacgaa | accgggtgcc  | tcgatccacc | ggacataagg | 360 |
| tttgcacagt | acctactcca  | ctcgggaaac | tctgtgtggag | catatccgcg | aagtccttgc | 420 |
| ttttcatacg | gacgaacaca  | tgtaaggccg | tccatggtct  | atatctccca | atccacagag | 480 |
| ttgggcacac | ctattctcgt  | catgagctgt | cggatctgtc  | caccttttgc | cgtgcaaacg | 540 |
| tctcctactc | taccttgacg  | gtgcccgat  | cggttcggcg  | atcatggnga | gacagaggac | 600 |
| aatccgaccc | tgaccgatat  | agccaccctg | accgatggtt  | ctacatcggc | g          | 651 |

## (2) INFORMATION FOR SEQ ID NO:359

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2441 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...2441

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| gggaaatcga | ctcttttttaa | ttgtttgtcc  | aatgccaaag | cacagtctgc  | aatttccctt  | 60   |
| tctgtaccat | tgatccgaac  | gtcgggtgtaa | tcacagtgtc | gatgagcgac  | tgaatatcct  | 120  |
| ggccgatctg | tgcaaacccc  | aacggctatc  | ccaaccacgg | tagagatcgt  | agatattgcc  | 180  |
| gggtcttgta | aaggcgcagc  | aagggcgaag  | ggttagggaa | taaattcctg  | gccaatatcc  | 240  |
| gtgaacggat | gcgatactcc  | acgtgctccg  | atgcttcgat | gatgacaata  | tcaccacgtg  | 300  |
| gacggatccg | tagatcctgt  | acgcgcacaaa | gaaatcatcg | acacgagcta  | caactgaaag  | 360  |
| accttgaaac | gatagagagt  | cgcatacaga  | aatccaaaaa | caggcacaaa  | cagggggcga  | 420  |
| caaacaagcc | aagctggctt  | acaagtgtct  | tcgaaattca | aagaagctct  | tgacgaaggc  | 480  |
| aggaatgtc  | cagcgtcagt  | ttcgacacca  | aagacgaaca | gcaaatagca  | cgcgaaactct | 540  |
| tctcctgacg | gccaaaccgg  | tcattgtacgt | ttgcaatgtg | gacgaagctc  | tgctcttagt  | 600  |
| ggcaacaaat | atgtggaagc  | cgttcgcgaa  | gcagtcaaaa | cgaagatgca  | gaaatcctcg  | 660  |
| tcgtagcagc | caagatagag  | agcgagtcgc  | cgaactggag | acatacgaag  | agcggcaaat  | 720  |
| gttcctcgaa | gagatggctc  | gaaagaatcc  | ggcgtgagcc | gtctgatcaa  | agccgcttat  | 780  |
| cactgtgtaa | tcttcaaac   | tactttacgg  | ccgggagcga | tgaggtaagg  | gctggacatt  | 840  |
| cctccgcgga | agcaaaagcac | ctcagtgtgc  | cggatcatc  | caaccgattt  | tgaaaaaggg  | 900  |
| tttatccgtg | ccgaggtcat  | caagtacaat  | gctttgtcag | tcttggcagc  | gaacaagccg  | 960  |
| tgaaagaagc | cggtaagatg  | gtgttgaggg  | aaaagaatat | gttgtgcagg  | atggcgacat  | 1020 |
| catgcatttc | gcttcaatgt  | ctgaagtctt  | tctttcatcc | ttatccttct  | cgataacaaa  | 1080 |
| acacagtacg | gcattcggaa  | taaccgtata  | tcccggcgaa | agaaacaaaa  | ccaaaagagc  | 1140 |
| gggtcggctg | tctttttgca  | aagttatggt  | tcaggattca | gcgagtatcg  | aacaaatact  | 1200 |
| cctgcatttt | tcttaagtag  | aaaaataaaa  | ctgcgcaaac | aatatggcga  | acaatgggaa  | 1260 |
| taacaagaaa | cccgaaaacc  | gatgcgtttc  | aacccgatat | ggctctatgc  | ccctgtattt  | 1320 |
| ctgtattggc | caccctcttc  | tttgctgac   | gggatattac | atcccagaaa  | gactcagctg  | 1380 |
| gaattgagtt | tcagaatatc  | gccaaaaaag  | caagccttta | cgatctcgta  | gtcaatcgga  | 1440 |
| aagagaacac | tctcaaggcg  | agggctgac   | ggccaaggtc | gattcgggtat | tcaagaaagg  | 1500 |

|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| cgacatcccg  | tcctttcaga | cagaggaaat  | atctcagact  | actatatcaa | cacgcaaatt  | 1560 |
| ccgtcgggtga | caaattctcc | gacttctacg  | acccaaaacca | aattacggct | aagggtgagta | 1620 |
| tgaagacagc  | aagttcagct | tcacctctat  | cctcattaca  | tggggccact | catccttttg  | 1680 |
| ctcgttttct  | ggttttggat | gatgcgccga  | atgagggcgg  | tggaggagga | agtggcgggtg | 1740 |
| gaggcggcgt  | cttcaacgta | ggcaatccaa  | agccaagctc  | tatgacaaga | ccaatatcca  | 1800 |
| cgttacattc  | agcatgtagc | aggtctgcat  | gaagccaagc  | aggaagtgga | agagatcggt  | 1860 |
| cattcctcaa  | gaatccatcc | aaatacacccg | aactgggagg  | aaagatccct | aaggagcttt  | 1920 |
| gctcgttagga | cctccgggaa | cgggtaagac  | tcttctggcc  | aggcagtagc | cggagaggcg  | 1980 |
| cacgttcctt  | tcttctcttt | gtccgggttcg | acttcgtaga  | gatgtttgtc | ggcgtaggag  | 2040 |
| cctctcgtgt  | tcgcgacctt | tcagacaagc  | caaggaaaaa  | gccccgtgta | tcattctcat  | 2100 |
| cgacgagtcg  | acgccgtagg | gcgtgctcgc  | ggcaagggca  | acaacttctc | cggcaagatg  | 2160 |
| agcgtgagaa  | tacactcaac | cagttgctta  | ccgaaatgga  | tggctcggct | ccaatagcgg  | 2220 |
| tgtgatcatt  | ctggctgcta | ccaaccgtgc  | cgattgctgg  | atagtgcctt | gctgcgtgcc  | 2280 |
| ggacgtttcg  | accgccagat | ctagtagatc  | ttcccgacct  | gaatgaccgc | aaagagatct  | 2340 |
| tccttgtaga  | cctaaaccgt | tgaagaccga  | caaaagtgtg  | gatgtggaat | tcctgtcgcg  | 2400 |
| caaacacccg  | gcttctccgg | agcagacatt  | gccaacgttt  | g          |             | 2441 |

## (2) INFORMATION FOR SEQ ID NO:360

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...549

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| agcaaaggac | aaattgaaag  | aaagccatcg | acaagtaatg  | gcattgatca  | gacatttttcg | 60  |
| aacgatgaat | tatttgccaa  | gggagtattc | gactggacga  | tacttcgact  | ctcgggtgcat | 120 |
| actgcgtatc | agccacttcc  | agtcattcga | ctgggcgatg  | aagaaaaataa | agctacatat  | 180 |
| caagaccggt | aagtgacgga  | tgcgaagttg | tttgtgtgcc  | aaatgctctt  | tcttcttgca  | 240 |
| gtatttatta | tgggcaaagt  | ggcagtagac | atctctccta  | aagagggtat  | ttttgctctt  | 300 |
| gtaacagggg | cttctcacag  | gtgaagacaa | tggagcttcc  | ggatcatggt  | tgaaaaaacg  | 360 |
| tatgaaggat | agggaaactca | ccgcagaaaa | tcgaccgttc  | gtaccttgag  | tgaaaaacgt  | 420 |
| gagcaaaacg | gatgtaagcc  | cgtagaaatc | gtcagcccga  | ctgacacaat  | cgccaagtat  | 480 |
| gggaagttgc | tcgttggtaa  | gtatcatttc | cgcactctatc | ggctatctcg  | tatcgtatgga | 540 |
| gagctgaac  |             |            |             |             |             | 549 |

## (2) INFORMATION FOR SEQ ID NO:361

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...5015

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| cgctatcgat  | aagctccaag  | aaaaagaaat  | ctcctacacc  | aattgcagaa  | tcgaaagtgc  | 60   |
| ggtatcgctt  | atcagtgagt  | tttccgcccc  | cacnttttca  | tccttcaagc  | atacgaaatg  | 120  |
| cctgtggcat  | agcttcgcgc  | ggtacacgat  | cgaagcttgg  | caggctgctc  | ttgccggtga  | 180  |
| tcccggatcg  | gcttttgccg  | catattggtg  | acaaatactc  | ctatcgatag  | ggagacagct  | 240  |
| caggaatcga  | caagattttc  | ttcgaggtga  | tcattgctcc  | cgactacgat  | aatgtgccat  | 300  |
| ggaatatctg  | acacgcaaga  | cgaacaggat  | tatactttcta | cagaagagcc  | tgtacgtgag  | 360  |
| cagtggcagt  | tcgcgtccat  | gtttggcggt  | gtctcatgca  | gcagggtggat | ggtgtgacag  | 420  |
| ccaagactgt  | tcgtttcaag  | ctgtaacacc  | cgtagtgcct  | acagcagatg  | aaacggacga  | 480  |
| cctcatcttt  | ccaataaggt  | agtgaagcat  | agcaagagta  | atgctattac  | tttgggtcaag | 540  |
| atagccaact  | ttgtgccagt  | ggagttgggc  | agacctccag  | agtcgatgtt  | tgcgacaggc  | 600  |
| tatcgataaa  | gcacggaatt  | tcggctttga  | cctgaatggg  | ctgtcatggc  | cagcgatgct  | 660  |
| ttctttcctt  | ttgccgattg  | tgtggaatag  | cagccgaagc  | aggtattcgc  | gctatcattc  | 720  |
| agccccggagg | ttccataagg  | acaatctgag  | catcgaagag  | gccacaaaaa  | aagggtattgc | 780  |
| catgtgatga  | cggtgttaag  | acattttcaaa | cattaacaaa  | aacatagaaa  | atagcctgtc  | 840  |
| gcaagagaaat | ggtcggggta  | tagcactccc  | gtaccgtcac  | aacacaggaa  | atgcttttct  | 900  |
| acagatacag  | aacaagatgg  | gattattttc  | tttcgacagg  | aattggccat  | tgacttaggt  | 960  |
| acggctaata  | cgataatcat  | aaagatggta  | aggtcgtctt  | ggacgaacct  | tcgtagtag   | 1020 |
| cattcgatcc  | cgcacggatg  | aagtgatagc  | agtagggaca  | gatgctcgtg  | agatgtatag  | 1080 |
| aaaggacacc  | agcatatcag  | gacagtacgc  | cccttgccag  | atggtgtata  | gccgacttca  | 1140 |
| aagctgccga  | gcagatgata  | agcggtagat  | tcgtagatc   | ggtaagaagc  | atcgctggat  | 1200 |
| ccatccatcg  | ctccgcattg  | tgatcgtata  | ccctcgggta  | gtacggaagt  | cgagatgcgt  | 1260 |
| gccgtgcgcg  | actcagcgag  | catgcaggtg  | ggcgtgacgt  | atataatgata | tatgaacctc  | 1320 |
| tggtgctgct  | gtgggtatcg  | gcacgatggt  | attggctccg  | gagggaaata  | tggtgtggat  | 1380 |
| ataggtggag  | gtacaacgga  | gatcgccgtc  | atttcaactg  | gggtatcgtc  | atggaccagt  | 1440 |
| ccattcgtgt  | agccggtgat  | gaactgacca  | tgatattatg  | gactatatgc  | gccgcgaaca  | 1500 |
| caatgtaaa   | atcggggagg  | tacagctgag  | cagatcaaaa  | tcaatgtagg  | tgacgcttcg  | 1560 |
| gaagacttgc  | ttcaccgccc  | gagacctatc  | tggtctgcgg  | tgacgaccag  | atggatacct  | 1620 |
| tccgaggaag  | atacccgtaa  | gttataagga  | ggtggcacat  | tgtctgagaa  | gtccatcgtg  | 1680 |
| aagatcgaag  | ctgccatcct  | caaagcattg  | gaggaacccc  | tcccgaactt  | tatgccgaca  | 1740 |
| tcgtaaggaa  | cgggtgtatc  | ctgacggagg  | aggagctatg  | ttgcgcgggt  | tggaacaagc  | 1800 |
| tctgaccgat  | cgttcgggtat | cactttccaa  | gtagccgatg  | agcctctggt  | ggctgtagcc  | 1860 |
| aaggcacggg  | gattgcgctt  | aaatacgtgg  | acacattcaa  | cttccgtgatc | catagagata  | 1920 |
| gtccgaaaaa  | ccttcttcca  | gcattgctct  | acattgcgtaa | ctcattgagt  | ttatagtacg  | 1980 |
| tcatacaacat | tggtctactgt | ttctttttcg  | gagacggtag  | cctttgtcgt  | actcttcaac  | 2040 |
| gatagcatct  | accatcgacg  | cagggaaatg  | cggtagccaa  | tgccctgacg  | gggcgcacat  | 2100 |
| atagcctacg  | ggcgaagtgc  | gcagttatat  | gagttctcgt  | gagaaaaatc  | gtatgctctc  | 2160 |
| gatgccaatg  | cacggttgga  | gttggagtac  | atttcgctca  | agagactggt  | gatgcagccg  | 2220 |
| tagccgattc  | tgtacgcccc  | ctactgttcc  | ggccgatctc  | ctcaatccgc  | aaccggtgga  | 2280 |
| gatggactac  | ctgagagcac  | aggggtcaat  | gcctcctata  | acagggtgga  | gaatttcatg  | 2340 |
| accatagata  | aggacgagcc  | gatggtgtac  | tgccggaaat  | gggtgtagtg  | tcggctacgg  | 2400 |
| ggtggtgggt  | gccgtaacgg  | ctgcttcaga  | tcattatgct  | attgtgatcc  | gatcatcaac  | 2460 |
| ccgaaattca  | aactcagttg  | ccgactcaag  | ggaagcgaaa  | tgtaggttcc  | attctgtggg  | 2520 |
| agaagccccg  | gagcaatgta  | gcccagctac  | cgatctgccc  | cgtcacgtgc  | agttagcaca  | 2580 |
| gggagatacg  | gtagtgaagag | cgggtattca  | tccatcttcc  | ctgctaacct  | gatggtcggg  | 2640 |
| cgtgtggcaa  | gataaagggc  | aaggatacgc  | ctttggccga  | gagaaattcg  | ttcaggccgt  | 2700 |
| acctgtaate  | ctgtctgcgc  | acttcggtag  | gctgacggat  | gtgttgtgat  | cctgaacaag  | 2760 |
| atcgatatag  | agaggcaaaa  | gctggaggag  | gaaacggcat  | acccaaaacg  | gaggcttact  | 2820 |
| gatgattcgt  | gagataaggt  | tttcttggca  | gctgtgctgc  | tggttctgct  | acagggtatg  | 2880 |
| gtgttcaact  | aatatttctg  | ttcaaagtga  | ccactccttt  | tggtctatata | tatactctga  | 2940 |
| gctgttgccg  | ctgaacgtgt  | ctgtttccgc  | ctctctgtgg  | cgagcattct  | aataggcatg  | 3000 |
| ttctctgatg  | tccttagtgg  | agtaccgggg  | ctgcatgcgc  | atcattgacg  | gctacggctt  | 3060 |
| tcgtccgcaa  | cgggctggca  | cgtccttctt  | ggaaaaggat  | tcggacttgg  | ggtattcacc  | 3120 |
| gtcggcacgg  | aatctgaagt  | cggatatatat | gtattcgtgc  | tgagacttac  | catcatacat  | 3180 |
| catctctcct  | tttcattctg  | gactcgttga  | gcctgtcgag  | tgtgccgtat  | atgcgcttcg  | 3240 |
| tacaggagca  | agcatcctgc  | tgacttatct  | gctattgctt  | atttgaactc  | gcttttcggc  | 3300 |
| aagagactca  | aaatgccaga  | aaatgagtaa  | acgcggaaag  | atcccaacga  | aaaacatcgt  | 3360 |
| ttcttattgg  | tgatagccac  | ttctgtgtgg  | tattcatcta  | tgcgatacgc  | cttttctatt  | 3420 |
| tgcaaatcct  | agtcggaact  | ataaggctcg  | tgccgatagc  | aatgctttct  | atcagaagct  | 3480 |
| gtatatcctt  | cgcgtggcgt  | gatatacgac  | cgcaacggag  | agctcctctg  | tataacgaac  | 3540 |
| cggcctatga  | ccttgttagcc | gtgacgaaag  | aggtagggaa  | ttcgacaccc  | ttgcctctgt  | 3600 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| tcagaccttg | aatgtggagc | cggagttgta | cgcaagcggt | ttcaggacat | aagggatcgt | 3660 |
| cgtatcaacc | ccggcattcg | ccttacgtac | ctcaactcct | gctggcgcaa | ttgaaccctc | 3720 |
| gcgagcggga | cgttttcagg | agcagctggt | caaattcccg | ggcttttcca | ttctcccctg | 3780 |
| gccatccgtc | aatataagta | tcatggagcc | gcacatgtgc | tggctatctt | tccgaagcga | 3840 |
| atatgctgta | cttagagcgc | gacagctcgc | tattgccggc | gactatgtgg | gtagaagcgg | 3900 |
| tatagagcgt | cagtacgaga | aacgctccga | ggcgaaaaag | ggatagaagt | cctgcttcgt | 3960 |
| gacgctcgcg | tcgtatcaaa | ggacactact | ccgatggcaa | atacgattcg | ccggccatcc | 4020 |
| cggacgcgat | ctgacccttt | cgatcgacag | caagctacag | acactggcga | acagctgatg | 4080 |
| cagggaaagc | gcggagctat | agtaatgatc | gaaccgagac | gggggaagtg | ctctgtctcg | 4140 |
| tctcttcacc | ctcctacgat | ccctcctact | tgcgggtaag | gacaggggga | aaaatcatct | 4200 |
| ggagatggaa | catgtcgaaa | caagcccctg | tatgcccggt | ccattcaggc | cacctatcct | 4260 |
| cccgtctcac | tttcaagccg | gcacaagggg | ctatctttct | gcaggaaggg | gtatcaggcc | 4320 |
| tacggatgct | tttagctggt | atcacgggtt | ccctcccctg | acaacagacc | ggcctgtcac | 4380 |
| agccacggct | ctccactcag | tctggtgccc | cattggccac | cagctgcaat | gccttcttct | 4440 |
| gctgggggct | ccgtgccatc | tggataacag | gcggttctat | ccttccgttc | aggaggcatt | 4500 |
| cgagcattga | aaaaaacaag | agccgcacac | gggggcgcgc | acacacgcgc | acacgagtc  | 4560 |
| ccccggagag | acgagacgat | atacccaaaa | caaaaaggta | caacaaacgc | ataaaaggcg | 4620 |
| agagaaaacc | cccacaacaa | tatccacatc | gagaggcaca | gcgaaaaatc | agacccactc | 4680 |
| cgctccaaat | agccaatctg | ggtgcacatc | tgccaacagg | ggacgctatc | gccgtccgca | 4740 |
| tgtggtgaaa | gccttcaggg | gatccccctc | gatacagctt | atacgaactg | gcagaatagc | 4800 |
| ggatcagtc  | ggcgaatatg | gagtatatag | tagaaggaat | ggcgagagcc | gaacgggcgc | 4860 |
| aacctgtcat | gcagccaact | tcgccccggg | ggaaatagag | tatgccggca | agacgggtac | 4920 |
| cggccgagaa | tcctcacggt | aaagaccatc | ggctttcctt | ggctttgccc | ctgcaacaat | 4980 |
| ccgaaggtgg | tcgtatccct | atgtggagaa | cggcgc     |            |            | 5015 |

## (2) INFORMATION FOR SEQ ID NO:362

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 556 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

|            |            |             |             |            |             |     |
|------------|------------|-------------|-------------|------------|-------------|-----|
| gcaagatata | caaactttta | atcgggagat  | tatcgctaaa  | ccatatgact | aaaaattgag  | 60  |
| aaggacgatg | tgctgaacat | ccttgctcagc | agtagagacc  | ggagctttca | acgccctaca  | 120 |
| accaagtgtt | gaccactcgt | gcactggccg  | caacggctat  | ggaacgaact | cgaacgaagg  | 180 |
| cttcctggtc | gattcgaagg | gtacatcaat  | tatcctatct  | taggccagat | ctatgtagag  | 240 |
| ggcctactcg | taccgaactg | gagaaggaga  | tacagaagag  | gattatttcc | agtgatttat  | 300 |
| caaggatcct | acggtaacgg | tgcagcttca  | aaattttcaag | gtgcgggttt | gggagagggtg | 360 |
| aatcatccgg | gttcgatgtc | ggtaaaagga  | gacgaataac  | tcttttgtaa | gcgatcggaa  | 420 |
| tggccggaga | cccgacaatc | ttggtcgccc  | gcgatcgggt  | ttttgtgatt | agagaaaccc  | 480 |
| gatgggcata | cagaggtttt | cagacggatc  | tcagaaaggc  | ccacttgctc | gcaagcccct  | 540 |
| gtactatctt | gcattc     |             |             |            |             | 556 |

## (2) INFORMATION FOR SEQ ID NO:363

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 685 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...685

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| gccgggtttcc | gtctggtaca | ccatcaggag  | ttcgggtacac | gaatgacgct | aagggtatcca | 60  |
| tactcgccaa  | gtatgggccg | ctgaacttcc  | gcgctacgat  | gctaacggct | ataagactcc  | 120 |
| cacgctgaaa  | gagctttttg | cacggaagaa  | ctcaccacta  | tgggttcgca | caatctctat  | 180 |
| ctcggcaatg  | cggatctaag | ccacagatgt  | cggattatta  | tgctttgggc | ttggagtaca  | 240 |
| atcaagccct  | atctcgttca | gtgcaacggt  | ttatgacaat  | gaacttcgca | atctatctcc  | 300 |
| tttatggata  | taccgacctc | acccgagcac  | gaagctcagg  | gaacaagaaa | accaagcagt  | 360 |
| atgccaacat  | aggaaaagct | cgcagccgcg  | gcttgatgtc  | ctatgtgatg | cctctatcgg  | 420 |
| ttgggggtatc | aagttaggag | cggatacagc  | ctcgtggaag  | ctaagaatct | ccagacggat  | 480 |
| gagtggctgg  | aggagctgca | cgtcactcgtg | ccaatgtgca  | cgcgatttgg | gttcaactacg | 540 |
| gggtcagtat  | agacttggcg | tgagcctttt  | cggccgtatt  | cagagcgacg | ttactacaaa  | 600 |
| gacggcaatg  | ctccggacta | taccttgtgg  | cgactcgcac  | atcgcatcgt | ttcgctcatt  | 660 |
| tccgccacat  | catcctggat | ggaac       |             |            |             | 685 |

## (2) INFORMATION FOR SEQ ID NO:364

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 401 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| tggatttggc  | acgtctatgc  | ggcatgcaac | cggctgcagc | cctcatagaa  | ttatcaatga | 60  |
| ggacgggtacc | atggcacgtt  | tgccacagct | atgggaggct | ccaagcgttt  | tggactgaag | 120 |
| atcattgcca  | tcaaagatct  | gatagccacc | gcctcaaaca | agaatccatc  | gtagaaaagg | 180 |
| gtgtagaagt  | ggatataccta | ccgaatacgg | acacttccga | ctcatacctt  | tccgtcaaaa | 240 |
| atccatggac  | tggagcacat  | agctttgttc | aaggggacgt | gggacgaaaa  | tgaacgatac | 300 |
| tcgttcgtat  | gcactcatcc  | tgtgccactg | gcgacatatt | cggctctatgc | gttgtgactg | 360 |
| tggcggccaa  | ttactgcaag  | caatggagaa | gacgagaaag | a           |            | 401 |

## (2) INFORMATION FOR SEQ ID NO:365

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 529 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double



- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...529
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gcgtgataag | gctgcggtaa | tactcgtgtg | tggagaggtg | cttggcgagg | accctcttac | 60  |
| acctcttttc | agcccgta   | tctccatgtg | ttcggcggtg | tgctctgata | cctgataagg | 120 |
| ctggcacggc | tcatcacctc | gtccgcaaga | ggcgtggggc | aggtgctttc | gtcctgtacc | 180 |
| tgcgccctgc | gttctctcct | tcttctgctt | cctgcgctcg | ccctgcacta | tcggcactac | 240 |
| ggtggatgga | tgtgcggcgt | ttcctcgtcc | atgtgcagca | ctgccgatac | gaggtttcag | 300 |
| ctccgtaggt | ctctctcagc | cacgccacgc | tgtcatcgca | ccatctccga | gcctcccttc | 360 |
| gtcttccatc | cgtgccatat | cctcgtgcgt | tcgctcagca | cgatgccgta | ttgcctgcac | 420 |
| ttggttcttt | ccaatcttac | gttcaatccc | gccgtgtcaa | ggcgggtggc | tatggctaac | 480 |
| gtgcggttgc | cacgccgtcg | ggaaacatta | ttaactcacg | gtttagatg  |            | 529 |

(2) INFORMATION FOR SEQ ID NO:366

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| catcagagac  | cctccttgaa | tatcgtttga  | tttgcaacgt  | caccttgccg | agaaggctcc | 60   |
| gaacaggctc  | gctatctcac | aagccgacat  | ccaaacagag  | ttgacgggat | atgtacattt | 120  |
| cccttcccat  | ctatggttat | agttcctttt  | tcatagttgt  | ttagtattca | ttgttctttc | 180  |
| gtctttccat  | cagccttcca | tatcctctga  | gattttcttc  | tccgaaatct | tcgcatagtt | 240  |
| ctgcggctgg  | taatggaagc | atgtcccatc  | atcttggtcaa | tgctttccgt | acattacctt | 300  |
| ccgagattaa  | gaacgatccg | aagctatgcc  | ttgcttgatg  | gtagacaggt | tctccttgcg | 360  |
| tccgatgatg  | acaccaggtt | catgtatttc  | aaccacatca  | tatccctgct | tggcaaaggg | 420  |
| aagacgggtt  | gtgtgtcatc | ttcgtgttgt  | atagattgat  | aatctgctcg | gctatcggat | 480  |
| gcaggggaat  | aatgattcta | ctttcgtctt  | cctgcgggta  | atccgtatat | aacgccgtcc | 540  |
| tcggccgtct  | ttcctatgtg | gtgcggatat  | agcaattgcg  | tatcaacaag | gcaagccccg | 600  |
| taaaacagga  | gaagatgaaa | gtccgtcgag  | ccagttcttc  | aacgggtcgt | tctgtggcaa | 660  |
| tttaagttcc  | aacaactggt | tcagttcgct  | ttgctgatgt  | gcatacgctt | ggcagggggc | 720  |
| ttctttctcat | attcgcttct | tctaattggat | tggctcggat  | aatctcatgg | tcaacggcaa | 780  |
| ggtaaccaat  | cgtttcagcc | aacaaaggca  | atggttggtc  | tcgatgtctc | cgagtttttg | 840  |
| tatcgtttca  | gataaacctt | gtattcccgt  | ccgaactcct  | cgtgatgtcc | aagaaagcaa | 900  |
| tgtcgtcatc  | gccttttgac | tccaaaaact  | ccgaatatata | atttggtaat | atcttgaact | 960  |
| tctgtatgtg  | gagtttgagc | tatttcgtta  | gctcttactg  | caagacgttc | tcgctccctt | 1020 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| tctcccatcg | gagtaaatga | atgggaacta | cgacatgtcc | cgcaatttca | tttttcaaag | 1080 |
| ttccgcactg | acaacaccat | atctcttaag | gagatcctca | taaagccttc | cgcatcactg | 1140 |
| cggaatttct | tcagacggtt | gtttgccgtg | catctgggtc | tctgcatttt | tggcggtcca | 1200 |
| ttggtggggg | tgcaggaaat | gccgtgtaat | gacgtgttct | ttccgtcat  |            | 1249 |

## (2) INFORMATION FOR SEQ ID NO:367

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2015

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| ttatactccg  | tccgatccgg  | atgattcagt  | agatattgca  | gacgggcacc | gctcggttac | 60   |
| cagcggcacg  | aggataaaaag | ccaaagtcgg  | agtgcggatt  | tgcccgatcg | tcgggcctcg | 120  |
| gaagcggcat  | cgatgaagag  | gtcgatactt  | tgttcctgta  | ctcgtaaccg | ccgctcgtgg | 180  |
| ctatcagtaa  | ggtatcgtag  | gcagttgctt  | gccggtcaga  | tgttcgcta  | cgtggagcag | 240  |
| tcgcttcgag  | cttctgcacg  | tcgcctctcg  | tattcttctc  | cttgtggcac | gaagtcgggt | 300  |
| cgaatccggt  | gggcagtagc  | atcggatcgc  | gttcgagcag  | ttgcggcatt | ctttggccgt | 360  |
| gagttcgctt  | accgtggcaa  | aggtgtccga  | ttgtgagccg  | ccgctttttc | tatcccgtgt | 420  |
| ttggcttcta  | caccgagttc  | gcagccattt  | gacgcgcgtt  | gtagcccggc | atgtaggcat | 480  |
| acagagcttt  | ttattgccgg  | cgatagaccg  | ccctgtgggt  | gtggcatgtg | tgaggaaaag | 540  |
| gttttcagac  | gaggtgtttt  | ccgcttgctg  | tagaggagtc  | ccatgccggc | atccattcgt | 600  |
| tgaatatacc  | tatggccggg  | tggctctcgg  | ggcagagtat  | tcacacaggc | tatgcacgtg | 660  |
| ttgggctgag  | gcaatgccga  | agagcggggc  | tcgtcatagt  | cgccgtaccc | gttgcgctt  | 720  |
| tggatgccga  | agtgcgccac  | atctcatagt  | agagcgttgc  | tttctgtgca | tggagggggt | 780  |
| cgaatccacc  | agtactacag  | ggggagaacc  | gggagttcgc  | cagctgccgc | acaatatcgc | 840  |
| aagtcacagg  | aggggtcgtc  | atcacgtagc  | cagctctcca  | agtggcaggg | actgtattct | 900  |
| caaaatcggt  | gggtaagtct  | tctgtctcgg  | tagcaggggg  | cctatgaaaa | tgatacgtcc | 960  |
| gtcgtggcgt  | ttcatcatct  | atgtgccctc  | gatgtaagca  | cagtgtatat | accaccctgc | 1020 |
| ttattgcaac  | ctcccagctc  | gtctccagca  | agagggaagg  | gttggggcga | aaatcattat | 1080 |
| tcgatcgcaa  | ttcgtttggt  | aaagtttttt  | ccggtcttat  | cctccgacaa | ccgccataca | 1140 |
| aaggccacgg  | ctacgggtac  | aacgaaacct  | gtggcagcgg  | aatcaaggct | gccagcagcg | 1200 |
| tccattttccg | gtctcccgtc  | tcttttatat  | gttaaaccagg | gtggtgctgc | aaggattgtg | 1260 |
| gagtaggcag  | aacacatgag  | attgatacct  | gtcagcatag  | tccaaccggc | ggcttcgaac | 1320 |
| agtgtgccgt  | ttcggtctgt  | ccatcggtct  | cgaacatgac  | gccggcaccg | gtcctccatc | 1380 |
| tattcccgtg  | gtcaggacag  | tcagcatcag  | tatcgtcggg  | acactatttc | attggccgga | 1440 |
| atggccaata  | cataggccag  | cagaatgaca  | cgttgagttc  | catcagccaa | ccgggtccgt | 1500 |
| ccagcagggt  | gacagatat   | cggtatccc   | gactccaccg  | atttggtatg | tgcaggtgag | 1560 |
| ccagataaag  | caccggccgg  | cgcggcaaaag | acaacggcac  | gccacaaaac | gacgagttac | 1620 |
| gggtctacgat | ggattttatg  | atcgtctgac  | aaaactgtgg  | cgggcgtagg | gtggaagctc | 1680 |
| cagattgaac  | gtggagactt  | gacctcgcag  | cagcgcgggg  | agagtaccca | agagaagaaa | 1740 |
| aacatgaaag  | cgatacccag  | caatcaatgg  | ccacgactga  | cccaatgccg | atcacgccac | 1800 |
| gcaaataggc  | cggacggcag  | gtgtgaggaa  | gatcgtggca  | aggagtattc | gtgtaggcca | 1860 |
| accccggttac | acagagagaa  | gttgttggtc  | agaatagcta  | tcagtctctc | ctttggctat | 1920 |
| cgatgatgag  | cgtattgatg  | attgctgccg  | cattgcagcc  | aagcccatcg | tcatggtcag | 1980 |
| agcctgcttg  | ccgtgcgcac  | ccgaacgaca  | agggg       |            |            | 2015 |

## (2) INFORMATION FOR SEQ ID NO:368

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...534

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ggcatttcaa  | aagcgataaa | cagcccttac | aatgaataaa | aaagtaccca | gctgtcagtc | 60  |
| tccaccgttg  | tgtaccgaaa | aaagttgaca | gttggggtag | cgggattcat | ataagtttac | 120 |
| acacataccg  | gttagtccta | tgctgggtta | caactgtcga | ttggattttc | cccttagggt | 180 |
| tacacaagca  | gatttaccct | ttgctcggga | ttcattcttc | tgtagttgta | gagttccgga | 240 |
| gcaatttccg  | agcctctctt | tgttgtgtat | ataaagagag | agatttgtgt | atatcgga   | 300 |
| tatatttccg  | tatataagaa | aatttatcgg | agtatatacg | aaatatattt | ccgcatatgc | 360 |
| ggaaatttcg  | ccaccttctt | ggtgcgataa | aacgctgacg | ctgaactact | tggtatcgga | 420 |
| ggcgagggtat | tcttcgagga | tcgaaggcgc | tccgaattgc | tgagatgttt | tgacattttt | 480 |
| ttcttgggtt  | tcgcacaccc | caactgcaac | ttttttcagg | ncacgacagg | atca       | 534 |

## (2) INFORMATION FOR SEQ ID NO:369

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 577 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...577

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| ccaaacgatt | ttgcttctgc  | accacgtaag | tttcggtgct  | tttgtctctc  | atthttccatt | 60  |
| gcctcctcca | agagctccac  | acaagatata | gtccgaaggg  | cttcttggtg  | ttcttaaaga  | 120 |
| gtgcgatcgg | tcagaaaaag  | acgaacccaa | atcagaagaa  | agtgggttccg | gaaatcctga  | 180 |
| aaacacgcgc | gaaaaaattt  | cgtttttggt | cgggaaacaaa | aaaattctcg  | aaccaaaacg  | 240 |
| aaaaattctc | agaccacgtt  | ttgcggagct | atactcggca  | aaatttacga  | acgaaaagcg  | 300 |
| tgcaagatga | gtatgcccc   | tctcgtgtat | tttgtatcgg  | aggggtagag  | agttttgtca  | 360 |
| gaggccttgg | ccatctaaac  | caaacggctt | gacacagagg  | actgaggtcg  | gtggaaaatt  | 420 |
| gccttacttt | tgggtatagc  | ccgccaccgg | attcggcgaa  | gaaaggatct  | gcaaatggat  | 480 |
| ggtttcgcag | atcgtttagc  | ttacgggttc | gaagtcgagt  | tgctttctgt  | ccagattgggt | 540 |
| tgggcaacac | gttacgggtga | tggtatcgcc | cagactg     |             |             | 577 |

## (2) INFORMATION FOR SEQ ID NO:370

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| aggcttttacg | ccgaaacagt | gtgctttctc | ataggccatg  | acggcgatgc  | cacaagagcc | 60  |
| tgggccgaaa  | ggttgtgatt | gatcagcgta | tgggccagaa  | gagtggcccg  | ttcttcaggc | 120 |
| tgaccatatg  | catagtggca | aagtgacgac | gccctcttgc  | aggccgacag  | tctgcttggc | 180 |
| cacttccgcc  | agatagtatg | cttgctgtat | atgcccggtga | tcatagcatc  | ggcatcccc  | 240 |
| aagcgaccat  | catcataccg | aaatagtgtg | ggtcgaacat  | cttgccagc   | gcttggtatg | 300 |
| attgcctccg  | cgccgccagt | tctgttcggc | aaagacacgg  | gcaaattgatg | accggcgagc | 360 |
| ctttttcttc  | aatcggaagc | cggtaattta | aagaattttc  | gatacccctt  | ccaaagatta | 420 |
| aattcccaac  | tcttg      |            |             |             |            | 435 |

(2) INFORMATION FOR SEQ ID NO:371

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| gtatctttttt | tgtcctgata  | taccgtagcg | atcagctgat | acacgtcgtc | tgacgatagg | 60  |
| gaacatcctt  | gatcttggtta | cagatctcga | ggttctgcc  | aagtcattgg | cctgataggc | 120 |
| acaaaccgcc  | gagaagaacc  | ctaccatata | gagttggaat | cctgtgcaga | gatttcggga | 180 |
| acagcagcaa  | acatcgagc   | tccttgattt | gcatgaactg | atcgaaggct | tcgagagctt | 240 |
| tcttaagtct  | ttcttctcca  | tgtagtaacc | accggcattg | atatagtaaa | gatgttacc  | 300 |
| ttgagagatt  | ccatgatctt  | ctttgtgaac | ttgggcttta | cctacccttt | tgatcaggca | 360 |
| tattgtccaa  | ctggctcggc  | ttcaaataaa | acgcaaaatg | cgcagcaaa  | catcgttcat | 420 |
| catagcacga  | tccggctcct  | gttcacagtt | tgcttgagat | tctctggatg | taaagagtct | 480 |
| ctcttcacc   | gaccggccac  | aaaccaagtc | ttggcatcgt | tcatcgctcg | gggttcttct | 540 |
| ggcttcaccg  | atccagcgta  | cgagctcg   |            |            |            | 568 |

(2) INFORMATION FOR SEQ ID NO:372

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

```

agcaaatcag atctatttgc cgatggtaga ttccagacct ttcaagggtcg taaatcgctg 60
cgtgagctta cgcaggcacc tgccggtgcc ccggaagagt atatgaatat gtcttttgtgt 120
acgaaaagaa tggcaagcga caggagtcga tatggatcat ctgcctgacg acagctggac 180
atacgtagat cggcacagaa actgattaaa aaaggctata cacctcccgt cactgacttc 240
cttttcttcg tgggggtgaa gatgttacat ccgaaatcgt caataaaaag gggatactct 300
cttgctcctt tcacccgatt gggagaatgc aagcgacgat aagtggacaa tatcagttag 360
atgtatgatt atgctcagga acatgcttgg gattctacgg cgtatcggct tccacttcgg 420
atgatatttc cacatggcga tcaataccgg tgctgattac ccgatgcttt tcctcgatgc 480
tgttaccggt agaccattac aacgcggcaa tccctctttg gttattttgc gggatggtga 540
atccgaggca aggttagtga tgcgaatttc cccggtgtgg gacaagccaa gcttttttcg 600
atcgttatat aggcaatgag ctttatcaac cttcttatgg ggaagggtgc ttgtattggc 660
tttgtgggtt attctccttt tgttcgatgt attcgcaagg tcgttttttg ca 712

```

## (2) INFORMATION FOR SEQ ID NO:373

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

```

gaaccgacga ggagaaagaa ccaaaaaaga atcgtttgtc ttgtcttctc ataattatat 60
caacgtttgt aggagttata caataacatc attcgccatg cggcagcagg cttgcagcgt 120
atgtatccac tggcaagcaa cgagaccgcc gtttccgttc gcaagcggct ctccaccaaga 180
gaaacgggtg caaatcggca agcaaggcgg actccacttc agacggagag aagtctcctt 240
ccggcctatt agaatcagta catcctgtcc tacgtggtag aaatccgacg gatacctcgg 300
ccttggggta tttcggctcg aacagcttcg tccacataag cgaaagacga acagctgtct 360
tcggagtgtc ggcaattaca gtttgtatgg ggtattgact tgaatcacgg gaaaaggagg 420
ctttgagcga ctgcttcatc gactaattgc gatgcgcttc caagcggttc gcttttgata 480
ccgcctacgc cggaatgg

```

## (2) INFORMATION FOR SEQ ID NO:374

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1192

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374

```

gagataaaac aggggtgaaga gccagaactc tttgcgacgg gcacggccct gaagtctaca 60
tatttgcgga gacaaagtat gaaccaacgc atagctgaaa ggataagaag ggggagagag 120
ttatttcacc ggcaaaaata tatcttttgg cgggtagata aaagctgtga atataaatct 180
catataacgg tggccgggat tgaccacaaa aaagcctgtt catgctttgc cgatagggca 240
tacatgatag gcttttgtct ttacagtctc tttgtggcga gactctgatt atcgtctata 300
gagacctttg aaaaataaagg aggtggaggg aaaagggtggc agtaggagtg aaagtagttg 360
taaatacccc ttgcggagct acctgcacga gccctcaagg gtggttatgc cttatcctac 420
ggatgaggac ataattatcc cggcgttctg cataaattaa agaagacctt tgcacggcaa 480
ttggcgtagc aggtctctta tatctgtaca gacactgaaa atcagtcaat tgacaatgaa 540
tctccggaaa atgccgtgcy acagtctcat ctatcggttt acagctcgac ggacctccaa 600
ctcccngaac ctgccatccg gcagagagca gatagcactt ccatcaatag accatagtat 660
cctctcatat gagaccatag tatccttcat gtgagaccat agtatcctct catatgagac 720
catagtatcc tctcagttag accatagtat cctctcatat gagaccatag tatcctctca 780
tgtggactat agtatcctct cataggagac catagtatcc tctcatttga gacatagtat 840
cctctcatat gagaccaatag tatcctctca tgtgagatca tatatcctct cgtggaagtt 900
cattctttgt atctcaagga aagatcaatg atagggtgat ggctgccaaag tgaatagaga 960
gcagtgcctt aatacgttgc aatcgataag catatcgact tggttcgaaa atacattccg 1020
tgctttcctt atcgattcgc tgacatgacg tccctgaacg aaacctcttc gtcggatggt 1080
ttccttgtcg tgccatcggt ttgtgtcatt gatcatacca taaacaccaa aacaatcggc 1140
cgacacacaa taaaatgaat ggataaatgg ataaaggcct gcttattgtg ca 1192

```

## (2) INFORMATION FOR SEQ ID NO:375

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...3446

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| gccttccgaa  | gagcaaatgc  | catgccaaac  | aatcccctgc  | cctcattata | gtcacttatt  | 60   |
| cgattggccg  | aagtgtccac  | tgtccgtttt  | cggacagtcg  | ggtgttcggt | tccgaacagt  | 120  |
| cggacacttc  | gccatcggag  | aaaacttcat  | attatcagcc  | ttttaagggg | agcggcataa  | 180  |
| actttgctgt  | cggaaagtgc  | aataaaaaacg | aaagaaagat  | gaagaaaaaa | agccttttcc  | 240  |
| tcctcccttc  | tgcttcgcct  | ccctgggtcc  | gactccatgg  | agcgagggtt | cggccagcag  | 300  |
| gttgccgcgc  | cggatccatc  | ccctttgtcc  | ctcacggaag  | ccaccggttg | gcacgaaagc  | 360  |
| agagcgtgga  | tgacgccgtg  | gcactgcaag  | agttcgagcg  | gcctactggc | agtggcgcac  | 420  |
| ctatcgggca  | gaattgtctg  | cggagtgaac  | ttgacagcca  | cactgccgga | ctacaggcgt  | 480  |
| gcctattcgc  | ctatcagcag  | cgggacggct  | cttacagctt  | cgtccgctcc | aatgctctgg  | 540  |
| cctgtcagga  | catatatccg  | tggatcagaa  | tatatggctt  | acgggttgaa | gctctctttg  | 600  |
| gtgagttcgc  | tcgagcatat  | caatccgctc  | ggcacggagg  | agctgacagg | catttcatga  | 660  |
| gcgtaccgat  | cagcctgacc  | ctgagcaacc  | gctcttcgga  | ctgaacgaaa | tgaatggag   | 720  |
| tcggccgata  | gaacgtgcg   | ttacgaagag  | gctcgccggc  | gattcgtcgc | caatacggag  | 780  |
| gagggagcgt  | aagctgtata  | gatcattact  | tttcggccct  | gctggcacgg | gaaagtacaa  | 840  |
| caatgctggag | accaacctcc  | gtaacacggc  | gaagctggtc  | gagtggcgcg | tgccaaaaag  | 900  |
| aagatcggga  | agttgtccga  | aaacgaattg  | cagccgtgga  | gatcagctac | gcttcggctt  | 960  |
| cttcggcaat  | tctttcgagc  | gtacagccct  | gcgcggagcg  | gagatgtccc | tgagcatttt  | 1020 |
| cctcggtttc  | agccggatga  | agtcctctcc  | ctctctatac  | cggccgatac | gatcttcaac  | 1080 |
| ccgtgagcta  | tgaacgggtg  | atggagttgg  | cgggacgcaa  | tcateccgtg | tcggagagat  | 1140 |
| gaagcgcagg  | atgctcgaag  | ccgatcgttc  | tctggccgag  | ccaaatccga | acgcttctcc  | 1200 |
| atcgaactga  | tgccccaaat  | cggattgccg  | gacaggcgga  | caatctgcac | gatgcatacg  | 1260 |
| gcggacgtct  | gaagacaaca  | gctctgtctc  | cgtaggcggtg | cgcatttctc | tcgtggattg  | 1320 |
| gggcgccggac | gcggtcggat  | acgcttggtc  | gagagcaacc  | gccgtctcga | aggcatcgac  | 1380 |
| tgcgacagga  | agaagagcgt  | tggcacccgc  | agatattcct  | gtggtggaga | aacacaacaa  | 1440 |
| ccaactctgc  | atcctcgaat  | tggcacgtcg  | accgacagta  | tcgctcaggg | gcgctatcat  | 1500 |
| actgcccgtg  | aaaccttcac  | gtcggggcta  | tttccacct   | cgatctgaat | gcggcacagg  | 1560 |
| atgccaagac  | ctggcgcgta  | cctcgctcgt  | cagagcattg  | catcactatt | ggagctatac  | 1620 |
| tacaatctgc  | gtagcctgac  | ggctatgatc  | cggtagcgga  | tgaggaatcg | atatacccat  | 1680 |
| ggaagaacta  | tagggacaaa  | ggaatcggac  | gatcaagcaa  | tgggaggaaa | ccgactgata  | 1740 |
| cccgattgac  | ctgaaaagggt | atatctggca  | aaccggagaa  | ttcttctatt | ttgcgcattg  | 1800 |
| ttttgcccga  | agtgggttaga | aatctttccg  | gccgaggcaa  | aatgctaagt | attattggac  | 1860 |
| aaaaactcta  | accattatgt  | actggacatt  | agaattagcc  | tccaaattgg | agatgctcct  | 1920 |
| tggcctgcaa  | ccaaagatga  | gttgatagac  | tatgcacaa   | ttcgggtgct | cctcttgaag  | 1980 |
| tcacgcagaa  | tctgcaggaa  | atggaagata  | aggggaaatc  | tacgaatcga | tagaagatat  | 2040 |
| ttggccggat  | tatccgagaa  | agaggatttt  | ttcttcaacg  | aagaagagta | ctgataatgt  | 2100 |
| aatctcctaa  | gcgaatatgc  | cccggatgtg  | caataatagc  | actcggggct | tcgtttacca  | 2160 |
| ccgtggcatc  | agtcttgcac  | aaatctttcc  | gttcgctcat  | tttgccctgc | tcctgaccgt  | 2220 |
| ggccggggga  | gaggatattt  | tcgctcaggg  | cgattattgc  | tggtcagta  | cacccggtca  | 2280 |
| tacggctact  | acaatccggc  | ttagccggtt  | tgcgcaaaga  | gattttcatt | actgcgtcgc  | 2340 |
| acaatagaca  | atggaaggca  | tgccccgaag  | tcctaagagt  | ttcgtcgtac | tggccgatgc  | 2400 |
| gctattcgct  | tcttcgacag  | agagcatgga  | gtgggagttc  | gggtagtgc  | gaaacgagag  | 2460 |
| gactctttgc  | catcaatgag  | ctgatggggc  | aatatgcctc  | aaacagaaac | tcttcggcgg  | 2520 |
| agatctgtcc  | gtcgccctcc  | aagccgggat  | gtcaatacgg  | ctttcgatgg | caccaagggtg | 2580 |
| gagctcgaga  | cggagaagat  | ccggccatcc  | cccttaccaa  | agtgaacgga | aaggccttcg  | 2640 |
| acatcgtgca  | ggatatatac  | accgcccga   | agaattgtac  | gtcggattca | gctctcccat  | 2700 |
| ctgaccgctc  | cggcaattcc  | gctcaatgaa  | cagtacatat  | tagactgaca | aggcattatt  | 2760 |
| atctccttgc  | cggatacaat  | atccgctcca  | tttttcgtta  | tttgcatggc | atccttctat  | 2820 |
| ctttgcagct  | actgacgggc  | acgttctcgt  | ttggacgtga  | cgatgggaat | gtcatacaac  | 2880 |
| aaccgcttct  | tgctcactg   | atgtatcgtc  | ccacacaagc  | cgtgggagtg | agcttggggga | 2940 |
| gcagttgggc  | aagttctatg  | ccggctatgc  | tttcgagtg   | ccgacatcgt | actggctaaa  | 3000 |
| gcctcatggg  | gaagccacga  | attgctggtc  | agctattctt  | cccattgagc | aatacgaaga  | 3060 |
| atagagatgc  | aaagtataaa  | agcattcttt  | cctctgaaaa  | ctgccttagc | gcaggattcg  | 3120 |
| gggagagcag  | cgaagcgata  | tataaataat  | gtatgtgtag  | aaagaacagg | tttttcgctc  | 3180 |
| ttgcagcttt  | tttctgtttg  | gagttttcac  | tatttcgctg  | tgccgctctt | ccaacgggct  | 3240 |
| gttggcggtg  | aactgacccg  | gtgccaagct  | atcttcatgg  | aatagccatc | gcctttcggg  | 3300 |
| atgatacagg  | ttccccgagg  | gaagtattgg  | tgttgggcaa  | ccaaagaagc | agacagctta  | 3360 |
| tggggcatat  | cttgccgaat  | ccgcctcata  | tctggtggat  | gccttttttg | atggatcggg  | 3420 |
| ccggagatca  | caatgcccaa  | taccgg      |             |            |             | 3446 |

## (2) INFORMATION FOR SEQ ID NO:376

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| tgcgatatga | agtcattgctg | atagagtacc  | gaggccgaag | cgaggagcaa | agaagcaat  | 60  |
| agaatataaa | tatggtaccc  | cagctcactc  | tggaacaca  | gaccgatctc | ctccgtcagg | 120 |
| cttcacatca | taggatccgt  | ccaatactgc  | tgaacggcaa | gaactccctc | ggacaaacct | 180 |
| tggcatagt  | tccccgtcga  | aaatgagggg  | tcatgcatc  | atgtatgata | cggtcagca  | 240 |
| gaccacgggc | aagtaacctt  | ccaaacccat  | agcccgtctc | aaagcgtacc | cgccctgac  | 300 |
| cagcacgagt | acgagcagga  | ggccgttggt  | gttcttttca | ttacgactcc | ccattgacgt | 360 |
| gccagcttca | aggtaaaatc  | ctccaatgga  | gctcacgat  | agacggaaga | gtaacgacgg | 420 |
| cnaactcaac | ggcatgactg  | cgcggtatgg  | tgcagccgt  | ccgttcatca | cctcctcctg | 480 |
| tgcattgctg | gcaagcctgc  | ttcgctccgtc | acgagtcgag | tgctatcggc | aagttggact | 540 |
| taggtacatc | ttccggc     |             |            |            |            | 557 |

(2) INFORMATION FOR SEQ ID NO:377

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 881 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| ttacagctca  | tggtacattc  | ggtagtgc   | tcagtgtctc | cgatgctttc | aaaaagcagg  | 60  |
| ccaatacgta  | ggcccggttcg | ggcacggacc | ataggcaacc | tgacctgaaa | cccgaaaagt  | 120 |
| ccatgacctg  | ggacttcggt  | atcggtacag | caatgcacgc | tgcgggatcc | aagccgacgt  | 180 |
| aaccttaacc  | tatttcacac  | cgaccacaaa | gatctgatct | tgtccagccc | tgactatgct  | 240 |
| aataaatcac  | cacatacatc  | aatgccgaca | aggctcgtat | gagcggatc  | gaggcctttt  | 300 |
| gtcttatgac  | ttcggcagcc  | tctttgccaa | caagttctct | ctcgcgcatt | tgcgaaatgc  | 360 |
| acgatcatgc  | tcaattccga  | gatgaagaaa | agcagaccga | tgccccttgg | agcgaaatgt  | 420 |
| actacgttcg  | caagcagaac  | acaccttcgg | tatcgaatat | cgtggcaaag | aaggacttga  | 480 |
| agtgatgctc  | acggtcgctt  | catgggacgc | aggatcgagc | aaaactggta | tgcttactac  | 540 |
| ccgaagtctg  | ccccgaactc  | cagcaactgc | ttgcagcaga | agagcctgat | tggtctgtca  | 600 |
| gggactgctc  | cgatcatccg  | aagcaatggt | gttcaatcct | ctgcttacta | ccacatgaac  | 660 |
| aagtattctca | ccttcggtgt  | gaacttaaca | acatcttgga | tgagctttat | acggagaaaag | 720 |
| acgggtacca  | catgccggac  | gtaacatcat | gggtaagggt | atggtcaact | tctaattctc  | 780 |
| tttccgagag  | cagatataaa  | agggagccgg | tctccctgca | taatcctcac | agacaaagcg  | 840 |
| gatattcctc  | tcataaccgag | aagcgggtat | ccgctttctg | a          |             | 881 |



## (2) INFORMATION FOR SEQ ID NO:378

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2747

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

```

ccgtaggtac cgacggattt gccgacaagt atcctctgga gatgtactgc ttcgccccgc 60
acaggtggac tctgacattg caccgatca tgaagagcca atgctcacgg ccccgatatcg 120
gaggaggtga agaaggcttt gatggaaaat acaaacaccc catccatcgc gagctggaag 180
agacggcgaa gaaagtggag gacacggcgg catggattac atcatggatt accgtctcat 240
ctattcctcc gcaatggcct gcccctcgat atggatgtgt acgatctggc cgaaggtgtt 300
gtctggcgga gctaagccgc atctccatcg aaaacggctc tgccctgtag ccatccccga 360
tttcacacgt ggcaattggg ataaaagtaaa ggctatcgac acgcaatggc agagtaaaga 420
caatcggagt atgaggaatt tctattgaca cttgcgga ctttgactgc cgcaagtgtc 480
gttttcggtg agaggcacag gtcacagagt cggggcttcc atattggaag gatattcgtc 540
ggtaagcgtg aacaaagaac cggcgcggtt gtcctttatg acctatgcga ccgaagcgaa 600
gctctcaccg gcaagtatga gaagagttcg tactacctct tctgaacggc acgtggcgat 660
tcttttatgc cgagagcgag gcacattgac tgccggcata acggatagct cggcaaatac 720
aaagggatgg cacgaatcca agtccccggc aactcggaga tacaagggca cgggtgtggc 780
atcttaccaa tcacggatac gagtttcagc ctcgcaatcc gcagccgccc aaatgccgga 840
agccaacccc gtaggtgtgt atcggcgcgga gatagaagta ccacggactg gatggagcgc 900
gatattctacc tccatatagc cggagccaag tcggactcta tgtctatatc aacggacacg 960
aagcgggcta cagcgaagac ccaagaatcc ggccgaattc ctcatcaatc cctatgtcca 1020
tgccggaaaa acacgctcac gctcaaggte tatcgttgga gtaccggctc gcatctggat 1080
gtcaggactt ctggcgcatc agtgggatcg aacgcgatgt attcctcttg cacaacccaa 1140
ggcggcagtg aaggatttca gcatcaaatc cacactgatg atagctaccg caatggtata 1200
ttctccctga aagccgactt acgcaccgcc gtggcggaagc ctccgagcta tctctgacat 1260
acgaattgct cgatccgaag gaaagaccat cgccaccgaa acccgttcga cctcatagc 1320
tgccggcgag agcgtaccct ctctttcgaa gcacagccgg gtacggtaca taatggacgt 1380
cggagcatcc ctatctctat aagctcttga tgacggtacg aagaaaggga aagtcacccg 1440
aggtaatacc gtcccgtgtg ggtttccgca ggatcgaaat caaacggata gaggaaaaag 1500
ctgccaacgg tatgccctag tatgcttctt tgtcaattga cagcccatca agctgaaagg 1560
ggtgaatagc acgaacataa tcccgccacc ggtcattacg tgccggaaga gctgatggtc 1620
gggatttgga gctgatgaag cagcacaatc tgaatgccgt ccggctgcac actaccgcga 1680
agatcgccgt ttctacgagc tatgcgacga atacgactct acgtgtacga cgaggccaat 1740
atcgaaaagt acggcatgta ctacacctgc gccgtggggg taccttgggc aataatccgg 1800
agtggctgaa gcccataatg atcgtatagc gaatatgttc gaacgcaaca aaaaccatcc 1860
gtcgttacga tctggtcgct cggcaatgaa gcaggcaacg ggtacaactt catcaggcct 1920
atctttggct gaaagaggcc gatcgcgacg tgatggcgcg cgggtgaact acgaacgtgc 1980
ccaatgggag tggaatacgg atatgtatga cccaatatc ccgatgcgaa atggttgga 2040
ggtatcgga cggccgggtg gaccgccctg tgatcccttc ggaatacgt caccgatgg 2100
gcaattcacc ggcaacctat gggggcagtg gcaggctatc tacaagtacc ccaaccgcaa 2160
ggcggcttca tctgggactg ggtggatcag ggtatccctc gtacaacgat aaaggaaagt 2220
cctattgggc ttatggagga gacttcggag tggagcaccg agtgacggca acttcccttg 2280
caacggactg gtcaatcccg acccacgcct caccctgcc aacggagggt gaagtatgtg 2340
catcaaaacg tcgcttcgaa gcagtggatg ccgccaaggg acatttccgt atcacgaatc 2400
gttctacttc accaacctca agaaataccg cctgcgctat acggtttcgg taatggcaaa 2460
gcattgcaaa gcaaggtcat cggcttagat atcgatccta gacttcatcg gacattattg 2520
taccgtaga cgggctgagg ccgactgcgg tatggaatac ttcggtgact tcagcgtaca 2580
gactctacag gcagagcgct gattcctata gggatgaga ttgctcacga tcaattccga 2640
cttccgctga tgcagagaga actgcctacc gtgctacagg ccctacattg cacacagtac 2700

```

ggaaggagat gaattgaagg tcgtttcgtc gaaagtcgat ttcgttt

2747

(2) INFORMATION FOR SEQ ID NO:379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| ttcttcttct | ttttttattg  | ccgctgttgc | tgggatgggt  | ggcagactat  | ttttaggaga  | 60  |
| tcctctttct | cttcgcgcatc | ctatagtcgg | cttcgggtcca | tgattgcatt  | cggagagaaa  | 120 |
| agattgaata | aaggaaacta  | ccgcaagtga | aaggcgccct  | catgtcgggtg | ttctatatcg  | 180 |
| ttgccgtttt | tcttttacct  | tattgatcct | cttgggactt  | gtttttgtct  | gtgtttatac  | 240 |
| catttgctgg | acgatttttt  | ccggattgct | gttgccattt  | ctgtggcttc  | tcttttttgg  | 300 |
| ctatcggcat | tttcttctgt  | ttggcaggt  | ctacccttat  | tcggaaagta  | cgtatgggtat | 360 |
| ttcgaaagca | agtcggaatc  | gttcgcgttt | gaagaaaggg  | ccgccaaacc  | agggttgacc  | 420 |
| gccgaaatcg | gtaagggccg  | cgaataccgg |             |             |             | 450 |

(2) INFORMATION FOR SEQ ID NO:380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| gaaattgtca  | tagacagggc  | ctcccctcgg | gataatcaca | gggtgggtgc | atagttccaa | 60  |
| caaataagtt  | ctgccgtatg  | gagatcgaat | acgagctgac | cctgtcgtta | gcgatatgaa | 120 |
| gatgattccc  | ttccgctcgt  | acttgacgt  | gggcatccgc | tcaggcagga | gggaagcaaa | 180 |
| acctctctct  | tgtgcagtgt  | aaactgttcg | gatgctaccg | tgtatccctt | atcggaccaa | 240 |
| gtggtgcttc  | acgaagggaag | agttcgaaat | cgatatggaa | gtcgcgagtc | gaatcattgg | 300 |
| aatatcggcg  | acgggtatcc  | tcaatgtagc | tttttctcct | gccgcaattt | gggcagatcc | 360 |
| acttctccgc  | tttcgatcac  | acagccgtcg | gaaggagctt | aaaacgaaga | ccgaatcgat | 420 |
| tcaaatccgt  | aaaggagtag  | gattgtgcag | agtgagcaag | tttgctttta | ctgtccgtat | 480 |
| gcatacgaatt | cacgtactgg  | atacactttt | cttcacttc  |            |            | 519 |

## (2) INFORMATION FOR SEQ ID NO:381

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

```

agtgttgtgt tatgggaagg gtgttgtttt atttatcatc ggaatcgnaa cagactattc 60
ggctacttgg atttctcttt ttatccctg atgcatatt tacccttttt aggccgaata 120
tccccttcaa ggctattgag gtagtgaagt catcgaaaat ttttagaagc cttctgagct 180
atgtttttta agccactaat ttactgatac cgccattttg tcagtttaga ggatccatct 240
ttatccgtta catttgtgat tgccaaatga atgtaaaatt acacttcaca acacactttc 300
gatttacatt cttaatccga tcagggtgta atcatattta atcgaattga atccacatat 360
gtaatcatgt caatttnacg cctgaaaacg a 391

```

## (2) INFORMATION FOR SEQ ID NO:382

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...3290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

```

acggctccga taccggcttc atgcagacgg gcatattctt ccgtggtcag ggctgaactt 60
cgagcgagag ttgggagaag agtggacgca gtcgccgctc atttctcat agtagcttgc 120
cggagtggct ttctcggaact ctcccgaacg agaaggaggt gtttgatcc gagccgaagg 180
atcgcttccg ctccccatcc acctcttcgg cagtgaagtc gcggcgatgg attttgttcg 240
accgatgaat ccgcagtata cacaggcatt gctacagata ttcgacaggt agaggggata 300
tagagctgca tcgtgtggcc gaatcgctct accgtcaggg catcgctgc cgggccatct 360
gctccagata agggatggct tgcaggcgaa atagcgtgat aaagtcttgg atggtgcggc 420
gtcggtatgc caacgaacgc tcacatcggc agccgtagca tcggccaaga ggttaccac 480
tcgctcccaa tataggggga ggcgtgcaag tgatcataga aagtcattt ccggaagaat 540
atttcagatt gaggaaaagag gtaaacggcg agctggcttc ggcttcgggc ggacgctgcc 600
gaacttggtc tcgaaaagcca ttcggccggc ttccacgcaa ggcggaaagc cgtcgccatg 660

```

|             |            |            |            |             |            |      |
|-------------|------------|------------|------------|-------------|------------|------|
| cttacgggat  | cttcgcgcac | ggctatgccg | tattcaccag | aacggcatca  | gcccccatct | 720  |
| ccatggcttc  | tgcggttggc | tgggcgcacc | gatacctgca | tcaatgacga  | ccggcacacg | 780  |
| actcgttcga  | tgatgatacg | gatcatttca | cgggtcttca | gtccgcgatt  | gctccgatgg | 840  |
| gagcaccacg  | tggcatcacc | gtggctgcgc | cggcttcttc | caatgcttgc  | acagcacagg | 900  |
| atcggcctga  | acgtaaggga | gcacgataaa | gcacgacgaa | ccaactcctc  | cgtggcacga | 960  |
| agcgtctcga  | tagggtcggg | agcaaatagc | ggggatccgg | atgtacttcc  | aacttgagcc | 1020 |
| agttggtttg  | agggtctccc | gtgcaagctc | ggccgcacga | atggcttctt  | tggcagaggg | 1080 |
| acaccogaag  | tattgggcag | gagagtgatt | tccggatggc | gggtgatcga  | ctgatcatgt | 1140 |
| cgtcttcttc  | gacgcgaccg | atttccactc | gtttcaggca | acggtcacca  | tacgagattg | 1200 |
| cgatgccaa   | accgcagcct | ccatcggctg | gaggaagcaa | acttacctgt  | gccgacgaat | 1260 |
| aggcgcgatt  | caaagttttg | ccggcaattt | gtaacgtttc | cattagattt  | tttctgtttt | 1320 |
| atcaaagatg  | atcgttcgat | acggaaggga | gatcatccga | ttagttcttt  | ttattttctt | 1380 |
| gataaggctg  | ccgctcacgg | caatacctcc | tatgccacag | tgcgaatgag  | gggaatgtct | 1440 |
| gcatectcta  | tcccaccgat | ggcaaaggcc | gcagtcggat | gccttcggct  | tgcatacagg | 1500 |
| cggcgatggc  | tttgtagcct | cgagtcogag | gacgggagct | aaacgctgct  | tcgtctccgt | 1560 |
| atagcgatcg  | ggcctatacc | cacgtagctg | gtccttcggg | catatgctcg  | gcgcacacct | 1620 |
| ccatcgtatt  | gcattgtcgt | cctatgatct | tattcgaacc | gaggatcgac  | gcgcttcgac | 1680 |
| tatcgccata  | tctcttttgc | ccaagtgtat | ggcgtagcat | ccacctgacg  | ggctattttc | 1740 |
| acacggctcat | tgcagacaaa | aagtctccgt | ggtgacggca | gacagccttg  | acggcacaa  | 1800 |
| ccgtgtgaag  | cattcttctg | ccgaagcctc | cttcatccga | agctgtaccc  | agcgcacacc | 1860 |
| taacggcaga  | cggcctccgc | ttcttcgagt | tccgacagg  | cgggctgacg  | ggcgtgatga | 1920 |
| actgcaaatc  | tatttcgctc | atcagcctga | cgaccggatc | accggcagg   | ctttgtgcat | 1980 |
| agcgagcaac  | cccgaagcac | gctcacgtat | cgactgacat | ataactgtgc  | catcccggca | 2040 |
| gccgtaaaag  | gttcttgcgc | aaggccaaag | cagctgcata | agcgggtgct  | tgggcacaa  | 2100 |
| ccgtgcctgc  | ttccccgtac | cgccgcgtaa | gagtcggaga | gcttcgcac   | gaccgtgtaa | 2160 |
| acgatccgat  | ccgttacgac | cgattctccg | gcattgcccc | ccttgggacg  | aggccgacac | 2220 |
| cgctccttcg  | atagaagtct | aacagggtct | catctccggt | tcgcagccca  | aaagggtggc | 2280 |
| agcttcggga  | agattcggcg | tgagaagtct | atccgggaca | aagccgttat  | atcttcaaga | 2340 |
| ttgaaacgat  | cccttgtccc | gcggagctgt | cggccgaagc | tctgagtacg  | ggatcccata | 2400 |
| catccgaatc  | gaggggaaaa | cctttttcaa | acaatccact | acgagagaga  | ggtgtccgag | 2460 |
| tcgcgatca   | ggccgatctt | ggcgacggca | ggctccatcc | ggccgacaaa  | gattcgatct | 2520 |
| gccggatgat  | gtccgcgcga | tccacccacg | ctccccccga | tagctgccac  | tccccgtaaa | 2580 |
| ggtaatagcc  | gtagccagg  | ataagcccg  | acgcccattg | tttcggccgt  | ccgcacatct | 2640 |
| gccgtatgcc  | ggctccggcc | gacggatcca | ctcctccgac | acagataaca  | gccgggtaca | 2700 |
| caattctctg  | caacgcacga | gttcccgcc  | ttcgaccaac | cacaatagcc  | gagtgcagct | 2760 |
| gccgaggcaa  | agcctgctct | acgaagctgt | ggcgacgatc | gggcgtaatg  | ccgcccagtg | 2820 |
| ccaccacggg  | cagatggagt | cgtgcagacg | atcgcccaaa | gaatcggggg  | aaaatcgtcc | 2880 |
| tgcatagccc  | acttgacacg | actgtcgaac | acggggctta | agaaacagta  | gtcgagtcca | 2940 |
| aggggaagga  | ctctatatcc | tctatcgctg | ggcacgaagc | tgacaccgct  | aaccatcagg | 3000 |
| gagctgtggc  | cgatcgggtc | tgcctttcca | gaccggttgg | gcagatgcaa  | accgcacagt | 3060 |
| ccgtagcggc  | cgacgagccg | gggatggcgt | gcaccacgat | tctccggcga  | tagcaagctg | 3120 |
| ccacagcttc  | gataactcgc | aatagtctc  | ttcgccggca | ctgggcaaac  | gaagatgcag | 3180 |
| ccgctcaagc  | cccggctcga | aaagtggctg | agcaggccga | tttgctcgct  | cgtagccttt | 3240 |
| cgggagtgat  | cagccacgg  | ttcatttgga | gactgcctct | ttcttttagca |            | 3290 |

## (2) INFORMATION FOR SEQ ID NO:383

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...655

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaggacaagc | agttggaatt | ggacaaacgc | tatctgcgca | tggcgcgcat | tgggcggaga | 60  |
| attcctactg | cgaacggcgc | aaagtgggtg | ctcttatctc | aaagagcaga | tgatcatttc | 120 |
| cgatgggtac | aatggtacac | cggctgggtt | gagaatatct | gcgaagacga | gaacaacgtc | 180 |
| accaagccct | atgtctgcat | gccgaagcca | atgctatcac | caaagtggcc | ggcagcacga | 240 |
| acaacgctcc | ggtgctacta | tctatatcac | ggcagctccc | tgtatcgagt | gtgcaagctc | 300 |
| atcatccaga | gcaaaataaa | acgggtgggt | tattccgaga | aattcgtctg | gacgaagggt | 360 |
| gtcgcttgct | ggagcgagcg | ggcattgtcg | tcactttata | gacatttccg | atattcagga | 420 |
| ataagttttt | tatgaaacgt | tatccggttc | cggcagcacc | ctctcataca | tccttatcgc | 480 |
| tgccatcttc | gcgcggttgg | tgctcttgcc | tcacatttct | atttcactca | caagaatcca | 540 |
| gcgatctgaa | tgaagtgttg | aatctgatcg | acaggaaact | atgtcgatcg | gtagatgtgc | 600 |
| cggaagttgc | agcacaaat  | gattccctat | ctgctgggca | gctcgaccct | cactt      | 655 |

## (2) INFORMATION FOR SEQ ID NO:384

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...343

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| aaagcatctc | ggcatccgtg | tcctgaatat  | ggaagtcccc | atacgggccc | tcatcatcac  | 60  |
| cttatctccg | ggttttagcg | agaaaatata  | tgaggaggaa | taccgggctt | gataccggcc  | 120 |
| ttccacttat | tggcagctct | gtcgaatgag  | gagtcgcat  | acgaacgttg | agcgtaatga  | 180 |
| tgttgccttc | agccggtagt | tggccattga  | ataggcacga | acggtctctt | cttcggttctt | 240 |
| acaagcaatg | accacgcata | catcttgctc  | caagtcgcca | cgggaagcat | cctgatatacc | 300 |
| gaagtcgagg | atagcggatg | tngtatttctg | gtatcctnga | tct        |             | 343 |

## (2) INFORMATION FOR SEQ ID NO:385

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1107

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385 .

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| tttcgntccg  | cttttccaag  | attttgcattg | aaatgagagn | caggacgtaa  | gatgaaaaag  | 60   |
| ctgtcttttcg | gatcggagaa  | agcagagcat  | gccattcggg | tatttttttc  | gcgcgaaaaa  | 120  |
| agttttcaac  | aacgaagacg  | agtttggatg  | attctaaata | agggggtaaa  | aagaagcgga  | 180  |
| ttttgaagtc  | tgaaagtcag  | agacgagcct  | tttcagttca | aaacatgctt  | ttcagaagag  | 240  |
| aggatacgtat | ctgtatataa  | accgttttcg  | atctatata  | agatcgtttt  | cgtttatata  | 300  |
| taaatcggtt  | tccattttata | tatagatcgg  | aagtcttttc | tattaaatca  | gaggctgaaa  | 360  |
| aaggccactt  | cgagaggcta  | taaaaagagg  | caccacacga | ttcgtggccg  | aacctatgcg  | 420  |
| gtgccttatg  | ccttttagggg | atataagagg  | ggttattcct | acttattcgt  | catagggata  | 480  |
| tgggctgttt  | tccgagtatc  | gagatggcat  | gataggctat | gggcgcgaaa  | gaatcggccg  | 540  |
| aaagatcggg  | ggtataatgg  | tgttcagtgt  | gtacatattc | aattattgtg  | agtctattat  | 600  |
| ccatgtattt  | ctattcaagc  | aatcggctct  | cttggcacia | cattcaactt  | ccgacagaga  | 660  |
| gcttcacccg  | gttggcaaa   | gtaacgaaat  | gctgaagtcg | aatgaatcgt  | aacagccacc  | 720  |
| gaatgtttta  | ctataaacat  | ttcatcggca  | agggtttatc | tttgtggcgg  | aatgaacggg  | 780  |
| gacttcggat  | atatatcatg  | gctgcaagag  | cagatctgct | gcattgtggca | gcattttgtcg | 840  |
| tgctgtggag  | gctatcggcg  | cacgggtagt  | ccaattcgtg | cgagggcttg  | atacatacga  | 900  |
| tccttgtgtg  | tggctatcgg  | tagcctacaa  | agagccaaat | ctctgttgat  | aaaggctctg  | 960  |
| atgcctatgg  | cccggacgta  | ccgattatgc  | tcggtattcg | cagagaggat  | acacctgtag  | 1020 |
| ggcgcatcga  | ctcgtagctt  | tcgatctgga  | ttcgacgctt | gtgcgcacgg  | agatcatgat  | 1080 |
| gaattggcca  | ccgcacacgg  | atgcctc     |            |             |             | 1107 |

## (2) INFORMATION FOR SEQ ID NO:386

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

|            |             |            |             |            |             |      |
|------------|-------------|------------|-------------|------------|-------------|------|
| cgcccaanat | gaaatccggg  | gaataacctc | acggcatccg  | cagaagatgg | acctataccg  | 60   |
| cttcatggaa | cgctgtacct  | tcagccgaac | gctacaacat  | ttcgctcgct | tcaagcggtac | 120  |
| agctgccgct | gacggcgcat  | tctttgtacc | gacgaaaact  | tcgatggaat | aaagactcct  | 180  |
| accggagaac | tgacagctgg  | acgatagaaa | attcgcctac  | ctatacgtac | gatgaggttt  | 240  |
| acctggcgat | ctgggtacaag | ccggctggaa | agggaactaac | tatgctccct | acacgactat  | 300  |
| atctgcttgg | atgcatggca  | gtacattttc | aatcacaccg  | atgaggcctg | atctcaccgg  | 360  |
| agttggatct | ttccaaagat  | ggcgggaaga | taacttgagt  | gtgaagctct | atgctacgaa  | 420  |
| atacgtcggc | gacgatggcc  | aggcaatcag | gtggaaggct  | atacgcgagc | agcgatcgcc  | 480  |
| ctcttccaat | cgacgagact  | gtcggagact | atgtgcagtc  | agagctgctg | tatctgaata  | 540  |
| atcggacgga | ctggtcgatc  | agtggaaagg | attcaacggt  | tctttgacaa | gggaacggag  | 600  |
| cgttcggtaa | tcggcatata  | tgcggtatat | gcaccggaaa  | tctctatgtc | gatgatctca  | 660  |
| agatcactca | aaagtataag  | gccggcaaa  | ccctgccgat  | cctttcctct | tcaagagata  | 720  |
| tttggaaagc | gaatcatcga  | tgtaaagtgt | cccgaagcag  | tattcaagaa | tgaaatgttc  | 780  |
| catcgggtgg | tgccgtgaag  | catggaggcc | aaggagtaca  | atatcaagg  | tacaaacgac  | 840  |
| tcctttcagt | ccgctccaat  | ctttcggagt | ctgtccttct  | ccacgaatct | gactccctcg  | 900  |
| gtaagcatgg | ccaaggctat  | ggtacagggt | acggagataa  | tatccatata | gacaatgttc  | 960  |
| atggcgaggc | tgtaagtatt  | atgatttcag | tggtcggttg  | gtttatagcg | attactcggg  | 1020 |
| caacgggtca | ttgttgtcaa  | cttaggccag | ggcggaacgt  | tcacgtgcaa | agtgggtatc  | 1080 |
| gctctatgaa | gctgacttac  | taagctatct | ctcacccttt  | cctaaaggta | taccgggggg  | 1140 |
| gtgtgccgga | agtgtgaagt  | gagcacttcg | gcacaccttt  | ttattatact | ctacgagctt  | 1200 |
| ttcaagcgag | ggaaataaag  | cgtttctggg | tattcatcag  | gcccgaagtc | ttaaatttgg  | 1260 |
| taccgcttan | tccccgaaaa  | ttatgaagaa | gaaatg      |            |             | 1296 |

## (2) INFORMATION FOR SEQ ID NO:387

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| tgccctgca  | tcctcgnngg  | gtttgtactc | tggtttgtat  | cggcgagtcg  | actgtggcac  | 60  |
| aaaacgcctc | cgaaacgacg  | gtatcgtagc | atacggatcc  | gccgtactct  | ccgaagccga  | 120 |
| tgtgcttcgg | atcgctctta  | gtgagaagcc | acagtgaag   | tggccgatat  | ggatgtgcgc  | 180 |
| aaacaggaat | atgcactagg  | gcagcacgtg | ccgatctctt  | cccgaagta   | gacctcaatg  | 240 |
| gcgttacagc | catacgctaa  | agaagcaggt | cttatatata  | gatatgcccg  | gttttagcagt | 300 |
| agcgaaggta | tcgaaatggg  | gcgtacacac | aatacgcaag  | gaggggtgaac | gtctccatgc  | 360 |
| cattggtgtc | ggcacagctt  | tggaaaagca | ttccatgacc  | ggagaacacg  | tcgatctggc  | 420 |
| tctggagaaa | gctcgcagct  | ccgaatcgat | ttgggtggcag | aggtgaagaa  | ggcttacctc  | 480 |
| agtgtattgt | ggccgaggac  | tcttatggcg | tattcaagcg  | cagctatgac  | aatgctctgc  | 540 |
| caattataag | aacatatccg  | acaagttcga | tcgtggactt  | gtggccgata  | tgataagatt  | 600 |
| cgagccaatg | tacaggtacg  | caacatcgag | cctaaccctt  | gcaagcgcag  | aactccgtag  | 660 |
| cccttgctct | ctggcgagctc | aaggtctgat | gagcatggaa  | gtggaaactc  | cgatcagact  | 720 |
| ctccggttca | ttgtcgacta  | taaagaacaa | gtctataaccg | gctattttgc  | cgccgatacg  | 780 |
| cttattccaa | caactcctcc  | ctgcgtcagc | tcgatataca  | gcgtcgtctg  | gcttcagtgc  | 840 |
| agacaagctg | aacaagtaca  | gcttcctgcc | tacactcaat  | ctggagggca  | gtacacctat  | 900 |
| tcgctcaaca | gcaacgacat  | caaatctggg | cagggacacg  | ctgacg      |             | 946 |

## (2) INFORMATION FOR SEQ ID NO:388

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtgtattctt | tggattaggc | gcataccttg | tatatatgtc | caaagcttaa | gctacttaag | 60  |
| tgacgatcca | cnagtttgta | tcaattgcc  | tgtaattggc | cttactatgc | cacttggcaa | 120 |
| catagttccc | acgcgatgcg | tgccaccgca | acgactgtcn | tgtgccacac | aacagtattt | 180 |
| ttagcaagta | ttatttaagg | catcagatgg | tctgcggcac | tcctatgtat | ttaccatgag | 240 |

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| gaacnacctc  | aacgcatgca | ggccatatcg | gcaagtcagg | cggtaatcta | tgacactgtg | 300 |
| tgcgttgcca  | cgctcaactc | aatcaagaat | ttgtccgtnc | aggatgctga | ccanggcgga | 360 |
| tattcg tact | gcagaagaga | aagcatgctg | ggctgccaca | ganatgtgcc | tcatggaggc | 420 |
| aaaaacagcc  | ttagcgcaac | gccaacggga | ttatatcata | cccaaagtcc | cctgttccgc | 480 |
| agtggcttan  | gcctatataa | g          |            |            |            | 501 |

## (2) INFORMATION FOR SEQ ID NO:389

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| ctcgggtgaa | ggaagtatgc  | gggagtaccg  | gtggaactga  | aagtcgtggt | atgttggcag | 60  |
| caatctgtcc | ggccttgccc  | ataccggaag  | ttatcagcga  | ccgttagagc | catgcacttg | 120 |
| acgaacaatg | aggctgatag  | ccgcctttag  | tcgttgctctg | cagggatggt | acggatggct | 180 |
| tcagcttcat | gtgccatatt  | tcggagatgg  | ttcgattgtg  | tatttctgcc | ttcatgctca | 240 |
| ataaatgccc | tgcaaaagta  | tttatttaat  | tttgcataatt | atgcttttaa | ggcttttctt | 300 |
| tgcactaaat | cttatttcgat | ttagaattgg  | aagggtggct  | aagaaaatgc | aattaagcta | 360 |
| aaacattgag | aaaagccctg  | aaagcatgat  | agcggaaggg  | tactatgtaa | cggatatgcc | 420 |
| gaatttataa | atggattatc  | actatacacg  | ctgccgagcg  | gtttgcatgt | ggtatataaa | 480 |
| ccgcatgccc | cgaagttaca  | taacccggct  | ttgccatagg  | cgtcggcaca | cgccacgaag | 540 |
| ctcgcggcat | catggattgg  | ctcatctgac  | ggaacacatg  | ctcttcaagg | caccagcctg | 600 |
| cgcaatagcc | ttcagatcat  | tcgtcgcgatg | gaagaggcgg  | tgnccgagct | taatgctttc | 660 |
| accgagaaag | aatccaccta  | tgtgtatgca  | tcttttc     |            |            | 697 |

## (2) INFORMATION FOR SEQ ID NO:390

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

|            |            |            |            |            |             |    |
|------------|------------|------------|------------|------------|-------------|----|
| aagccgaaca | tgcgtggtac | gntgaccagc | gtgtagcata | gtaccggcag | tagatgggtca | 60 |
|------------|------------|------------|------------|------------|-------------|----|



|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| gataggccag | ccccttgcca | aagacgatac | ggagtgcgcg  | gagtagtggc | tgatatcggt | 120 |
| aggtacgagg | tcgtgaaact | tattccttca | cgcgcgcgtac | cggccgagag | tcctatgccc | 180 |
| agcaggagcg | tctgcttatg | atcaggatga | gtacggcagg  | tagcaggaag | gaagcgaaac | 240 |
| cgacgtcggg | ttatacagtg | ccacgtcttc | atagtcgatg  | gggtaagaga | tgattctccc | 300 |
| tgacgtctcg | tagctcctac | gctgcgcgct | atcttgatct  | cttggttcac | tccagcgaaa | 360 |
| ccagtgtatt | ggcaatgagc | aggcttttgt | agagagcaat  | ccgctcatat | cgcagtaaa  | 420 |
| agagatatgg | gccttcctgc | cgtattgaga | tggttcggaga | aatcctccgg | aacgtagatg | 480 |
| atgccatagn | attgcgcctg | cggatttgct | ccttggcctc  | ttccatatcg | gtgcagtgtc | 540 |
| tacgatgctt | acttcgggtg | tggcatctac | ccttcgcagg  | tattcgcgct | cagtgtcgag | 600 |
| ttcgatctgt | ccaccacat  | ggccggcaca | tcgcgtacac  | ttccgtggct | gtatatatag | 660 |
| ctgtagagga | gtgggtacag | gaggggacta | tgatgaaaaa  | gatgaccata | cccatgtctc | 720 |
| tgaacgtctt | gcacactcgt | ac         |             |            |            | 742 |

## (2) INFORMATION FOR SEQ ID NO:391

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...4129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| gcaagatcca  | agatgcttac | acacaggcca | cgaatggcaa  | tatcagccaa | agatcaacgt  | 60   |
| cagtgcggac  | tacgacatca | gccgcagtgt | tacctgcag   | cttattacga | ttgggatatg  | 120  |
| aaccatccgc  | ttgtcagctc | agcctcctcc | ctatcacgaa  | cagcaatttc | ggcgtcagct  | 180  |
| tccgtttcaa  | tctgaccagt | agcctaacgg | cattaccac   | actcctcgta | tcgcatttca  | 240  |
| gcgaagccac  | ctcccatctc | tgagatagtt | gtatccatag  | tattcggata | ttcatagtga  | 300  |
| aatccatata  | gtgaagaaag | tatgaccgat | atggatagga  | tacatggtct | catatgagag  | 360  |
| gatactatgg  | tctaacatga | gaggatacta | tgtctcataa  | aagttagaaa | tgagagaagag | 420  |
| aaaatgccgg  | atccctaccc | tccacgaaca | ttagatcgat  | cagatacgat | aatcatgctt  | 480  |
| cggagatgaa  | ccaatcgctt | ttttcaagca | gaaagccgat  | atgttgtgct | tttgagtgtc  | 540  |
| ctgattacct  | ttgccggaca | ttactttttc | aggattataa  | taatgatcat | cgagcacttg  | 600  |
| tccgatcccg  | agttttgcaa | caagcatatg | tgtattacat  | cgagatgatg | ctgatataca  | 660  |
| atctgccgaa  | aaagagttgc | tcaacatctg | gagcagacat  | acgacctata | cctatattat  | 720  |
| ctcctcttgg  | ttccgagctg | acaagactgc | atgcggaagc  | cctcgaagcc | aacaagaaca  | 780  |
| agcattagcg  | accgaaaagg | acaaaaaccc | caatctgcgt  | atggtacgca | accgcttgcc  | 840  |
| gaaaagatcg  | agagctgcag | gcctttgtgg | gtaagagccg  | aaagaatgct | ctgaattggc  | 900  |
| gttccgaaga  | agcttttctg | cgacgcctgc | taaaaagatc  | catttgtccg | agactttcac  | 960  |
| ccgttatatg  | agatccgatg | caccgatgac | ttcgaagccg  | accgcttggt | ctggaacgaa  | 1020 |
| ctgatgcgca  | catcatcctc | cccgatgaag | aactggcaga  | agtgatggaa | gagcaaatga  | 1080 |
| cttctggggac | aatcaaatac | aactcatcga | ggaaaatcga  | gaccagagaa | gcttccgaca  | 1140 |
| tagaggaggt  | ggaacagtcg | gtacgacaag | cagttgcgat  | ggcaactacc | aaacgatccg  | 1200 |
| acaggaaaat  | gcacctatcg | aaatctgaag | gagttcgtcc  | tcaagacaat | ccgacggatc  | 1260 |
| gagcaagaca  | ccgaccatcg | gctatcctgc | ttcctgcata  | caaggagaaa | gacgatgccg  | 1320 |
| tatcggcacc  | accctaactg | gcaatgccat | catcaacgga  | caggaatata | gcatatcatc  | 1380 |
| cgtgaaaaat  | tgatcaactg | ggaagtggat | cgcatagcgg  | aatggatatg | ctgatcatgc  | 1440 |
| aactggctat  | gcggagctg  | ctccacttcc | gaatatcccg  | gtcttggtaa | cgatcaatga  | 1500 |
| atacatcgac  | ctctccaagt | gttcagtaca | cccaagagcg  | gaacgttcgt | aaacgggttg  | 1560 |
| ctggatgcgt  | ggtcaaaaag | ctcagagaga | aaggcaaaact | actcaaataa | gagcagggca  | 1620 |
| aaacagctat  | ccccagatt  | tgacaaatga | cagacgacaa  | aaagatcggg | cagccatcgt  | 1680 |
| aggctacggc  | aatatcggtc | ggtatgcctt | gcaaggctta  | gagaagctcc | agattttgaa  | 1740 |
| atagccggca  | ttgtccgccg | caatcggccg | aggttccctt  | cgagctccag | cctttccgtg  | 1800 |
| tagtatccga  | catgagcaac | tccaatcggg | cgatgtggcc  | ttggtttgct | caccaagtcg  | 1860 |

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| tgagtagagc | gaacagcctt | ggagatat    | aaaaagggaa  | tatgcactgc  | tacagtttcg  | 1920 |
| acatccacga | cggtattttt | gccttgcgtc  | gatcggttggg | gacgcgcgcg  | gaaaaagtgg  | 1980 |
| ggcggcagcc | gtcatcgctt | caggctgggt  | ccgggcagcg  | actctgtagt  | gcgcacactg  | 2040 |
| atgcaggcta | tcgtacccaa | gggatcacct  | acacgaactt  | cggtccgggc  | atgagcatgg  | 2100 |
| ggcacacgta | gccgtaaaag | ccatagacgg  | tgtaaggcc   | gcactttcta  | tgaccatcct  | 2160 |
| ctcggaaacg | gtgtacatcg | tcgcatgggt  | tacgtagaac  | tgcttcggga  | cacaacttgg  | 2220 |
| aggaggtatc | ggctgccatc | aaagcagacg  | agtattcggt  | catgacgaaa  | cccacgtgat  | 2280 |
| acaggtagat | gaagtggatg | ccccatcgat  | atggggcatg  | gcgtccgcac  | ggtgcgtaag  | 2340 |
| ggtgtaagcg | gcccacacaa | aaccagcgaa  | tgctattcga  | catggagata  | aacaaccccc  | 2400 |
| cctcaccgga | caagtactgg | tctgtgcagc  | tcgagcagcc  | atgcgccaac  | acccggagct  | 2460 |
| tacaccttac | aggaaatccc | cgtcatagac  | cttctccccg  | agacagggag  | cagtggatag  | 2520 |
| gaaaactttg | ttgaaaaaga | ttactcaata  | aacggttaat  | cggaacatta  | tgacactacc  | 2580 |
| tgcattcatc | acatgggttt | cgatccgggt  | ctattttacc  | tcttcgggca  | ccctattgtc  | 2640 |
| tggtacggtt | gctctttgca | ttggggctga  | tcattctggg  | cccttgagata | gagaaaaaat  | 2700 |
| gtgggaacac | gagaagctgg | attccaaatg  | gttcgagtc   | ctggcgctta  | tgtctttgta  | 2760 |
| ggtactatcg | tcggagcgcg | tttgggacat  | gtctattcta  | tgacccggca  | tactatttgg  | 2820 |
| ccaatccggc | caagatatct | gtacttggga  | gggtggcttg  | gcaagccacg  | gcggtaccat  | 2880 |
| cgggatcatt | aagcctgctg | gctgtactca  | cgcaggggtga | cgcgcaaatc  | tattctatgg  | 2940 |
| tattagatcg | tttggctgtg | cctacaggta  | tcgtggccgc  | catgatccgc  | tgggcaatct  | 3000 |
| gaccaacagt | gagatttttc | gcccgcgcac  | gacattactt  | ggggcttcgc  | ctttattcgt  | 3060 |
| tcggaagagt | atcgtaactt | ggtaaccgaca | tggaatggg   | atgtcatcct  | actcagatat  | 3120 |
| acgaagcttt | atgctatttg | cggctctttg  | cctctgtatg  | tggctatact  | ggaagcgcca  | 3180 |
| tgctgccgac | gctactccgg | gctgatcggt  | ggggttttcc  | tgacaggtat  | cttctctctc  | 3240 |
| gctttatcat | cgaacgcata | aagatcggtt  | aggaaccatg  | ggactaaagc  | tcatacgaatc | 3300 |
| agtcggcctg | aatatgggac | agctgctcag  | caaccttttc  | ttcttgacag  | catttggtct  | 3360 |
| atcatccgtg | ccgtaaagaa | tcgattacgc  | agaaattatc  | ataacaacaa  | ataattataa  | 3420 |
| aaatatccaa | aatatgatgt | atcaagttcc  | tcaagtaaca  | gactccgttt  | actacgtggc  | 3480 |
| gtgaatgacc | gctcgaaaag | tctcttcgag  | aatatgtggc  | cgttgccaac  | ggtgtatcgt  | 3540 |
| acaattcata | tctcatcggt | gacgaaaaag  | tagccctatc  | gacacagtag  | atgtttgcta  | 3600 |
| ttcggagatt | ttcttcaaga | agttgggtaca | gtcctcaaaag | gacgccctat  | cgactatctt  | 3660 |
| atcgtcgata | acatgagccg | gaccatagtg  | gctcgatagg  | cctgctgcgc  | caacgctatc  | 3720 |
| ccaaatgcaa | atcgtcggga | acaagaagac  | tcattgggatg | ctcgaaggct  | acccacatt   | 3780 |
| accgaaggac | ttctagaggt | aaaagaaggc  | gacaaactct  | cctcggcaaa  | aatgagctta  | 3840 |
| ctttcatatt | cgtcccgatg | gtacactggc  | cgaagtaatg  | ttcacctaca  | tgccaaccca  | 3900 |
| acaggtcttg | ttctctgcgc | tgctttcggt  | acgttcggta  | cactcgacgg  | acatatattc  | 3960 |
| gacaaggatt | ggatctctct | ttccgctggg  | aggagatgta  | ccgctactac  | gcctgcatgt  | 4020 |
| gggcaagtac | ggcagctttg | tacagaaagt  | actcaccaag  | ttcaaggagc  | caatctgcct  | 4080 |
| gttcaatata | tatgctctac | gcacggcccg  | tttggaaaccg | gcacacttc   |             | 4129 |

## (2) INFORMATION FOR SEQ ID NO:392

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...646

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| aattggcaagc | gtcttgcccc | tgaagtgtac | aattctcttag | gcgtaaagga | tttacctctc  | 60  |
| agctgccgcg  | aggatccggc | tcttatacgc | tgccgggtgt  | ctgcagcgtg | gtgtgcatat  | 120 |
| cttcgcgcat  | acagaaggag | gtaagccgcg | tttgttcaga  | agtatctgat | taagtaataa  | 180 |
| tgggagtagc  | gccaaacctg | cacgatttgg | aggctaagga  | cgtttttccc | aagataaaaag | 240 |
| aggctcctcg  | gagttcgaca | tagacttcgg | ggcagttctc  | tcgttatatt | ttcagtcact  | 300 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gaatctgatt | gaggaaggat | tcggcatcat | ttctatatta | gattagtgcc | gacatttgtc | 360 |
| atccgaaagc | agacagtaat | actttatcat | caggcaaaga | tattggtggc | atttaacacc | 420 |
| gtgagcgagg | ggttcgaccg | gttaccgctc | gtcacgaagt | ggttttcccg | cccaaagggc | 480 |
| gcgattttac | caagaagaaa | tagcagagcg | tatcgtggat | tgcgatgttc | tctgttccga | 540 |
| ttcgacattc | cgatcggtag | ggatttgatt | gacaaaggcc | cgatcgctaa | gttgatcgct | 600 |
| aactatgctg | tcgggtacaa | taatatcgat | gtgactttgc | agcatt     |            | 646 |

## (2) INFORMATION FOR SEQ ID NO:393

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...3018

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| cttcacacgg  | ctcatcatcg  | atattccccc | caataccatc  | agagagaggg  | gacgcagagt  | 60   |
| atataataga  | tggtaggact  | cattggctgc | ctcettctct  | ttcttgctaa  | acatacggag  | 120  |
| catgcggtgc  | gtgacaccga  | aacctccacc | acattgatgg  | tagcgaggat  | gatggccagt  | 180  |
| cctccgaaga  | tttgccgagg  | atgagtttgc | cgctcatgcc  | gaacttgaaa  | gataatccgg  | 240  |
| cagctcaata  | gctccgatta  | cggttactcc | ggagagagcg  | ttcatacccg  | acatagcgga  | 300  |
| gtatgcagca  | agctcggcac  | attgctgata | agcttgtagc  | cgaaagcggtg | gaagctatca  | 360  |
| gcacgatgat  | aagaatgatc  | ggattcatta | tttatgagtg  | attggtgtat  | tagctcaaat  | 420  |
| gagtaagagc  | caaaggacgg  | cacttgagag | gggtcgcttc  | ttggctcttg  | atattaagat  | 480  |
| gtaggaacag  | tcgattacag  | acctattgct | tcacgagtac  | cggcgtgttt  | gatttcgcct  | 540  |
| cgcgagttaac | gaggatcttg  | ctgcaaaact | cgctcgttcat | atccaattga  | tccgaccggt  | 600  |
| ctttgtgagg  | tacttcatca  | gattgtacat | gttctgtcga  | acatccaagt  | agagcttttc  | 660  |
| ggaagcatac  | cggggatggt  | cttgatcctt | ggatcatcac  | tccgtgcttc  | acttccttgg  | 720  |
| ttcccttcgg  | cgtgattcgc  | agttaccgcc | ctggctcgata | gagatgtcca  | cgattacgga  | 780  |
| gccggcttca  | tacccttcac  | catttcttcc | gtgatgatga  | tcggagccac  | cttcccggga  | 840  |
| tcaatgcgct  | acagaatacg  | atatccatat | cctgaatggt  | ggcttgaggg  | cttcgcgttc  | 900  |
| tttgccaggt  | acatcatcgt  | gccatttggt | gcataccgc   | cttcggcgat  | agccagttcg  | 960  |
| gcaggaaacgg | tcggtatcca  | gatttggttc | ccaagctctg  | agcctgttgc  | gcagctgcag  | 1020 |
| ggcgaatatg  | gcagcataag  | tgatggctcc | cagacgctta  | gccgtagcca  | aagcctgcag  | 1080 |
| ccagccacac  | ccacaccgat  | caccattact | ttggcggggcg | gaatcatccg  | acagccgtac  | 1140 |
| ccatcatcgg  | gatgaagctg  | gcgaagtctt | cggcagcatc  | aggatacctt  | tgtagccggc  | 1200 |
| acaagtactc  | atcgaagtca  | gtgcgcgagg | ttttgtgcac  | gtgagatacg  | ggggatacca  | 1260 |
| tcgagagtca  | gcgaataaca  | ccctgttttg | ccagattgcg  | taccatttcg  | tgggttcacc  | 1320 |
| ggtaagccgg  | atgaatgaat  | gtgatcagat | actgaccttt  | gcgcatacag  | tcacttcgtg  | 1380 |
| cgtatttgagc | tgttcgttga  | acaaaggctc | ttttaccttg  | agatcacttc  | ggcaccgtca  | 1440 |
| taaacggcct  | tagctccgtc  | taccagcgta | cacctgcctg  | ggcatattct  | tcgtcatgat  | 1500 |
| actgagcacc  | ttctcctgcc  | ctttttcaaa | cagaactttg  | aaaccgctctg | ctacaaattt  | 1560 |
| ggccactggt  | caggggtagc  | cgacacacgg | tttctgcctg  | gcataatctc  | ttttggatgc  | 1620 |
| caataatcat  | tgcttagatt  | ctttttgaat | gtgattttct  | aaattaactg  | ccggagggtta | 1680 |
| acatcggtcg  | ctccgaacgt  | ctgccgggtg | atgagggtag  | gcgtccaaag  | gtcatcgggg  | 1740 |
| tgtaagccgc  | tgagcgacca  | caaaatagaa | aagaaatgta  | tataatgcac  | ttattacgga  | 1800 |
| cacttttctt  | caacggaaacg | cttattatca | aagagtaaac  | ggaaaaacaa  | agaaaccact  | 1860 |
| accaaactat  | cggcagagcg  | tgcattgccc | atattcgata  | gttgtgagta  | gggtttctct  | 1920 |
| ttattttctca | cccattcccg  | gtcggccggg | cggagggtat  | tcctcgccat  | ttgcggccaa  | 1980 |
| gagtagggga  | gactactgtg  | cttattgtct | ttgagcaaat  | cgcgaaatctc | tgtaagcagt  | 2040 |
| tcgatttcag  | gtggcgtaga  | gcaggagctg | caggtgcctc  | ctcttctttc  | ctcttggcag  | 2100 |
| ccatgatgct  | ttgatcatca  | ggaagatcac | gaaagctaaa  | atcaggaagt  | ccaccgagtc  | 2160 |
| tggataaaat  | tgccatagtt  | ccatgacact | tccggtttca  | cgaccctccg  | ccttcgacga  | 2220 |

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| cagccttgc  | caataccaat | ttcagatctg | tgaattgacc | ccaccgcgtca | gcaaactgat  | 2280 |
| gggaggcatc | atgatgtcgt | tcacaacgag | gtgacgatct | ttccgaatgc  | gccaccgatg  | 2340 |
| atcacaccga | caccatgtcc | actacgttac | ccttaagggc | aaacgctttg  | aagtcctgaa  | 2400 |
| taattttctt | ataatacgct | ttgtttttga | tgagatctgt | ccgccttggt  | ttgcaaaactt | 2460 |
| agattgcata | tctacagaga | gttcccatac | atgagttaga | tctctaatta  | aacgcccaca  | 2520 |
| gcactctttt | ttcccgatgg | aaaaatcggt | ctactacctg | tcaaataatag | acacaaaatt  | 2580 |
| atcgaaatga | cctgtacgaa | aaaaatcgta | tggtgttttg | tagtagatag  | gattgctgtg  | 2640 |
| cttgtcactt | gggaactcct | gccgagagat | tcttaatcaa | ggggcgaggc  | tacaacgaac  | 2700 |
| aacttgggca | agcaggctta | tattattggc | ccaaggagac | tcttataaca  | caacgaagga  | 2760 |
| gagacaccgg | aagttcctct | cctttctatt | gccaaaactg | acttttagga  | cactattgat  | 2820 |
| gcagatccga | tatttatggt | ttggaaggta | tctggtgagt | agttttatcg  | gatatcgggg  | 2880 |
| ctctcctcct | cctcttcttc | tttttgtacc | cacatcaact | ttttctgtgc  | gagtttttac  | 2940 |
| catctgcggc | tcgtgttttt | cggaagaggt | ggcgcgagat | ttttttcgtc  | tggcgcgtaa  | 3000 |
| aaattttact | tctcgcgc   |            |            |             |             | 3018 |

## (2) INFORMATION FOR SEQ ID NO:394

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| gtcatcagtc  | cgaacgggtca | taagtatatc  | cgcgaaatata | atgtggataa | ataccggcca | 60  |
| ccatcttttcg | cgtggggagga | gtgggtactca | agcgcgaaaa  | gtattctgcc | actacatcaa | 120 |
| tcgtgccata  | ttcaaataca  | cgctgatgaa  | gcacatagcg  | atagctact  | gcgctttcgt | 180 |
| cccttgcttg  | ctttcagagc  | gtggcagctc  | tcactcacga  | aaacgggcag | atcgaacgtg | 240 |
| gacattccccg | gcccgaaacg  | gcatagggat  | cagcctctac  | aagggttata | cccactcttc | 300 |
| atgcagttca  | gcaaagaacc  | cgaataccgc  | gaggagggat  | attgtacaaa | gacttcgaat | 360 |
| accccaagga  | aaaagagcgt  | ggatacgagt  | gtcggaggat  | ctttacatgc | ccggcacatt | 420 |
| cgagattccc  | ataaaaaaag  | ggaatccatc  | tactttgctg  | ccggtctttg | aagaggccaa | 480 |
| tccaaatacc  | ttcgaacgac  | atttgtcaag  | gaaagtagca  | gagcgcatte | cacgccgaaa | 540 |
| atttttcagc  | tgccttg     |             |             |            |            | 557 |

## (2) INFORMATION FOR SEQ ID NO:395

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...905

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| gcgaaattaa | ttgtaaatat | gactgtcgtg  | aatacagggg  | aaattttaagt | aaggtaaaaa  | 60  |
| tagaatgaga | aaagcttggt | tcatgggcct  | gggtataaag  | gtctgccaac  | ggcaattgta  | 120 |
| actgccaaaa | gtggaataga | agtattaggg  | tagatataaa  | caccaatatac | gttgcaaaaa  | 180 |
| ccaattcagg | aaaattcact | ttgtggaagc  | aggtatggaa  | gatcttttac  | aggaagtatt  | 240 |
| acaaaagaaa | cattccgtgc | ttctacaaca  | ccggaggata  | gcgatgttta  | tctgttgtgg  | 300 |
| tgcctacacc | cttcaaggcc | aatcatgagc  | cggacattac  | atggtagagg  | ctgcaacaag  | 360 |
| atcaatactt | cccttgctca | agaagggcga  | ttatttatta  | tcgaatctac  | ctctccgata  | 420 |
| ggaacaacag | agcagatggc | tatctaattct | atcgagagcg  | tcccgaactt  | aaagaccaat  | 480 |
| tatatatggc | tactgtccgg | aacgtatcct  | tcccggtaat  | gttatattatg | aactggagcc  | 540 |
| aacgatcggg | tcatcggggg | cttaagcgca  | gaagcgaccg  | aacgggcaaa  | gagttctatg  | 600 |
| ctcattttgt | taaaggaacc | ttgcatggaa  | ctaatgccgt  | acagcagaac  | tctgcaagct  | 660 |
| tacagagaat | gctagccgag | atgtacgac   | gcgtttgcc   | acgaactttc  | tttcatttgt  | 720 |
| gacaaagccg | gaatcatgtg | tgggaactta  | tcgaactggc  | caataagcat  | ccaaggggtga | 780 |
| atatcttcag | cccggtagtg | gagtagggg   | gcattgtatt  | gcggtggatc  | cgtttttaat  | 840 |
| ctcttcggct | ttcctctgga | gagtaaactg  | attgccgggtg | ctgtgaatca  | atactaccag  | 900 |
| gcttt      |            |             |             |             |             | 905 |

## (2) INFORMATION FOR SEQ ID NO:396

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...535

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| ggaatgttcg | ctcgagttac  | agatattact | cacaagagta | tagaagagta | aaaaatcttc  | 60  |
| gccatttggt | atttaaatgga | ataactgttg | gaactgaacc | ggagatgac  | tgacattatt  | 120 |
| gcatatgaat | aagaaaacaa  | cttcagcgaa | acgatagaaa | acctcaagaa | gtttgaagag  | 180 |
| gcaggcatag | aatattttgt  | tcctatctta | caggattggc | cggtgccgga | aatggagaaa  | 240 |
| gaaatcttta | gctacttcgg  | atatgtttta | tcaattacat | ccttatatca | tttcgttgta  | 300 |
| tcattaacga | tttttcctga  | cacagttcta | tttcaagaaa | ttcacagggg | cttttttagag | 360 |
| aggcgtctga | acatgagaga  | ttaaaagagc | tagcaccttt | ataagtaatc | tgaaaatcaa  | 420 |
| tacgaatttc | ttcgcaaata  | cgtatcta   | cctgttccat | taacgggata | cttgcccaat  | 480 |
| gataaaaaga | attgatcaat  | gagctttccg | atgttattaa | tgccgtagat | gaaag       | 535 |

## (2) INFORMATION FOR SEQ ID NO:397

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| aggcataccc  | tttttcaggc | gagagaaata | ctgttcggag | acgtcgatgg  | gagcttttacg | 60   |
| ggagctatct  | gttctaccac | atagataggt | ttcgtgggga | agccatatcg  | ccgctatcat  | 120  |
| aattgcgtgc  | ggtaatcaca | ccgataaagg | gcttcggagc | acgggtgttct | ccagcagatt  | 180  |
| gttgtaagta  | gtctcgccac | gtcgagctgc | gttttgagcg | catccactg   | ctgtttggct  | 240  |
| atgccccat   | tttgtacagc | tcatccatac | gctggaaatt | gggtgcgcgta | ttctcagttg  | 300  |
| tactttggcc  | tgggtcagtt | ggctccgac  | caactcggcg | agccctgtcc  | gcgtccact   | 360  |
| cgatcaccta  | cttcggccgt | aaggcgtagc | atctattgcc | catctgaggg  | gtaatgttgt  | 420  |
| tggtcacttc  | ggcccgaacg | gagctgtgaa | actcagtacc | tcattcagcg  | tgtcgggtctt | 480  |
| cactatagtc  | tctccaccaa | tttggctgcc | atagctgccg | aatcagcagc  | agacggccgc  | 540  |
| tctctttctt  | gccattgcag | ctcgtgagaa | tgaggaaacg | caggactaga  | ggaggatagc  | 600  |
| actgcccagt  | gtattcgatc | ttttcatatt | tatcataaag | tgtattttgt  | tactatttac  | 660  |
| tttttacgct  | cattgttcgg | gaatcccatg | ccgttcactt | tgtccaattc  | ggcctttgcg  | 720  |
| gtcataaaagt | cgaattggcc | tgattataat | tgagtcnagc | ctgcaaaaaga | gccacatcgg  | 780  |
| catcggttag  | ctcgacgaga | gtgccttcgc | ctgtctgata | gcgtttctct  | gcttctgata  | 840  |
| gcccttttct  | gcacttcgga | cagcctcttc | cgaggccaca | aactctgcat  | acaggtacgc  | 900  |
| agacggtcat  | tttggttctt | gattcccatt | cgatggattg | ctctatgtgg  | ccgtcgttgc  | 960  |
| atctcgatct  | gacggatcga | aaaagcactt | tgcttcacgt | tgtac       |             | 1005 |

(2) INFORMATION FOR SEQ ID NO:398

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| aggaacgagt  | cagagccatc | gaggcacagn | tgcgcgaaga | gttggtccccg | ccattncggt | 60  |
| cgatgggtgtg | gccgaagnac | gtgtcctcgg | agccatcgtg | hagaggagat  | gaagcggccc | 120 |
| gtggatatgg  | ccacgctgca | gcagcganca | tccgagaggg | aatctgggta  | cgccccctcg | 180 |
| gtcgtctgnt  | gctatcggag | ccacccttna | tcatatcgcc | ggaagatcta  | tcgtatcctt | 240 |
| acgcaggact  | tctccgtgta | ctcggtcagg | atcganccat | tncattttacc | cgataataca | 300 |
| aganntatgt  | ccgaaacaaa | ngaaagactc | tgcatatacg | ccgctnccca  | ta         | 352 |

(2) INFORMATION FOR SEQ ID NO:399

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| agctcttttg | ctgcagagca | gattcttagt | gtcttcggga | aaggtcaaac | tccggtatat | 60  |
| gggcacacca | agcaaacaga | aattttccca | agtttccata | gagaagtact | cctttcctcg | 120 |
| tcaaataggc | gagaaataag | aaacgatgtc | agctgattct | tgcttcctgc | atgatgcagg | 180 |
| acgcgattgt | cagctgttct | tgcttcctgc | acgatgcagg | acgcgattgt | cagttgattc | 240 |
| ttgctcctgc | acgatgcagg | acgcgattgt | cagctgattc | ttgcttcctg | cacgtgcagg | 300 |
| acgcgattgt | cagctgattc | ttgcttcctg | cacgatgcag | gaccgattgt | cagttgattc | 360 |
| ttgcttcctg | cacgatgcag | gacgcgattg | tcgttgattc | ttgcttcctg | cacgatgcag | 420 |
| gacgcgattg | tcagttgatt | ctgcttcctg | cacgatgcag | gacgcgattg | tcagctgatt | 480 |
| cttgcttcct | cacgatgcag | gacgcgatt  |            |            |            | 509 |

(2) INFORMATION FOR SEQ ID NO:400

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aggccgctct | ggcagaagcc | gtgtggggag | actatataga | ccaagcggaa  | attatgactt | 60  |
| tgtctatgct | caaatcaaaa | atctgcgcaa | gcagatgacg | atgcaggggc  | gacgatcgag | 120 |
| atcaaatcgg | tatatggatt | cggttataac | tcatagaaag | agaagaagat  | acttgaaact | 180 |
| atcctatcga | atagtatgcg | ttttgtcttg | ctgtcttcct | cgtgggtattt | accgcctggg | 240 |
| tgatactttc | tattatgtaa | tcgtcgaaga | aatnaacgac | gagacgaacg  | attcttggag | 300 |
| aactactccg | aacatgtcat | ccgcaatatc | ctctccgaca | atctctttcc  | accggctgaa | 360 |
| aacgacctta | acaacactta | ctccattcgg | gaattacccc | acaggaggct  | atgcggttcg | 420 |
| ctcacgatat | ttactacc   |            |            |             |            | 438 |

(2) INFORMATION FOR SEQ ID NO:401

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| gattctcaag | aatttcaatt | gaaatthtga | caaaaagttc  | tatatttgca | cttaatcatt | 60  |
| agtacttgaa | gctctatttc | tcttaagttt | cgcccttaat  | cagcgtagaa | aattatcacc | 120 |
| gctatgggga | accgaagaca | aacagatctg | acaagtccgt  | atcgaaaaca | aaacaaccct | 180 |
| accctatttc | gcttattcga | tctgtataa  | ttttcgcaag  | atgccgccac | gtcccgacca | 240 |
| aaatgatccg | aagaggcaga | aggacggtta | tttgctcaag  | ctatcatcca | acggagtaca | 300 |
| ccaccgagga | cctttgtcgg | gacatttcgg | acagggtcgtc | cttagctccg | gcgacatcac | 360 |
| gggactgatg | atagccatgg | aggagttagt | atcgagtatc  | tggttcggg  | ctatagcttc | 420 |
| cggtctggga | atatcggcac | atatcggcc  | aagtaaaatc  | gcgcggagta | agagacaaaa | 480 |
| aggaaatccg | tccggttccg | tccaagcccg | tgatatcaaa  | tttccgttcc | acaccgcaac | 540 |
| caaacgacgg | atgcgcagca | tgagtgtgaa | gcgcggtccg  | agctt      |            | 585 |

(2) INFORMATION FOR SEQ ID NO:402

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...4412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| gccgtggatc  | ggatcgtagg  | cggattggag | aaaaagaaca  | aaatcaccaa  | gaggaggagc | 60  |
| gtcgcagcat  | cgccatccac  | gaagccggac | acgctacttc  | agttggatgc  | tacgctatgc | 120 |
| caatcctctc  | gtcaaagtc   | ctatcgctcg | cgaggcaagg  | cactcggtgc  | cgcctggtat | 180 |
| ctgccggaag  | agcgctgatc  | acgacaacgg | aggctctgca  | ggatcagctt  | tgcgcccttt | 240 |
| tggtgtgacgt | gccgccgaag  | atctcttctc | cggacgtgta  | tcgaccgggtg | cagcaatgac | 300 |
| ttggagcgcg  | ttacgaagtt  | ggcttacgcc | atgggtacct  | atttggcatg  | agcgacaagc | 360 |
| tgcccaacat  | caactactac  | gaaatgcaaa | acacggctgg  | aatctgacaa  | agccgtacag | 420 |
| tgatactacc  | gccgagggtta | tgatgccgaa | gtaaacagaa  | taatattccga | acaatacgag | 480 |
| cgcgccaaaa  | cattctgcgc  | gagcatgaag | ccgggcacca  | cgaactggca  | gatctgttgt | 540 |
| caagcgcgaa  | gtgattctgg  | ctgatgacgt | agagcgtata  | ttcggcaacg  | cccctgggct | 600 |
| tcgcgtacag  | aagaattgct  | tggtctgaat | gcaccgggtac | cgccacagaa  | gagacaacag | 660 |
| cggtatgccga | agcaccatt   | cccgttaggg | agaagagaag  | acggaagaac  | atcccgaata | 720 |
| aaatataaag  | agacttcgag  | cttacgttat | gaaagcagtt  | ttgattcgca  | gcctcagtgg | 780 |
| tctgtctata  | tgccctgat   | cattcttccc | gtcgtactaa  | gggaaccggc  | tttttcttag | 840 |
| cggtttttgc  | cgttttcatc  | gtgttgggac | tgccgggaatt | cgctcgctgg  | tcaatctgaa | 900 |
| tcgcacacgt  | ccccttcggg  | cattcatgga | cgacttttcg  | gtgccttctc  | ctttgcggcc | 960 |



|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| atcttcctat  | acggcagtg   | cgaatggatg  | tcacgatatt  | tatcccgtat | atcttctatg | 1020 |
| tcctctacat  | atgggtgcgca | gtctatatct  | ggatcgccat  | aaggccggat | cggacaatgc | 1080 |
| cgcactttca  | tggggcatct  | gtatatagcg  | gcaacgcttg  | gtttgggagt | cttctgctcg | 1140 |
| tgccccgaaag | tatcggcagg  | gagttggcag  | taggagagtg  | gcagacttca | cgcctcacta | 1200 |
| cttcctcttc  | gtttttgtgc  | tgataggctg  | aatgatacag  | gagcttttat | tgcaggttcc | 1260 |
| ctctttggca  | agcaacactc  | ttcaagggtca | tatcacccaa  | gaaaacatgg | gagggcttta | 1320 |
| tcgagggctg  | ctgttctactg | tggcaggtgc  | attgctggca  | ggccactatt | ccgttcggcc | 1380 |
| aagcatccga  | tggagctggg  | cttctttgct  | ctactggtaa  | cgccatggcc | acttggggcg | 1440 |
| atctgtatga  | gtccaatctc  | aaacgcaatg  | aggagtgaag  | gattccggcc | atatcattcc | 1500 |
| cggacatgga  | ggtatactga  | ccggctggac  | agtctctct   | tcgtattccc | ggcgtctat  | 1560 |
| cttttcatct  | gatcttcgga  | ttgtaagcat  | ttttcccggc  | cacccattcc | gacgaggaaa | 1620 |
| gagaccggcg  | gaagctctga  | taaaagcaac  | ccccgaaag   | ccgtgggttc | gggggttcc  | 1680 |
| tgtattatac  | cctcactctc  | cttgccatgt  | ctattgcaag  | gagagtggaa | gaattgggtt | 1740 |
| ttcagcacia  | ctcactattc  | actttcagag  | aagacgctgg  | ctgcgacgaa | tgaattcggc | 1800 |
| caaagcctct  | ccctcagcaa  | tccgcttcgg  | agcagagcca  | agtcgatgag | ctgacctatc | 1860 |
| agtcgttgct  | ctgagcatat  | ttggtcagtt  | gatcgttgat  | actgccttcg | gtttggcctg | 1920 |
| ttcgacggcg  | ttgttctcct  | tggcttcctt  | cgtggcaaca  | ggatttcttc | cggtttcttc | 1980 |
| ccttttctct  | catcgagcag  | cttggcctct  | ccgctttcag  | ctcgcgatt  | ttcgctctaa | 2040 |
| gctctgtgag  | cgaaggctta  | ccgattcttt  | ctcaccggag  | agtaacctgt | cgatgagcgg | 2100 |
| atgatcgat   | taagtaccag  | attgtacgaa  | tcggggagtt  | cgccgtagaa | gctcatccc  | 2160 |
| gctgcagctg  | tgccatatcg  | cgcatacggc  | gcatagaatt  | ggctttgtga | taaggatggc | 2220 |
| ttcaccttcg  | gctccgagcg  | attcgaaagc  | tacatgaagt  | gcttcttctc | gtcccggtgc | 2280 |
| aggcgtgctt  | cgaacagctt  | cacagagtgg  | cgcgtccgt   | atcgacagct | ttcacttcgg | 2340 |
| ctctttctct  | ctcgggatca  | gattgttgat  | cgtatcgcta  | tcgacacgga | caaagtgtgt | 2400 |
| ctctccaact  | tttgcctcag  | caggctcagc  | atatgcggat  | ccaactgacc | tccaacagca | 2460 |
| tcacgctgta  | gcctttgtcg  | gatgcacggt  | tcacgtggcg  | tactgtccat | gcttgtccgt | 2520 |
| agcatagaga  | tacactacct  | gtccgtccta  | tccgtctgta  | caccttcgac | gagcgttcgg | 2580 |
| tattcgtcga  | acgtgtattg  | tgtccgtcca  | tatcggtgaa  | aaggagaagt | ttggctgcac | 2640 |
| gctcatgaac  | ttctcatccg  | tcagcatacc  | gtattcgacg  | aagagcttca | gactacccat | 2700 |
| ttctcctcga  | atgtggggcg  | gtcgtttttg  | aaaatttctt  | ccagcggctt | gccaccttct | 2760 |
| tgggtgatatg | agacgagatc  | ttcttcacat  | tggatcgctc  | tcagatagg  | agcgcgatac | 2820 |
| gttgagggga  | atatccggcg  | aacgatgacc  | ccgtgcagga  | gggtgaggaa | gtccggcagc | 2880 |
| ataccctgta  | ctcatcggtg  | acgtaaacct  | gattgcagta  | gagctgaatc | ttgttgcgt  | 2940 |
| cagatccaag  | ttgtttttga  | tcttcgggaa  | atagaggata  | cctgtcagat | gaacggatag | 3000 |
| tccacattga  | ggtggatcca  | gaagagaggg  | tcttcggaat  | gggatagagc | gaacggtaaa | 3060 |
| attccttata  | gtcttcgtcc  | ttgaggtggc  | aggctttttg  | gtccaggcag | gatgtgtgtc | 3120 |
| gttgatctga  | ttgtcccgtc  | cgtatcttgc  | atcttgccgt  | ctttccattc | ctgcttcttg | 3180 |
| ccgaaatgat  | cggcacggta  | aggaacttac  | agtatttgcc  | gaggagcccc | tctacttttc | 3240 |
| ttttttgagg  | aactcgctat  | tctcctcatc  | gatgtgcata  | acgtgtcggg | gccacgggtc | 3300 |
| gccttgctcg  | caggttcgag  | cgtgtattcg  | gggatccgtc  | gcagctccat | ttcaccccg  | 3360 |
| tagcatcttc  | tcggaaagag  | ccgtgatcac  | gtccactcgc  | tcggacacca | tgaaagccga | 3420 |
| gtaaaatccg  | gtccgaagtg  | gccgataatg  | gcggccttgt  | cgtcttttga | cttttcaaga | 3480 |
| actcttcgcg  | actggagaaa  | gcaatctgat  | tgatgtactt  | ctccacctct | cttcggtcac | 3540 |
| ccctacgcgg  | cggctcgctga | ccgtgatcgt  | gcgtgccctt  | catccacgct | gaccgttaac | 3600 |
| cggaggtcac  | ccgtctcgcc  | tttgaatcgc  | cgacggatgt  | aagcgttttc | agcttctcgc | 3660 |
| tagcatccac  | ggcatggaga  | cgatctcacg  | caggaataatc | tcatggctcg | tgtacaggaa | 3720 |
| tttttgatga  | cggggaatat  | attgtcgctc  | gttaccccg   | ttgttctttt | cttctcatag | 3780 |
| tgtattatta  | tctgttaatg  | ttttgttgtt  | ttctattccg  | tcaaaggaa  | gacaaatccg | 3840 |
| atgccacagg  | gtccgggaact | gacaatctgg  | ccattctttc  | attcagactg | cctttttcgc | 3900 |
| ttccgaatga  | ttgacgtgta  | tgaaaaatcc  | ggtgtatttc  | agttctgaaa | aacgtgggtc | 3960 |
| gagaaaattt  | tattttgggt  | cgggagttga  | aaaaatctcg  | cctgagaacg | aaaagatttc | 4020 |
| gcaccatttt  | tgggggattt  | tggtttcaga  | tttgggcgat  | tttcggtcga | gtttctatgc | 4080 |
| gattgataac  | ctcacgtcag  | ctcgacgtaa  | gaaaagccaa  | tggatcaatg | aacccttttc | 4140 |
| gcctccgcgg  | gaagaacaaa  | atcagtcctt  | ccgtaggcag  | ggggatccc  | ctcaaatccc | 4200 |
| aaaagtcttg  | tattgagcga  | ctcagctctc  | atactaaaaa  | ctccccctc  | taagcaaa   | 4260 |
| tttgacact   | attgatttga  | tagcggtttt  | tctatacaaa  | cgatgatccc | ggccctgct  | 4320 |
| tgaaactgaa  | ttttgacaca  | ccctcttctg  | gtagttgggg  | taatttaggc | cttgcgtttt | 4380 |
| ttttctgcgg  | aaaggttgcc  | gtctttaacc  | ta          |            |            | 4412 |

## (2) INFORMATION FOR SEQ ID NO:403

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

```

ggacgaatcg tccgtgctgcc gcacgcagcc cgactgtttg ttttcgaatg cagctctgcg 60
ccgggtttttt acttccgacg cttgcgctgt ttggagtcaa cttgtcgtag aaacgtcctt 120
ccgtcgggtt ctcttttgcga cctttgtttt gcgtgaagtg ggattttcac tacgtcgccc 180
gtcgaaatct ttgcgagagc ggaaaagttc ttatctccgc cttttttccc cccggcatag 240
tcttttttgt atccgcatac tctacatgga tgcggcgacc atccacttcg taccattgag 300
ggtttctact acgttcttgg cttcgaactc gtctacatcg aagaagcgaa tcgggggcac 360
aggctgatcc gtccgatatt gacacgcccc ggatacaacg gttgatcagc tcgatcagtc 420
ggttgggaaa catttgatcc acttgccaaa attgatgaac agacgggtca tcccttcttc 480
tgcttcgccc ctccctcgttt tcggttttta cgatctcccg aaacctcgtc tttttttctt 540
cgaccacttc ttcacgtct tccgcacgtt ggtaatagtc gagcatgcat tgaactccaa 600
tgccattacc cgacgaatca attcgtcttt ttcaatcatt cgagcttctt gttcacttcg 660
ttcaagacag agtcgatggc cgttgtttct ctatatccac acgttctata cgatcggcca 720
gattgaacag ttgctttcgc atatctctgc tccggaaggg atgctgtcac gttcgatctg 780
cttcgcacgc tgcgctctat attcttgatt ttgcctttct ccttgacatg gcaatggcga 840
tcgaaagacc tgttttccct gcacgagctg tacgacgcgt gcgtgggtgt agctctctac 900
atcatcgggg agaccgaagt gaatcacatg gtcagatcgt tcacatccaa tccgcgggca 960
gccacatcgg tggcaacgag agttgaaggt tgcggacgcg aaacttc 1007

```

(2) INFORMATION FOR SEQ ID NO:404

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 497 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

```

ggctcccag tatctcttca tcgtctttgt aacgcccgtg gggccgtatt caaagaagga 60
ttcaaaccga ccaagatggc catcttccgc gactatgacg tgcagctcct ctgggtacgg 120
gtacgatcaa agtgggagg aactatgagc cggtatgac cccacagtga aagctcacga 180
aatgggctac tctgcactat cttcttggat gccaaaagaaa agaagtacat agacgaagcc 240
ggtccgcca cttcttcgcc atcaagaaca atacttatat cactcccgaa tccactctat 300
cctgccctct atcacaaca agagtctgat gcagggtggc cagatctggg tctgaaggta 360
gagcgtcgtc cggtagccga agaagagctt gcactttcga agaagcagg gcttgtggta 420
cggcagccgt gatcagccct actccgagat tgacgaactt ggagaacaac aaacagtacc 480
gtcatcagca gggacggg

```

## (2) INFORMATION FOR SEQ ID NO:405

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| atatacgaccg | atgcgaacga | aacgacaagc | gcaccatcga  | caacgtcatt | atcgcgacgg  | 60  |
| caagtcgcgt  | cgtttctata | tcaaacgttt | cagcgtcacg  | gtgttacgcg | agacaaggag  | 120 |
| tacaacctta  | cgcaggaaac | ggccggtgtc | gggtgatgta  | tttcaccgcc | aataaaaaatg | 180 |
| gcgaggcaga  | gaccgtagga | tcatcctcaa | accgaaagct  | cgccagcggg | tactttcttt  | 240 |
| cgagaagact  | ttagcaatgt | cgccatcaag | gggcgaagca  | gcaagggcaa | tctgtgacca  | 300 |
| aagcagaggt  | gcacaagatc | ctgttcaaac | agcanggggtg | cttcaccctc | ggagggcgga  | 360 |
| aangtttggt  | tcgatcgggg | cgtgatgcga | ctaactacga  | ccgagcangg | gcgaatatct  | 420 |
| ttgggcgaaa  | ttcccaaagc | caaccgattt | cgatggcttg  | gtaaatcctt | tgggattaaa  | 480 |
| ccggggggacc | ggcttattac | ctaacaattc | ccataa      |            |             | 516 |

## (2) INFORMATION FOR SEQ ID NO:406

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| gacgctcatt  | accgtttccga | ccaatgccag | aatgctgaag | aggagaagaa  | accgctaagt  | 60  |
| gaacgttcct  | cctcgctgtg  | cgaggctatg | atgtcttcga | acgcaggatt  | tcggtatagg  | 120 |
| gctgccccgt  | aatacgggag  | taaacggctg | tatgctttga | atcaactgct  | ccggatcggc  | 180 |
| cccttccgaa  | tagccgccag  | tacggaccac | gaccaggcgg | atgactgggg  | ataaggggatg | 240 |
| aagagttagct | cggatgcggc  | tccttgaatc | cgccgaagtg | aacctcgggg  | gcatgccgca  | 300 |
| ataatagaac  | tcaccggctt  | tgccccaatg | aatgacaccg | tcgcagatt   | ggctacatcg  | 360 |
| aaatcgttgt  | aggccgatcg  | gctgagatag | aggtgcgatc | gggcttgctg  | gccttgcgac  | 420 |
| cgttgggctt  | catcttcaga  | tgaacaggct | cagtgccacg | gagtctatgg  | agaaaatctg  | 480 |
| catggagaga  | gcctgccacg  | gtattcgga  | gagttgttgt | tgcctccgtt  | cagcggagtc  | 540 |
| cacgcgtgag  | gcctataccc  | gttatgccgg | ggattttggc | tatttcgggtc | tcatcgctact | 600 |
| gacgatctgc  | ggatccagtc  | cgaaaacgtc | tatgatcggt | tggttcctgta | atcgtagccc  | 660 |

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atgtcggagt | tggatcatata | gtcgattgca | cggccattac | catggtacag | ctcagcagga | 720 |
| tcacgtgaat | ggcatctggg  | aaatgaccat | aatctgcgag | aagctgcttt | tgaccacacg | 780 |
| gcgaacttgc | cgctgaccac  | ctcgatcgga | cgaaaccgcg | atatgaacca | tgccgcaggg | 840 |
| ccgcacacac | gatgctcagc  | aggagcatga | agccgattag | cataggatga | gcgtgagcga | 900 |
| aatatgccgt | gccagataga  | gatgcgtatc | gacaggcgat | cgaatacggg | ttcaaggggc | 960 |
| aacatgccga | atacggccag  | agcgtgctc  |            |            |            | 989 |

## (2) INFORMATION FOR SEQ ID NO:407

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| gatccccctgc | ccgaatttttc | gtatgcctat | cgcaacaaag | gtacatttttc | ttttattgta | 60  |
| aaggtctatt  | tagcattttt  | atgcaggcac | agcagcagca | ttcgacccat  | cgtttaccgc | 120 |
| tccggatcgg  | cgtccaggca  | gaataccaca | ttccgaagag | ctgagagaga  | acggggagaa | 180 |
| aatcgagttt  | acgctcagaa  | ttgttccacc | caacgcccct | aaaaacgtgg  | cgcgagattt | 240 |
| ttttcttttg  | gtgcgggaag  | gaaaaaattt | acgcgcgaga | acgaaatagt  | tttgttcgtg | 300 |
| tttttcagga  | aaacacacgc  | cgcaatctgc | togtttacgg | ttctaaatcg  | cgaacgaaaa | 360 |
| tgtgcgaaga  | aaaggaaagg  | atactttctc | tgatcgattg | ttcagtcgga  | ttttgagtgt | 420 |
| gcccgtatcg  | gattggctct  | cgctatgctc | cgctttatct | tttgcccttg  | tcctaaattt | 480 |
| gcaccacgtn  | gttttatacg  | ggagagaact | actcccctcc | cctactgact  | c aa       | 533 |

## (2) INFORMATION FOR SEQ ID NO:408

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gggaagaact | gagcattggg | gaatctcttc | acatagtctg | atactacgtg | ttaccgctgt | 60  |
| cacggaggtc | aagcatgcat | cggaatttct | ccggtgtgtg | atacgcgtcg | ggtcgtaaac | 120 |
| atagccgtca | ggaccggaga | tcgtaacacc | ttaatgccca | actcggtagc | tttctgagcc | 180 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acaccccaag | caacgtaccg | aatccggaga | tagcaagagt | tttgcccttg | tagtctacac | 240 |
| cgtttgctta | cacatgttct | gtacgaagta | aacagcaccg | aaaccggtag | attcggacgc | 300 |
| agacgagaac | cgccgaactc | gaatnccttg | ccggtaagcg | tactgtgtgc | tcgcgagcga | 360 |
| gcttcttgta | cataccgaac | atataaccta | cttgcgaccg | ctacgccgat | gtcaccggc  | 420 |
| aggaatgtcg | gtgttagggc | catgttgcg  | cacaaatttc | ggcatgaag  | ctctggcaga | 480 |
| aa         |            |            |            |            |            | 482 |

## (2) INFORMATION FOR SEQ ID NO:409

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1900

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| tcttcagtct  | tggcaaagat  | gaactgactc  | agaaaatgat  | ggtcaattca | ccggacgcaa | 60   |
| atgggagttc  | actttcacta  | cattgggttac | tttcgggagag | ctctctttgc | ttcgtttcct | 120  |
| cttttctata  | gcaccagctt  | cggaggacat  | attgggtatg  | gatgctgac  | ctcttctgct | 180  |
| tcattatcca  | agctgttcc   | acgagtatca  | atccaaacat  | ggtaatgtat | gggggaggaa | 240  |
| aacctccaaa  | tactgtttt   | catcaatggt  | gtactggctc  | cggttctgct | cggaccgctg | 300  |
| tttccacatt  | ctttacgggc  | agcagcttcg  | tggtaaacia  | gatgcgatgt | tcgacctctc | 360  |
| cggcggcaac  | cagatcggtt  | ctgcctggca  | gccttcaatg  | ggtggcaact | gagaggcctt | 420  |
| gaagctgttt  | tgaacctgtg  | gacgtggttc  | tcggattggc  | tgtattcttc | cttgccagag | 480  |
| tatcggtctt  | ctttatttca  | tcaataatat  | cgatgacgaa  | agtctctatg | cggcagccaa | 540  |
| cgccgacttt  | gggccaatac  | ggtcgcattc  | ctgattttct  | ttctggcaac | atagctttcc | 600  |
| tgctgactac  | ggaaggattt  | gccgtgaatc  | ccgtttcaaa  | gaggtgtata | tggagccata | 660  |
| caagtacctg  | tacaatttct  | tggatagccg  | gccgttctgg  | ctgtattcct | gttgggagta | 720  |
| atcctcgta   | ctggcgata   | ggtttgactc  | tactgcgtaa  | aggcttcaaa | cgcggaatct | 780  |
| ggctcacggt  | acgggaaccg  | tactgactgt  | gcttgcccta  | ctactgttag | ccgttggaac | 840  |
| gatacgtctt  | ggtacccctc  | cacatacgat  | ctgcaaagtt  | cgttacgatc | gagaatgcca | 900  |
| gctccagcca  | tttcacgctg  | aaggtaatga  | gtacgtctct  | ctccttattc | ctttcgtttt | 960  |
| ggcttacatt  | ttctatgctt  | gcgcgcactg  | gacatttctg  | aaaatcacaa | aaaaagaaat | 1020 |
| ggagcaggag  | atcacgtcta  | ttgatctctg  | acagataatt  | ccacaatctg | aggctgtgca | 1080 |
| ttgaggttcg  | atcccttgat  | acagcctcat  | tgtctttata  | tatttcgcaa | taatcatgac | 1140 |
| cgacgatttg  | aaaagacggc  | tatatattacc | tgaccaacga  | tagcaatatg | gctcagtcac | 1200 |
| catatcaaac  | cgcaccgcat  | cggatggctt  | ggctcttagc  | ggcggagcgg | ccaaaggctt | 1260 |
| tgcacattcg  | ggagactcca  | tgtctttgag  | gacaatggga  | ttcgtcccga | catcatagca | 1320 |
| ggtcgagtgc  | aggagcgttg  | gtagctgcac  | tctatgccga  | tggatacagg | ccgaagagat | 1380 |
| tcacacaatta | ttccgaggca  | aaaatttcag  | attcctaaca  | ggtggcaaat | accacaaaga | 1440 |
| ggtgtattca  | gcattccaacg | cttcaagagt  | ttcttcgctc  | gactttacgc | cacaagaata | 1500 |
| tcgaagacct  | accctttcca  | tcagaatagt  | ggcaacggac  | cttgaccgtg | gagttgtcaa | 1560 |
| agttttttac  | aaggctctct  | cgtcgagact  | gtcacggctt  | cctgtagcat | tccgatctat | 1620 |
| tcaaccctgt  | agagatagat  | ggaaccacct  | atgtcgatgg  | aggactttca | aagaccttcc | 1680 |
| ggcttctgtc  | attcgtgaag  | actgccgtta  | tctcaaggag  | tacacctcaa | tcccaaagag | 1740 |
| ccttccgact  | ataaaaagag  | tctttcggca  | ttgcagagcg  | ttgcttcggc | tacatcttcc | 1800 |
| gagcgaactc  | cctcccgatc  | gcaagctgtg  | cgatttgctg  | atcgaatcaa | gagaaataat | 1860 |
| cagttcaaac  | cattccacgt  | ggagccggca  | gaagaaattg  |            |            | 1900 |

## (2) INFORMATION FOR SEQ ID NO:410

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

|            |             |             |            |            |            |      |
|------------|-------------|-------------|------------|------------|------------|------|
| ctgcattgga | cacgttggct  | catcgttcga  | tgaacctatc | gtcatctgtc | gatccggaaa | 60   |
| ccaaactcat | gcgcggtaga  | aatcaggatg  | gtagtttcgg | acaccttttt | cccccttcaa | 120  |
| atggggagat | gtattcacgg  | agggcaagcc  | tggcactaca | cttggtcggg | ctttcatgat | 180  |
| gtgcaggggc | ttatcgcttg  | atgggaggag  | atcgcccgtt | cgtgtctatg | ctcgattcgg | 240  |
| tattcatact | cctcctatgt  | tcgatgagag  | ctattacgga | tttgtcatcc | acgaatcaga | 300  |
| gagatgcaaa | tagcggatat  | gggcaattat  | gctcatggca | atcacccata | cagcatatga | 360  |
| tatatctgta | taatcatgcc  | ggtcattccat | ggaagctcag | gagagactac | gcgaagtgat | 420  |
| ggggcggctc | tatcgctccta | cccggatggg  | tattgcggcg | atgaagacaa | cggacagact | 480  |
| tcggcttggt | cgttttctct  | gcttttaggct | tctatcctgt | tacaccgct  | acggatcaga | 540  |
| tgtgctcggg | tcgccgattt  | tttccaaggt  | aatactctct | tttcccgagg | acacaaaacg | 600  |
| gtgttgcatg | ctccggccaa  | cagtgcggat  | acgccttcac | ccgctcgatc | agcgtagaag | 660  |
| gaaaagaatg | gagctgcaat  | tacctgctca  | cgaacagctt | cgctcttctg | catccattca | 720  |
| atggatgatg | gacacaaacc  | caattataat  | cgtggtatga | aggaaagtga | cagaccttat | 780  |
| tcctctccac | ggagcaacag  | cgtcgcgcta  | atcacagtaa | ttaatgatac | attccccact | 840  |
| tcggactatg | aatacgaaca  | aagcatttac  | gccccgacga | tcatactgat | gagcttgctt | 900  |
| ggctttttcc | tccttggtgt  | aagctctgcc  | gatgtaaaga | tgatgtccag | accgacatat | 960  |
| ttaaaggggc | tgtggactac  | tgaatcctta  | tatgggcaat | atcagtcac  | tgctcattcc | 1020 |
| cacttttcca | ctgtgcattg  | gccca       |            |            |            | 1045 |

(2) INFORMATION FOR SEQ ID NO:411

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtggtaataa | aactattacc | cgattcgctt | cggatacaac | cgctgatcta | aaattaattt | 60  |
| gacctctcta | aacgaaattt | ttcattcaga | attcgacact | cttattaatc | aaccaaacgg | 120 |
| aaaaggatat | gaacaaaaag | aacattacat | cggatcaatc | atcgcagtac | tcgccatact | 180 |
| gcttatcacc | tctttctgtg | gaatagagat | gtacgtaata | aattgcggat | cgctcagcac | 240 |
| aatgtgaagc | cgcattggac | tccattcggt | acctcaaaga | tgccaatgga | aatcctatgc | 300 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggaaaagaaa | tcgttcatcg | ccactatcag | cgaattgaaa | gaatgaacac | tgagatgtac | 360 |
| gagaatatcc | agtctttgca | aaagaaactg | caaagaaaat | tctggcaggc | tccgatatag | 420 |
| gcgtagtcgt | agtggacacc | attatcagga | caagatcatc | gaatacacgt | tagacagtct | 480 |
| ggtaaatatc | ccttctccga | tcagaccatc | aatgccaaac | gcctcgttcg | catacatcgg | 540 |
| acaatatccg | tctgcaacaa | ttcacatata | cttggacatt | cc         |            | 582 |

## (2) INFORMATION FOR SEQ ID NO:412

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| aggatccccg | caaaagagtc | ttcttcggtc | gtggtgctga | tggtaatatg | ccaaagtgca  | 60   |
| gttcactgac | tatcaggatg | cagaactcaa | aaaaggagca | tcactttcac | ttatacatatc | 120  |
| cccgttaaat | aagttaagag | ggaaatagaa | aagtgtagta | acaaagcagg | ccctcatcgg  | 180  |
| cctgcttttc | tttagttaag | tatatactcc | catgcggcca | accctccggc | ccaacctacc  | 240  |
| gacacatcgt | atccggcaat | atcgcaactg | aggatatagt | ggtgaccggt | agcctacagc  | 300  |
| ccgtctgctt | aaagatgtac | ctgtccccac | aaagggtgtc | aagccaaaga | tatcaaagct  | 360  |
| atagccccat | cttctttcat | tgacgtactg | catatattct | tcccgggatc | gagttttacca | 420  |
| agcatgggtc | cagagatcag | ccaatgctca | gggatttgac | gaaagttcta | ttctcttcct  | 480  |
| cgtcgatggc | aattgatttc | aacgggatct | accagtggaa | tagacttcga | acgaatcaac  | 540  |
| cggatgacat | cgagcgaatc | gaagtgttcc | gtggagcttc | ctctgcttgt | acggatctaa  | 600  |
| tgccatcgga | ggtgttatca | atatcatcac | ccgtacacca | aggatccttt | tccggtatct  | 660  |
| gcttcggctc | gatacgatag | tcgcgaggac | agaaatacga | tgtggcagca | ggagtgaaac  | 720  |
| gtgggatctt | caccatcagt | ccggcgtaga | atatagagca | gacaaaagtt | atatcttggc  | 780  |
| ccgacagttc | gagcaggaac | tgaatgttgc | aggcaatacg | acatggaata | taatcaagaa  | 840  |
| gtttacaatc | tctccgacgg | aaaacttatc | cttcaacctt | acggactggt | gaatctgcgt  | 900  |
| aagcagcact | ggacggataa | gategatttt | cgtacaactc | ctacgatgtc | aaagccgggtg | 960  |
| ccaactggcg | tatcagcgag | cttcggatct | ggacgtctct | tatcattacg | acaaatatag  | 1020 |
| ccgtgatact | gtctgatcaa | gactgagaac | caaaagaaac | ttcccatttt | cgatgaggta  | 1080 |
| tgcaccattt | gcgagcacia | tacaatctca | atcttgctga | agtccacttc | tcaatgtggg  | 1140 |
| tctggagtat | atccatgata | atgtagcatc | gccccgcttt | cctctccgaa | cgacccgggg  | 1200 |
| gaaaagtccg | tgaacaacaa | aatccatacg | gacagtacat | atataaagtt | acccccaaac  | 1260 |
| tcgtattgag | ctatgaaggc | gcttggacaa | gcactccgga | ttcggcttgt | actatacatc  | 1320 |
| gcgctgtctg | ccatgttcaa | gtgcagccat | gtcaccaate | gcttg      |             | 1365 |

## (2) INFORMATION FOR SEQ ID NO:413

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...449

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtcgaaaatt | cggaaaactt | tacacaaaac | gcaaaaacaa | taacacacta | taataagtgt | 60  |
| ttttatgaaa | agttttcgga | aaacttttca | acaacgaacc | ttttcctatt | gtccaattaa | 120 |
| tatatacttc | ataacattgc | aggcacaaca | gaagttat   | acataaaaca | ccatgtcacg | 180 |
| caaaacgtac | acattcacga | ggcatacaaa | gcctcgcttg | cctattttga | tggcgatgag | 240 |
| cttgcgccaa | agtatgggta | atgaagtatg | cgctgaaaga | tgcccaagg  | aatactacga | 300 |
| aaaaagccct | atggacatgc | acaagcgtat | agcctccgaa | atactcgcat | cgagaaaaag | 360 |
| tatcccaatc | ctctttccga | ataagagctg | ttgatctctt | cgatcacttc | cgctacatct | 420 |
| gtgcctcagg | gaagtcggga | taccgggtat |            |            |            | 449 |

## (2) INFORMATION FOR SEQ ID NO:414

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...449

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| ggcgtaatgc | ctgatgtcca  | tggactctcg  | gcacaggatg | ctttgtacag | ctacagctct | 60  |
| cagggttgaa | agtaaggacg  | aacggatggg  | gacatgtatg | gctcagtcog | ttccgtacgg | 120 |
| ctctaaagtg | aaagtggggc  | agactgtgtc  | atagacttat | ctatgtaaag | aacaaggaat | 180 |
| gggaatgaaa | ctcgaataata | tctctcgga   | ctgcggccga | tagctgtcat | tggcaatata | 240 |
| gaacagaagt | atcagatatt  | gcattctgatt | ctcgcaaggc | tacggacggg | gcaccttcgt | 300 |
| agccgttcgt | ggaacactga  | cagatgggca  | cagatacata | ccgaagcata | cacacaaggc | 360 |
| tgtcgcgcct | ttgtcgtgga  | ggaccttccc  | gagaaaagcc | ggaaggatgc | tgttttgtcc | 420 |
| aagtgtcgga | tacagccgaa  | gatttgctt   |            |            |            | 449 |

## (2) INFORMATION FOR SEQ ID NO:415

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:



## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1086

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

```

ggaatacgtg tcggcagatg gagaggaggg gtatccgggc gagctgggtct tcggatcatt 60
tacagcgta cggatgaggg cgcattgcac atagactacg tgctactgcg gatgctccta 120
cggttctgaa tctgaccaat cactcctttt caatctctcg ggtgcaggcg atccctccgt 180
gcatgatcat accctctgat acaagcccg cttatctccc ccacagacga tacggccatc 240
ccttaggcga gcctgccgag gtcgagggga cgccgttcga ttctctcacg cctccggcat 300
aggggatcgg atcgacagtg cgatggatca gctcatttgg gcaagggaata cgatcatacc 360
tttatcgtgg acaagccgtc gggggcatat ggttttgcgg ccgttgcgta tcgccaaga 420
ccggaatcgt attggatgtc ttccaccga accgggtatg cagggtgata cgggcaactg 480
gatgagcggg agctgagggg gaagtccgat cggcgttatc cggctcgctc ggccgtttgt 540
tcgagacgca gcactatccc gattcgccga acaaaccgaa ttatcctaga ccctcttgcg 600
cccgggcgaa gtgttcgagt cccggacggc gttccgatcg gtatcgtcga gtgatcttct 660
cacaaggatt ttgtatcaaa ccaatctaaa caagcagaaa ttatggaatt agacttcgta 720
aggagtagat tcatcagcac ttgacggat ctacgggtca gatcttcaact tctcccgggc 780
gcataatctg atcggcgaa acacggacta caacggcggt ttctgtcttc ccgtgctata 840
gacaagggcg tcatggccga aataaaaccg aatggttcgg acaggtaagg gcatattcga 900
tcgacctcaa ggactatgtg gagttcgggc tgggcccggac gatgctcccc gtaccacttg 960
ggcaaagtat atctatggcg ttgtcgcgag atgatagccc gaggcgtaga ggtaaaggga 1020
ttcaatacgc cttctccggg gatattccgc tcggagccgg catgtcctct tcggcagctt 1080
ggaagaag 1086

```

## (2) INFORMATION FOR SEQ ID NO:416

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...480

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416

```

gaagaggaag ctttcgatct gggacataaa gctgtgagag aacgtttcgc tctttcgtgg 60
aagatgccaa acgattaggg cgagccatcc gcacgggac aatcatggct ctctgtccga 120
acgtatgctt acgcgctatg gcgatacgtg gaaggcatgg taaaaagctg catggaatac 180
ctcgatgtat gccacgacat gagttcgacg atgtgggtgat gtcgatgaaa gcacgaata 240
ctttgtcatg acagcagctg tacgccttct tgtggaacga atggatgctg cagaatgcac 300
tatccgcttc acatcgggtg caccgaggct ggcatgggtg agggggggcg atcaagagtg 360
ctgtcggcat aggttcgctt ttggctgatg gcttggcgat accattcgtg tttcactgag 420
tgaggatccg gagcatgaga tccggtagcc cgcaaattgc ttgcctatat agagaaacgt
480

```

## (2) INFORMATION FOR SEQ ID NO:417

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: UNKNOWN  
(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION 1...773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| gtaggcagg  | gaattttggc | ccgatccggc | acgggcacgg  | caccggcatt | tgtctgaacg | 60  |
| cttgttttag | ctgctataga | cgagctgaaa | agaggagttt  | ggttcaagga | ggattgtcgc | 120 |
| gtatggatgt | atcgcgaggc | ttgggcaagt | gggaaataga  | ctacatagag | atggccgtcc | 180 |
| cgatgagtc  | ggacgactcc | gcttcaaacy | aaacagcatc  | ctcaagcatc | agtcgcaa   | 240 |
| ggagtcgccc | ccttccttgg | cgatgacgaa | cggctcttct  | ggcagagggc | ggaaatcgga | 300 |
| acagacaaac | ggccaccctg | tacgaaaaac | tgggcttggc  | ctctatgaag | ccatagaggc | 360 |
| attcgtacag | tataggcctg | tccaatagag | aacgggtataa | atacaataag | agaggcttcc | 420 |
| ttcacttgtc | cattcgggac | gagaaggaag | cctcttttatt | ttggtaccga | cctttgccaa | 480 |
| cggcaggcgg | gtttatctcc | ggcgagctg  | atgatcgatg  | aagatcagat | tctgctccta | 540 |
| gagagacgga | tctgttcgac | gatttcggca | gcagtggctt  | cctcttctcc | tgctcgcgga | 600 |
| tatacttcca | gaagaagtc  | tgtgatgcca | tatctccgct  | tcggaagcag | cccttacgac | 660 |
| agcctcgatc | atttcgggtc | ctttgcctcg | tgttcgtaca  | cctgttgga  | tacctccaat | 720 |
| acagagcccc | aactttgggg | cacggcatcg | atagcttcta  | tcttcacctc | gcc        | 773 |

(2) INFORMATION FOR SEQ ID NO:418

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 5489 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: UNKNOWN  
(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION 1...5489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| cagcctgacg | gatactactt  | acgaattaca | aatcccttct | actttgaatg | gcacagaagc | 60  |
| accacttgaa | tctggaattt  | cgtcttattt | ccgagcctag | cgtgctcacg | gacatttcaa | 120 |
| ttacgctgtg | tttgtggatg  | gccatcgatc | ggtagcggaa | tgggcatgaa | taagaaagaa | 180 |
| gctcatcaga | atgctgacat  | gatgccctgg | aaaagttaga | gcgtgcgcg  | gattaccgac | 240 |
| aaaaaagaaa | tcgatcatcat | cttcggagcc | ggaataaaga | ctcgcaactc | gcaccaataa | 300 |
| cttgtgctgc | attttcttat  | tgtattttca | gaaaaagaag | caacccaatg | acactccact | 360 |
| ttgtgtcggt | gggggttggtg | ctttagaagt | aatgatcaga | ttatttctta | gctgctttgt | 420 |
| tgagcttgcg | cttttggatc  | tgtaggcaag | gggtgtagca | acaaagagcg | tagagtatgt | 480 |
| accgataacg | taccgagcag  | gatcgagaac | gtgaaactac | gcacgtagc  | acctccaaaa | 540 |
| tgaagattac | caacataacg  | ataaacgtag | tcaaagacgt | atttaatgtc | gacccaatgt | 600 |
| tgaattaagg | gcacgttgta  | tcacctgata | gcgatcttgt | tggggtacaa | tttcatcgtc | 660 |
| tctcggtatc | ggtcaaatac  | aaccacgtgt | cattgagcga | gtaaccgatg | atagccagaa | 720 |

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| tagcagcgat  | gaagtctgat  | cgatctccat | ggtgaagggc | agaatcttcc  | acagcaacgc  | 780  |
| atacagagcaa | taatgcagaa  | tgtagtagcg | gccacagata | cgaatacccc  | ggcgagaaag  | 840  |
| aaatgtcacg  | gaagcgaatc  | agaatatata | tgccatgaa  | gacatcgata  | acagcacagc  | 900  |
| ccaaatagca  | cctctcgtga  | tgtaactcga | ctactgggac | ttactttctg  | agagctaatg  | 960  |
| atattgtcca  | agaactgatc  | gcagtaggct | gctgggtgta | gaaacctttc  | aggctctgat  | 1020 |
| acaatttgta  | gtaatctctg  | cttcagtttc | ttcgctttcc | tcctggatct  | tatagttcta  | 1080 |
| gatatacgca  | cctctgtccc  | ttcagtaccg | atggaggtaa | ccaatacttt  | tcctgcaggg  | 1140 |
| gagaagacaa  | ggccgaacga  | acggcttcgg | aagataaggc | tggtcgaatt  | taactacgta  | 1200 |
| gttacgtcct  | cgggagaatt  | caatacccta | ttgagaccga | ttgtaaatga  | agctataagt  | 1260 |
| cccaaaacga  | tgatatcacc  | ggaatgataa | agccggtctt | gcgcttacct  | aagatgttgt  | 1320 |
| atggggattg  | acaaggagat  | tgcgagtaat | gctcgtagt  | aatgtaatct  | taccaaacga  | 1380 |
| ccttttttcg  | ccagttttct  | gaagacgata | cgagtcaaga | aacagccgta  | atgaaagaag  | 1440 |
| cgataagacc  | gataatcaac  | gtagtggcaa | accgcgaatc | ggccccgtcc  | cgtagaggaa  | 1500 |
| taggatgata  | cgggtaatat  | agtcgtaacg | ttcgagtcga | agatggcaga  | gaaagcgttg  | 1560 |
| ccataaccct  | cgtaaccgga  | cgaatcggag | tcttaccggc | acgaagctct  | tctttgaacg  | 1620 |
| ctcgaagata  | agtacgttgg  | catccacagc | cataccacgc | gtcagcccaa  | acctgcgata  | 1680 |
| cccagagagg  | tcagcacggc  | atggaaagaa | gccaaacgcc | caatgtgaag  | aagctgttta  | 1740 |
| caatcaatgc  | gccgttttgc  | ataaacccgg | caagaaaccg | taagccagac  | acatgtaaca  | 1800 |
| catcaggata  | accaagcgag  | caggaacgac | aagaatccgg | ctttaatgga  | ctcgccaccc  | 1860 |
| aggtaggacc  | aatcacgttt  | tcctgttcga | tgcttaccgt | agcatccatt  | taccggagtt  | 1920 |
| gagtacgttg  | gcaaggtcac  | cggcctcctc | cacggtgaag | gccccgagat  | ctgagagcga  | 1980 |
| ccgcccgtga  | tctcatcatt  | cacgttcggg | cagaataaac | cacaccatcc  | aaaacgatag  | 2040 |
| cgattgcccc  | tcccacgtat  | cctttgtgat | acgcgcccct | ttacgagcac  | cttcttcatt  | 2100 |
| catcgtctcg  | aaacgatcgg  | ttcggaacga | ccgaagtcct | tttgatatac  | actcttgccg  | 2160 |
| aagtcactac  | atcacctccc  | aaatcaggat | ctcccgtacg | attggacgaa  | tagcatagag  | 2220 |
| ttcgtagagg  | tcggtctcct  | ttttggtttc | ggggcttcga | ttgcttttag  | accccagagg  | 2280 |
| aaaagcacat  | cttcacgtgt  | aacttcagat | cgtgagcttg | ctggagcatt  | tcagatatct  | 2340 |
| gagccatatt  | agacgacgag  | ccacaccac  | tactgcaccg | ccacgattca  | cgggagtaag  | 2400 |
| cgagagaaga  | gtgcgtcttt  | acgagtagca | tccttggcct | ctttttgtgc  | acagttagag  | 2460 |
| aatcagctac  | agcttgtaga  | gcagcagaat | cggctgttga | gctacagagt  | cagtagttgc  | 2520 |
| aggctctgtt  | tcgggggtag  | catccgtgtg | ttcatagcca | attcgctcag  | acgatcattg  | 2580 |
| gcagcgatca  | agtctccctg  | acctcttcga | atltgtatgt | acgccagaac  | tgtaggttgg  | 2640 |
| cactgcttgc  | aaaagggtag  | gaacacgctc | agggctcttc | actccgggga  | gttcgcaagg  | 2700 |
| atacgccctt  | gcccttccaa  | tcgctgcaaa | ttaggtgcaa | ccaccgaaa   | gcacgcgatac | 2760 |
| gagcacggag  | cacattgaac  | gaagcttcta | cagactatta | tatttttctt  | tgagcagacg  | 2820 |
| cactacgtct  | gcacccgtag  | acttgccgta | atctggtcgc | gaaggtcacc  | cgaaccgaag  | 2880 |
| ataacggcca  | acgaccgttg  | ggatcgagct | tgcgatattc | cttcacgaaa  | atatcgatga  | 2940 |
| gtcgggattgc | tcggtgctct  | tgccagcatt | ctccagagct | ttgttgaaat  | gggatccaaa  | 3000 |
| ctttttgttag | agaggttacg  | aagcagatcg | cttgcgtag  | tttcaagata  | acgttcatac  | 3060 |
| ccccctttaa  | gtcaaggcca  | agaccaattg | ctgggcttga | gcttctttca  | gcgtgtagcc  | 3120 |
| gaaccagacc  | ttctcatcga  | catggaatca | agataggcca | ttccggcaac  | atcgccccat  | 3180 |
| gccttgccct  | cttttctgtaa | cggttcgtaa | cgaagagaaa | tgacaggtaa  | aacgcagat   | 3240 |
| gatggccaga  | gccgatgtga  | taacaatcac | aaatcctttg | tttgcathtt  | gtctgttact  | 3300 |
| tattttattg  | ttagattttt  | ttcatctata | cagcatattc | atagggcgca  | aagttacgtt  | 3360 |
| tttttttaca  | ctatctctca  | cttatatata | gaaaatagcc | gatgattcgg  | gtcatcggca  | 3420 |
| gcaaaaaacag | gggacattgc  | ctcggtagac | caaagattgt | ggtggctcta  | taaccaagac  | 3480 |
| cacagcaagg  | ataactgcag  | ctaccactt  | ccagctgct  | ttaaagagcat | ttttcgaaag  | 3540 |
| cgatatatgg  | caaaggcttc  | tgcttcatat | ggaaagacaa | acctgccggt  | agccaaggcg  | 3600 |
| acggaaaagg  | ctctgcgcag  | ccgtatgggg | ctatacgtat | ctatgcgtat  | gcaagtgcgc  | 3660 |
| ccttggttcgc | gagcttcgtc  | tcggcagaga | aaagcatggc | agcggcatac  | cccttgcgga  | 3720 |
| gcaggaggaa  | tgaacaccca  | ggcgggtgat | cgtataggct | ttcccttcgg  | tctccatggc  | 3780 |
| aacgagccgt  | attcggccgg  | catctgatca | ttcacagcca | ttcccccaaa  | ggagtacccg  | 3840 |
| ctatatccaa  | caggaaggct  | tctccacggg | catatcctct | tgagcttcgg  | tctcgcccg   | 3900 |
| atacgtctcc  | tgccactgag  | attgtcggaa | gcaagcatcg | tgtgccgggc  | atcctcccat  | 3960 |
| agggaagat   | gctgtcgtaa  | tcggatggaa | gagcccgacg | gatccgataa  | tgatcagtga  | 4020 |
| gagacaatat  | cctgtctgct  | tgctgtccaa | tgctttctct | gtcatgtaaa  | tcaataagat  | 4080 |
| ggttgccaccg | tctttgtgcc  | tttgggatac | agtctgtgca | cgagtgtctc  | agccgattcg  | 4140 |
| tcctaaatagc | tgttcgggtc  | atcgatacga | ggagttcggg | acagcttacg  | atagctctgg  | 4200 |
| ccaaaaggag  | acgcgtagct  | gtccgcgct  | caaateccat | atggggcggt  | tgagcagatc  | 4260 |
| ggtatccgga  | agcaccgggc  | agcagttctt | agaagttctt | tgtgcgaacc  | tcattaccct  | 4320 |
| ccccaagcaa  | accggatcga  | atgacctcct | ccacgcgaat | agaaaagctc  | tgtcgatacg  | 4380 |
| attgagctga  | ggcagataac  | cgatcgaagg | cttacacacg | gcattccctc  | ccgattgtag  | 4440 |
| aacgtaagac  | ttcccgatcc  | agtggcagca | ggccgattat | tgcttttacg  | agggtggact  | 4500 |
| ttccccca    | ttgcgtccta  | cgataccgag | aaattcgcca | cgaacgatat  | cgagcgatag  | 4560 |
| tccttgaata  | catttttcgg  | tccatagccg | aacgagccg  | acttcagctg  | agcaataagc  | 4620 |
| taccgttcat  | gagccaaagc  | gcgagcaata | tgtaaatctt | ctcctccac   | gagctgcgca  | 4680 |
| gaggattgat  | ccttaccgga  | cgagaccgat | ctcgcgtgcg | atgtcctccg  | cctgacgcgt  | 4740 |
| ttcaaattcg  | ggtggataaa  | tacgattctg | acaccatcgg | cacgtgcctg  | atcgatcaca  | 4800 |

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| cgccaagggtg | ggcagccgta | ggctcttttcc | catcttcttc | tatgacgata | tccgcaggcc | 4860 |
| gaactcttgg  | gcgaaaaagc | tgagcgatgg  | gtgatatatg | cgaaggcttt | gtctgctttg | 4920 |
| ccattggcaa  | acatggtatc | gacgagtctt  | tcacgctgtc | gatacgtcg  | ttgagacggt | 4980 |
| cgtgcccttt  | gtcccattgt | ctttctcggt  | cggataaagc | tccacaagcg | cgtcgtatgc | 5040 |
| agcacgatga  | gtgcctttgc | ccctaccaca  | ctgctccaat | agtgcggatc | atgggctgca | 5100 |
| ggtctgtatg  | agaatgatct | gtgcaggagc  | cgtggagatc | tgcactccgg | catccgccaa | 5160 |
| ggctttgccc  | atttcgaaaa | gagggagctt  | aggggtattg | cccgaatggc | agcgagattt | 5220 |
| ctttgctcga  | accccagtc  | tccatataga  | agtaggcata | tgcttcggac | aaacgcttca | 5280 |
| tcacggtagg  | cgagggtcgt | attcctccgg  | attgctgccg | gccggtacca | atgccaccac | 5340 |
| cgcaccgact  | tatccgcaat | ggactcgatg  | aagtattttc | gtggctcgat | gtcacagcca | 5400 |
| gcgtacgatc  | ggagcctgaa | gcagtacccc  | ctccacaagc | ggcaaagcag | tagcggcgag | 5460 |
| gatgaaggcc  | gggaaaatcg | taaaaaaag   |            |            |            | 5489 |

## (2) INFORMATION FOR SEQ ID NO:419

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cagcagttcc | cggtagtaga | aaccatcacc | agcataatgc | tcagccgaaa | accagcatct | 60  |
| tgcgcactta | cccaatactt | gacaagcttg | gtcccttcag | tctgggtgta | accaaatagt | 120 |
| tatccggagt | taaaacgcca | atcatcgtaa | gtacgaagg  | gatgcaatac | acttctcact | 180 |
| gtcatgtcca | tacatatcca | aggataatag | tcccaattaa | cattgtcgcc | atcagcatca | 240 |
| atcaaaacca | gccttcagga | atacttcgg  | cctcaaagcc | ttcatataag | ataagtccga | 300 |
| ttgagaatca | taaatcagct | tatcgcaaac | cgattgggac | tcgtattgtc | gttataaacg | 360 |
| gcagtgcac  | aatattccac | ttccacctga | tctctcgtga | agaataagtc | tcatcgatat | 420 |
| actccaaaac | agtcgggtct | ttatgtgaac | aaggagcgag | ccgtttgcat | agatattgta | 480 |
| gccggcaagc | gcaatgggtc | tttatcatca | gtcttatcgg | gttcgtaagc | cgttaggata | 540 |
| ttccacttta | atcgctccct | gttggtttca | ataagcgaga | caacgaaacg | gtaacaggtt | 600 |
| cgggctctga | tgcaggagtc | ccgaatccag | gtgatatgtc | caacttcaag | aaatattata | 660 |
| tcgg       |            |            |            |            |            | 664 |

## (2) INFORMATION FOR SEQ ID NO:420

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...567

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

```

ccccgtaaag cagtgatcgc atcggaatca gccaaagaaag tattggctgg aacctgagac 60
aacgcgctca caaaatcgct cagatcaaga aagaggctaa gaaaaagctg catcaatgca 120
gggcatcagc ctgacgatca aggccaaaca agcagcacgg gcacaatctt cggatcggta 180
acgaatatcc agatcgagaa gagctggcga aaaaaggcgt ggaagtggat cgtaagatca 240
tcgtctcaag cctgccgtta aggaagtggg caactatacg gctgtagtgc gcctcacaag 300
gaagttactg tagaaattcc cttcgaagta gtttctgaaa atgaactatc atagaagcaa 360
agccggaaga agctcctgtt cccgtagcgg aaagccgacc gctgagacag aacaagcaga 420
agttgctgct tgaataagca cctgagattg ttccttttta gcctgtcctc caatgcttgg 480
atggacatgg taaaggaata acagctttgt cagcattcag aataaaaacga tatgagaagt 540
ggacaaaaac gcatagtttt ggctcac 567

```

## (2) INFORMATION FOR SEQ ID NO:421

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...433

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

```

gcctttgctc tacggccaat aataatgtgg gcgaagaagc ctacgacgac aaaaaaagac 60
cgatcatcaa gcttttgctg ctgatcgaat tcgtgaatcg gggatggcca gtacccaaaac 120
gccaacgagc aatatgatgg ctcccaatat tttccgattc cttccattgt gagtatgttc 180
gttttatttg ttttcgtttt atctctgcaa ataaaacaat aatctgccga atacagaaat 240
tattgacgaa agattcatta cttttgtccg taatcaatac gaaaaagatg aatatatcgg 300
acgctttcct tttctcatct atttctgcct gatcggcgcc cctttttcct cctgctcact 360
atattgacag cactgactac cactgtaggc tgatgctggg gaggcaagta agaatatcca 420
agttaattaa tcc 433

```

## (2) INFORMATION FOR SEQ ID NO:422

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...730

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

```

aaagcgtagc gtttcagcac cgccgaacca cacggcaatc tgccgacgcc atcgccctgc 60
tttacatccg ccgttttcaa aacgtttctc gcatgtgttc gtgccgactt ctccggtttc 120
cgctcgggat caagccgtat ttccgctcag ctcatcgggg gatccgtttg ctgcgtcttg 180
cttcgaactt gtaaggagct ttttcccgta gctgtccaca cgcagggaga cgatatggat 240
atgtcgccg cgatgtcgtt gtgcttgaat acgatgtaag gctgtttgcc gtatccatct 300
tttccatgta ttcccgggcg atgtcctgta actgctccgt tgtagcctgt cgtccggatg 360
cggattgagg gaacagtga acaccgtctt ttcgtgcgga taccgcacgg gatgcgcata 420
tccatatcgg tcaatgctcg tcaaagtctg tttctccgtt tgcaccacg ctcatcgagg 480
aggtcagaat acggaggcgt ttcccgccgt tactttggaa aagttatatc ccaacactta 540
cccatgcttt tcggagcggg tatctcggca accatcgttc ttcgaaagta ctgtgagccc 600
ggttcggttc tccagaagcg caaggagtcc tccggtgatt gtcacagctt tgcagcaaaa 660
cgcccgccgt tttgacggaa tgggtactgta atggagcgga cggcctgatg tagagcacgc 720
caaccttgcg 730

```

## (2) INFORMATION FOR SEQ ID NO:423

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...364

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

```

cggctcgggg atattgacga aataaagcac tacaaaagcg agtgcaaaat acacatggcc 60
aggatgatag cgggataagc ctgcttgata ttggcctgtg aacgttgctc ccgataaagt 120
aaccacagag cacgggtacc agagtcgcat cagcgaattg aaagagccac ccacctggat 180
aagctgggta ccgcggtgcc tccgccaccc aaggatttga gcatcggatt gactaccgta 240
ttgagataca catggagaaa cgggcaacaa atgcgccgac caaataaata gagagctacc 300
catctcttcg gacaagagct gtattcctat gcctacaaat ccgcagcgat ggccggataaa 360
agct

```

## (2) INFORMATION FOR SEQ ID NO:424

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...3297

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaccaaactcg | gcacctgttt  | cttccgcttt  | ggctatagcc  | atggcgagac  | tgcaggctct  | 60   |
| tcgggattgg  | gagaatgtac  | cgtagggaag  | tctccgctac  | aacatcctgt  | tcgggtacgt  | 120  |
| gaatgatatt  | ggcaaaacca  | tattcactaa  | ggcacggggg  | accaccgtac  | ttccgggtacc | 180  |
| gtggataggg  | gtgtatcgat  | cttcataatcc | cgatgacggg  | caatgctttc  | gggagaaaaga | 240  |
| ctcaggccctt | gacttcagca  | atgaaagccg  | aatcgatatt  | ctcacctatc  | atccaatcag  | 300  |
| ctcgggcttg  | gcttcgaatt  | tgatctcatc  | aacggagcga  | atttattgac  | ctcggcaatg  | 360  |
| atattacgat  | cgtgtggagc  | tataatctgt  | gcccgtcttc  | ccaataagcc  | ttatagccgt  | 420  |
| tgtattcctt  | aggattgtgc  | gagctgtaat  | cattacaccg  | ctcttacatc  | ccagatgacg  | 480  |
| aatggcgtaa  | atatttccgg  | tgtgggacga  | agttcctcaa  | acagataaac  | cccgatgcct  | 540  |
| tggccgagaa  | tacagccgct  | gccgtatcgg  | caaaaaaacg  | actattgtcc  | gacagtcgta  | 600  |
| gccgataaacg | acactgatat  | ttgaagaacc  | ggcaaaccgc  | gcaagagata  | gttgagaggt  | 660  |
| ccttgagtag  | ctgcgcctac  | cgtatacggg  | tcatacgatt  | ggttccggct  | cccatgatgc  | 720  |
| cgcgaagtcc  | gcctgaccaa  | actccaaatc  | tcggtagaat  | gcatccacga  | gttcgggtcgt | 780  |
| atctcattgt  | ccagcatagc  | ctgaacggct  | tttcgagagg  | agtcgtcata  | ttcgttccga  | 840  |
| gccaaattcg  | agctttggca  | cgtacttgat  | ccaataattt  | gttgtttcca  | taagtatttt  | 900  |
| gtgtttctgc  | aactacgcaca | aagataaggt  | tccgcaccgt  | tttccgggta  | gaaataaaac  | 960  |
| agttaaatcga | acaaagtcga  | agaatgtcgg  | gcgtcttcaa  | cagagggaaa  | ggcggaaggt  | 1020 |
| gaaagcgatg  | tagtccacca  | gataatccaa  | acctgtcttc  | gctcagctct  | cgaaagccaa  | 1080 |
| agctttcata  | ttatcgaatg  | taatacgact  | aaagagctgt  | aaatatgcga  | ttgatggggg  | 1140 |
| ggaattcccc  | ttccatgagc  | aggagcattc  | ggtacgagcg  | accatcagca  | ggatcgaacc  | 1200 |
| aacgcggaat  | aacacttctt  | ccgaatgtaa  | atcgggtatc  | aaccccaatg  | gaacaagcaa  | 1260 |
| acgaaaaaga  | aaagcagatg  | aaaattagcc  | atcggccgct  | ccatttcttc  | caacttatct  | 1320 |
| atgaaaaagc  | cacaaaatca  | tacagattcg  | tatcggcttc  | cggcagtcgt  | aaatcagata  | 1380 |
| aagaaattct  | gccagaaaaga | gtgctatact  | attccttacc  | gatcggactg  | aatacggcca  | 1440 |
| tgcaaaactgc | atagtttggc  | ttctttgata  | agtgc aaatc | gcgggtgctgc | ttgtgttcgg  | 1500 |
| ccgtaatctc  | cagttcgtta  | gaggagaaat  | aagcaaaccg  | aagctaccgc  | cacttttccc  | 1560 |
| tcgcttggtg  | aacgtggtat  | cagataggac  | actctgccac  | tctctctact  | gaaaagaggg  | 1620 |
| ctatactata  | actatcgtta  | taagccgtat  | tgtggagaac  | tattgcctgc  | tgactataat  | 1680 |
| catgactaac  | cgaagatcga  | tacaaatata  | gtctatcagt  | cgtctgaaac  | aatcgttttc  | 1740 |
| cacatagact  | gtcgataaac  | ctgtgaaaat  | tcgctgataa  | aaacttggtt  | attctcttgt  | 1800 |
| ccgatccgaa  | agatcttcat  | ataaaattat  | tcttctgcaa  | agacaaaaaa  | gttagcagca  | 1860 |
| aatctcatca  | acttttgcca  | aggattactc  | acagctcggc  | acaaaaacaa  | aagaccgaat  | 1920 |
| tgaccgtaga  | aacaaaagtt  | ttccacattc  | cgatggaaac  | cattggctat  | cagcattcaa  | 1980 |
| cgaagtgtat  | aacctgttag  | taagctatcg  | tatctatttc  | aaatctgtta  | atccccctacc | 2040 |
| ctattcacccg | agtagttaaa  | gccttatcaa  | cagtttcaac  | cgacctcctt  | cttccctatat | 2100 |
| attttttttt  | tcaaaaagga  | atatataata  | aaaagaaaat  | cggttgccca  | cctgttaaag  | 2160 |
| gtgaagcaac  | cgatcgtgtc  | acagatatag  | aaaagtagct  | atgaatttat  | ttgatcagta  | 2220 |
| gccggattat  | cggttggtgg  | atcagaaatt  | gatcttgtag  | cgacgaaaat  | ccttctgggc  | 2280 |
| tgcataggac  | cgtatacgta  | agtgaagctc  | tacccggtcc  | cttgtccgtg  | tctttctgat  | 2340 |
| agctgttgaa  | tagttctgta  | ttccggcatt  | caattccaag  | gtcatagtgg  | aagcaaggtg  | 2400 |
| gagtcgtggc  | tcagcttgag  | gtctatatcg  | gcgaaggccg  | gagtcctgac  | agcttggcat  | 2460 |
| gaccttcggc  | caaacccttg  | aattgctgac  | cattcattta  | aagtcgaacg  | atccgtccgg  | 2520 |
| agctatgtgt  | tctgcgggaa  | tatcgccctca | taggcttcgt  | gtactacatc  | cattttgccc  | 2580 |
| gtgaatgtac  | cggagagttg  | atggcgaggt  | gctcggtagg  | acgtaccgta  | gcaacgaaat  | 2640 |
| agccgtcaga  | ttcggagtg   | gtacatagtc  | tttcacagag  | atctcggctt  | gtcccttggt  | 2700 |
| ttgtccgctt  | ccacagcggt  | atagatgctt  | ccgtagcggc  | ttcttgccat  | gtaccgcgga  | 2760 |
| ctgggaggtc  | gaacgatttg  | ttgtaggcga  | ttctccctcc  | agattcacac  | catatacctt  | 2820 |
| cgatactcca  | tccttgctgt  | tgagatggta  | cgaatgtatc  | attctttgce  | atcgctcgtg  | 2880 |
| gtttcgacct  | ttcggatggt  | ttgaactgat  | tgctgataaa  | gggtggagaag | gcttctccca  | 2940 |
| gatattgaat  | tgccattcgt  | cggctctgtg  | gtaataatcg  | aaagaagcat  | gatgcttcgt  | 3000 |
| gaacgttctt  | ctttcagatt  | gggggaaagg  | acacggctat  | aggagtacca  | ccggccaact  | 3060 |
| ctacgtgcag  | atcttcatcg  | aaatactagg  | agcgcggaat  | ccttcgctgt  | atgagagtcg  | 3120 |
| gaagctgaga  | ttcttatggg  | attgtatcgt  | acgttggtct  | taggactgaa  | aatgaagagc  | 3180 |
| ggatcatata  | gcgtttgcca  | tcctgattga  | ggagaacata  | gtcgatacgt  | gctcgataag  | 3240 |
| ggcacttaac  | ttctccgtct  | tatattccgag | ctggctcgtac | tgataaaaagt | agaggta     | 3297 |

## (2) INFORMATION FOR SEQ ID NO:425

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

```

gggattttca ttgaactctt ttgctgcaga gcagattctt agtgtcttcg gaaagggtcaa 60
acctccggta tatgggcacc gagcaaataa aaatttcaca agtttccatc agagaagtat 120
tcctttcctc gtcaaatcaa tgcttgctcg ataggcgaga aataaggaat gattgtcggc 180
tgtttcttgc tccctgatga tgcaggacgc gattgtcagc tgattcttgc ttctgcacg 240
atgcagacgc gattgtcaac tgattcttgc ttctgcacg atgcaggacg cgatgtcaac 300
tgattcttgc ttctgcacg atgcaggacg cgattgtcaa ctgttcttgc ttctgcacg 360
atgcaggacg cgattgtcaa ctgattcttg ctctgcacg atgcaggacg cgattgtcgg 420
ctgttcttgc ctctgcacg gtgcaggacg cgattgtcaa ctgattcttg ctctgcacg 480
gatgcaggac cgattgtcaa ctgattcttg ctctgcacg gatgcaggac gcgattgtcg 540
ctgattcttg ctctgcacg gatgcaggac gcgattgtca actgattctg ctctgcacg 600
gatgcaggac gcgattgtca gctgattctt gcttctcacc gatgcaggac gcgattgtca 660
gctgattctt gcttctcacc caatgcggac gcgattgtca gctgattctt gcttctcacc 720
caatgcaggc cgcgatgtca gctgattctt gcttctcacc cgatgcaggc cgcgatgtc 780
aactattctt gctcctgca cgatgcaggc cgcgatgtc agctgattct gctccatcaa 840
tgcgctaact atcagctgtt tgcaactatt ttataggact ttattgaagt cttttgccgc 900
agagctgatt cttaagtgtt ttccagatta ctgaggtttg cagagagatc gcatgaagct 960
ctcctttctt cgtcaaatca tgcttggtgc tgtcttgatc aatatgagag ggggagaggg 1020
ttattgtgca cagtctcttt aataataaat tgtatttctc gtttattcat tggtttagta 1080
gtatttttgc gctatcatga gattatcaga attacatag ggcatcagc agtaatcgta 1140
cgagtagaag gtcgcggggg accccg 1166

```

(2) INFORMATION FOR SEQ ID NO:426

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 730 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

```

cgcacaantt ttcagcttaa atgtttcttt cagatagatg atctcgccgt ggtcaagaga 60
tgatcaggcc ccaaactgga acccgaaagt gtatagatcg gacgttacgc ttagtgacgg 120
taggagtaag atcggcatag gtgcgggagc acccagttta gcctgaagcg tcatcgcccc 180

```



|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| cacccctgtg | aggtagcttc | atcgggatac | tctatcgaaa | gataaaactgt | ctgggtcggg | 240 |
| ttctggaacc | attggttata | gaaaactctc | gtacgatggg | ctccccaatc  | tgctgttcac | 300 |
| ttgcggcgca | ggctgtttga | tcgtcagggt | cggatagttt | accaatagga  | gtttgattcc | 360 |
| ttgctatcac | tatgatcgcc | gatagtcacc | gtaccttgtc | tttgaagaca  | aaaccggttt | 420 |
| cggcagcatt | aatggcattg | cccatgcggt | acagacagct | ctcctcttaa  | tcgtcagctt | 480 |
| aacgatgggt | caagctctac | cacattgttt | ccatccgccg | attttaccgt  | aaatacaggt | 540 |
| cgttcggatt | agaaacattg | gtttccgcca | ccgtcactgc | attgcccttg  | taacacttac | 600 |
| gacagccgtt | ccgaccacat | actcgacacc | gncggcagtt | tcacattaac  | tttgatacca | 660 |
| ttcgaatcct | nctggactac | agtnaatcaa | tgatcaatgg | ctcttctnca  | gaacatacag | 720 |
| caatggacna |            |            |            |             |            | 730 |

## (2) INFORMATION FOR SEQ ID NO:427

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

|            |             |             |            |             |            |      |
|------------|-------------|-------------|------------|-------------|------------|------|
| tagaggatcc | ccgcgactat  | gtttcttttcg | gtttggcggt | agaagatggc  | gtttgacaaa | 60   |
| cgccggattg | ctttttgccc  | accaatgtcc  | gttacctgca | gcagagtctt  | ctgtacacgc | 120  |
| tggaatgggt | tgcaaaggag  | atcagtgatg  | aagatgcgac | ggatgatgca  | gaatacagtg | 180  |
| gcaatctgat | atacttttaa  | aaagtgccac  | tgagtttatt | cgcagaaaata | cccgcaaagg | 240  |
| atggataaaa | cagctaattg  | aagagtggag  | aaaccgcact | atgccgaacg  | tgctattttg | 300  |
| agggagtggg | gaacgctctt  | atccatagga  | catatgattt | tcggggactg  | aagttcatgt | 360  |
| gaaaatgtat | gacgaccggt  | tagttatctc  | attcccgggg | gaatctatgg  | agggggagaa | 420  |
| ttggagccca | tgagcgacgg  | ccttatattt  | ctaaaaggcg | taatccgata  | ttagctgaca | 480  |
| ttttcagccg | ctaagggtata | tggagcgtcg  | gggaagcggg | ataaagaaaa  | tctttgaaga | 540  |
| acgaagaatc | tttatggcta  | tacggaagaa  | aaaaagccgt | ttttcctttg  | aataaacaga | 600  |
| atgacttctt | cctgacgatt  | ccgaacgtta  | attatcgtct | gagtctgtta  | ccacacatga | 660  |
| caccatacat | gacaccatac  | atgacacata  | catgacacca | tacatgataa  | aatcgccctg | 720  |
| ttactttcct | tctgtaaaacg | cctcgcagca  | gagaagagat | gatggagttt  | gtgggtttta | 780  |
| gaaacgcgat | catttttcaga | agaaatacct  | ccgtccttta | ttagaacagg  | aaagatcgaa | 840  |
| atgaccattc | ctgaaaagcc  | ccaaagtaag  | aaccagaagt | atgaacgaag  | gaggtagtca | 900  |
| aataacatat | ccattctcta  | atataagcgt  | taacaaattg | agtttttata  | agaaatatct | 960  |
| tcctgtgggt | atgaaagagg  | ggtgactcat  | tgtctggatt | ctttcgtg    |            | 1008 |

## (2) INFORMATION FOR SEQ ID NO:428

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...768

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

```

atccccggcc gtacacggct ctaatccggt acccccttat gcctatgtac ctcatatctg 60
tggacacaga aagcattcaa agcggatgtg atgatgcatt cggcacgcat ggcagccttg 120
agttttatccc gggcaagcag atcgcacctc ttctgaggat tggacagacc gcctcgtaa 180
tgacctgcct catatcacta ctataccatc gccaatatcg gtgaaggaaat gatcgccaag 240
cgcagagcta tgccgggtacg gtatcttatac tggctcctcc ttctatcgaa acgccatgag 300
gggtcaagta agcgagttcc tcagcttgac ggataaatac ctgagcagga caacgatgat 360
aaagccctgt ctctccgcat caaggctttg gcgtgaagaa cggctaccat cgggatctga 420
aactcgactc catccttgac aaccttatac acgtgagcaa atcatctctc ttcccgactt 480
tgccgaagaa ttgctgtcag caagatcccg ggtggtatgt acaagacagg cgttatgttc 540
cggaagaaaa gatccgctct tccgtgaagc atattgctac agatcctatg cttatgcttt 600
ggccgctatc gaccgtcagc gtggacgcta cacacagagc agcaagatag cgaacgattc 660
tttaccaccc actatcgctg tcttgcaag cactggtaga gcgttacctt ggacgcnagg 720
cggtagatgt gaatgagcat tgactacgct ggggtgtactg tccagcga 768

```

## (2) INFORMATION FOR SEQ ID NO:429

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3453 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...3453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

```

tcaaaaaaaca aattcattgg tgtttttctta acgtcgaact gacgttctan ggaataaccgc 60
tatgtctcctt gtggtatagt tagtcgtcag ttcgatccga cccaacttcc ctattttgcgc 120
ttagatcgaa ctggcatctc tgatcttatg cggtaaaatc tgccacttcg ataaattacg 180
aaccgaaaaa gctcggttgt ggtctgtaaa tccagagaaa acggcgcgag aattttttcg 240
ctttgcgcgt aaaattttta cctcccgaac caaaacgtaa aaaatcacac gccatctttc 300
atggctgtaa agccggcaat ttttgagacc taaaccatcg cgggagaggg agtagcgatg 360
tgtactttct cggacttccg agtacagatt cagcactgta ttgagcaggt tgccccgggtg 420
tctcaggtat tggttgtctt aggcgaaaac gccgattgcg tggcattaag tcaccggctc 480
ttagcagtcg cataacctat accgaccgat cgaaacctct ctccgaagca ctgcttactt 540
attaatgaat aactctctaa agccggcttt cggtaggctt tctttgcact gaggtactga 600
taataatgga ctatactcgt atttaatgtc agttcgacta agcgcaaata ggggagttgg 660
gtctggatcg aactgacgtt atagttaggc aataaggttt gcgacatcct cgtttagttt 720
aggaacagca atatggcatt atgcttacct ttgctcatca aggagccgca accgcatggc 780
tgtagcttcg gatgcatttc caataataca catacgacaa acaaatgaac ttttagaaga 840
actgcgttgg cgggttatga tccacgatat tatgcccggt acgaggaaca cttgaacaag 900
ggtatgacct cggcatacgt aggcattgac ccacggctga ttcgttgcac atcggccacc 960
tcgtgggtgt gatgatgtg gccatttcca gcgtgccggc catcggccca tcgctcttat 1020
aggtggtgca cggaatgat aggggatcct tcgatgaagt cggccgaacg agttctctgg 1080
acgaagccac tcttcggcat aatcaggact gcacaaagca gcaactgcca agttcctcga 1140
tttcgatagc gatgcacca atgccgcaaa gctcgtaaca attacgattg gatgaaggac 1200
tattctttcc tcggtttcat tcgggcacat gcaagcatat taccgtcaat tatatgatgg 1260

```

|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| caaaggattc | tgtgagaaac | gccttagtgc  | cgagagcagc  | accggtctgt | cctttacgga  | 1320 |
| atttcctacc | agcttctgca | aggctacgac  | tatctctatc  | tatatcgga  | tggggctgcc  | 1380 |
| gcttgacgat | ggcggttcg  | gatcagtg    | gcaacattac  | cccggaaacg | agcttatcag  | 1440 |
| acgcaaggac | ggaggagagg | cctttgccct  | acttgctcgc  | ttattaccaa | agccgacggt  | 1500 |
| ggcaagtttg | gaaaaacggg | agcggcaaca  | tctggctcga  | tcctgccaga | acttctcctt  | 1560 |
| atgccttcac | cagttctggc | tcaatgtgag  | cgatgccgat  | gccgaaaaag | tatatcagat  | 1620 |
| cttcacggga | ctgaatcagg | acgagatagc  | agaactggca  | agtcgtaggc | cgaggctccg  | 1680 |
| catctacgcc | ccttgacaga | gagattggca  | gaagaatcac  | cgatcatggt | cacagtcgtg  | 1740 |
| aagcctacga | tgctgctgtc | gaagcagcga  | gatcctcttt  | ggcaagagta | cgacagagca  | 1800 |
| attgcgcaag | cttacgaggc | cactctcttc  | gatgtctttg  | ccggtgtgcc | gcagtatcat  | 1860 |
| gtgagcgag  | caggatagcc | acaggaattt  | cattggctga  | tttgctggcc | gtgctaccga  | 1920 |
| tatattcccg | tccaaagggt | aattgcgcaa  | gacggtgaaa  | ccggcggagt | gagcctgaac  | 1980 |
| aaagagaaa  | tagccgatgc | ggaacaaacg  | taggagagga  | cgacctcttg | tccgaccgct  | 2040 |
| atctgctggc | gcaaaaagca | agaaaagcta  | ttacctgata  | atcgtggagt | gaacacacgg  | 2100 |
| atagcgcttc | atgaaactat | ccatcggtat  | tgtcaattat  | cgtgttccgt | atttctggaa  | 2160 |
| cagtgccttc | tctccgtgcg | aaagtctgcc  | caagggattg  | atacgaagtg | tgggtcgtag  | 2220 |
| acaataattc | gggggatggt | tccgtagaat  | atctcaaagt  | cgtttccccc | aagttcattt  | 2280 |
| tgtagctaac | gaggagaatg | tagtttctct  | cgcgccaaaca | atcaggctat | ccgtctcagt  | 2340 |
| aaggggcaat | actactcttg | ctcaatcccg  | atacccttat  | cggagagagt | acgtgcgta   | 2400 |
| cgtggtggac | tttatggatt | cgaagcctaa  | tgcaggcgga  | ctgggcgtaa | aatgctcaat  | 2460 |
| ggatcatggc | gctttttgcc | ggagagtaag  | cgagggtttc  | ttctccatgg | gtgtctttct  | 2520 |
| gtaagtgtgc | cgggcttaac | cggctcttcc  | tcatctgtct  | cgtttcaatc | gctatcacct  | 2580 |
| cagttatctc | agccgtgcga | ggtgcacaaa  | gtagagggtac | tgtccggtgc | ttttatgctg  | 2640 |
| atgcgtggga | ggcattggat | aaggctgggt  | tgtcgcagca  | gcgttttttt | atgtagggtga | 2700 |
| ggatatcgac | ctctcttata | gcttgatatt  | gggcggatac  | nacactacta | ctatccgact  | 2760 |
| cctattcttc | attacaaaag | agaaagtctg  | tctgtctccga | tgttaaatat | cttcgttcgt  | 2820 |
| tctatggggc | gatgggtttg | ttttcgataa  | atactataga  | aacaggatga | atccactgct  | 2880 |
| tcatggactg | acaatgtcgt | catcaaagca  | cgtacagctc  | ttgccttgat | gcttcgcagt  | 2940 |
| tgaggaaggt | tccggcggca | gagaaacctg  | ccaaaatatt  | ctattggcac | cttctgaggg  | 3000 |
| agaggctgct | atatctgcct | atcacgaccg  | cagccatacc  | tgatcaatac | cgatgagggtg | 3060 |
| acttgatgat | gcctgcttct | gactatgaga  | aactggctga  | taggaagcat | actttccatc  | 3120 |
| tgacgaatga | caccacaaaa | gggtgatctc  | accttgatac  | atcttccctt | agaaaggaaa  | 3180 |
| tctccaactg | ttttttttga | aagaaagagg  | ccgtgtgtga  | tcgtattcgg | atcgcatggc  | 3240 |
| cgtttttgtt | tctcttccct | acggcataga  | gtatactttt  | cgttcacgat | aaattcaact  | 3300 |
| tcctattgaa | ttgcgaggca | atctgtatca  | agcaaaaaga  | gacctttgca | aaatcaagaa  | 3360 |
| gtatcttttc | ggtatcggtt | taccctgtaga | gcgtgtcgca  | caagtcatag | aggagctgag  | 3420 |
| gtattcatac | tataacgaca | cagaaaaaca  | gtc         |            |             | 3453 |

## (2) INFORMATION FOR SEQ ID NO:430

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| ggatccccgg  | gattggttct | tcctcttctt | ccggtggaga  | cacggcgccct | ccgagacact | 60  |
| gaggttgggc  | aaagagaaa  | ccttggtatc | gcttttggat  | agaagcagtc  | gatgccgagg | 120 |
| ccaccggatt  | ggaaagggga | ttcgacacga | aagaggagct  | tccgatgagg  | acagtctcgt | 180 |
| tgccgggtatc | attggcccat | tgacccaaag | ctgccaaaccg | ctgccaaactg | cgtatgtgac | 240 |
| cgtaagctcg  | tgaatggctt | tgttcccagc | gggtatgcgc  | taccatcgat  | gagatatcgg | 300 |
| atcgagacat  | gctgctctcg | cctgaaggga | gaacgcggag  | tcgacatcca  | gcagatccac | 360 |

```

ccctttcgag ccgctacccc agcgaagagc taatagtcga actcggagtc gctgatctct 420
ccataacagt acaggtagca aagagatagt tgttgatggt cgggcggaag tccagcttga 480
catcgccctt catgtttag tcttgaagta cgggacggtg atagctatgc gcgattcgtc 540
aagtcgtcgg gatattccac gtagagcttg agttgtttt tgatgatgca aagtctgcat 600
ctgt 604

```

## (2) INFORMATION FOR SEQ ID NO:431

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```

attctgaaca agaaagggtac atttgccggc tttgaagaca catacaagcc atgttcatga 60
actacgagcc agggcggttac acaccggtag aggaaaaaaaa aatggtcgta tgatcgtcac 120
cgtagccaaa aagtatgagg gagatataaa gatttcgttg attggaaaaa ccaacgcggg 180
ctccgtaccg aggtgaagtg gcagaagata ttgcttctcc cgttacagct aatgctattc 240
agcaatcggt aagcaagaat acgagaaaga aggtaatgat ttgacctatg ttctttgatt 300
ggcgatcaca aagatattcc tgcncnaatt actccgggga tcgatccgac caggatatag 360
gacaaatant angtaatgac cactacaacg aatcttcacg ggtcgtttct catgtnagag 420
ctnagaggat ctganaacnc aatcgatcgg actattcact atgagcgcaa ta 472

```

## (2) INFORMATION FOR SEQ ID NO:432

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

```

ttttggagcg tgacgtgtac ttgaaaagca ttgtgccgag taacgctaca cttcgggtcga 60
ggagttgcat agagtagcaa tagtggggag agagacgcat ttccacgcat tcgtttcttc 120
ttgcgttaaa tgtccgtaaa tgtcagaaga gagtgtgttg atgggagcag aaacgggtgt 180
ttccggtctc ctgcatgctg caacgagcag gaaacagcct acaatcattc cttaaatttc 240
tgcgttgctg ccgccacggc cgaatgggtg gttcagtgat cgagatagat gaaaacagg 300

```

```

ttcttacggc caatcggacg gtggatgaaa agggattcat gcaaaagcca atcggcccggt 360
cccctatcgg catgaaaaaa gacccttgca caaaagtaca ggggtctcgtc aatatatatt 420
cggaatttc cgtttcgggt ctaatggatt gg 452

```

## (2) INFORMATION FOR SEQ ID NO:433

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 758 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...758

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

```

ctntagagga tccccgggaa aaagattcgc tttaagcggg aaatgctttc gacttttcgc 60
attttgtaaa caaattcttc ttcttgccaa cgactgatca caaggaggac ttaaggggtt 120
ctcctcaacg ggacgtttta tttcctcaa acacggatag atagtttcct gttcgatacc 180
gagttttatct gtctggtaag agaaaaaaag tgtgcatagc agtcgtcagc ggctccattc 240
gtcctacatc tctctgtcgg taatgaaagc caagactatc cttcgtgaag tctaaaaatc 300
cccaaattga tcaaagcaag atgggttctct tgagtttcga tatgaggagt tcgatgtacc 360
ccttgagcag ggatataagg acttcccatc ggagaacaat tgcgcatcag tcgtcaaggg 420
acagaagcca tctccatat atgagaaaaa aaggcggttcg gtccaccttc ttcagtaccg 480
ttactttctg gaatcattgc cggaggatct gcgaaagggc atttacacgg atggacacga 540
ttggcctctc atgggtgtgt tcaactctct ttctccaaag agcaccttcc gaatctcgtc 600
agaagctcgc ttctctgtgg gatggtaccg atgtctgggt ttccggatgc cacgtatgat 660
gcccgttggc gatgcgaaa tagccgagcc ggttacttgt acaattcttc gctcaatccg 720
acttgatatcc ccggtgctac aatcatctct cggctcgg 758

```

## (2) INFORMATION FOR SEQ ID NO:434

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 460 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...460

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

```

taaccggccg agcgaacccc tcgtgcccgg tggtcgcgat cgagctgaac gatgtatagg 60
tcatattgga tcttgtggcc gaacagtgga tgactataat ttgatgggat tcattgtttt 120

```

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| ggatgttgat | agatgaaaaa | attaaacccat | tatagaaaaga | caaaggccgg | agacaaaagc | 180 |
| aaatttcctt | gtctccgcct | tccgattaga  | ttcccgtccc  | tgctcgaata | caggaggaat | 240 |
| acggacagaa | ttagagaccg | ccgcctccgc  | tgcttgctc   | accgccgcc  | tccgagaatc | 300 |
| aggaacagag | ggagtaccac | cttgctgttc  | tccgggacga  | agctattgat | ccctttcaga | 360 |
| cgaatttgcc | gacaggcgcg | gcgaatatcc  | ccccgggcag  | aaagagcacc | cgtgctcggc | 420 |
| ggatattttc | cacggtaaat | ctctccttct  | ttggcggcct  |            |            | 460 |

## (2) INFORMATION FOR SEQ ID NO:435

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| gggattgagg | acttcatatt | ggcctttaag | agggaaaaga | tatgttgccg  | cggtaacgctc | 60  |
| gttgacgctc | tcaaaggggc | actcattaaa | ggggagtaat | ttccaccggt  | ggaaaaccgg  | 120 |
| tgtgtaccaa | atagtcgcct | gacacagaat | aaaaagaatg | aacaaaagtg  | cctgcttatt  | 180 |
| gtgcaaaggt | cccgaaaata | gaagaaagag | gctaaggata | cagtataaag  | atacagtata  | 240 |
| aatttcaaat | gaaataaccc | tggggttaca | tcagatttga | gtagggagat  | attgtatggt  | 300 |
| tagtcgggga | gaacaagctt | tcgtttcgct | gtgatcatat | ctattttaatg | cgatagatag  | 360 |
| cggtatgtgg | catgccgctt | tcaacggcct | tacgaacaaa | tccattttct  | ctggcgtgta  | 420 |
| cttctcgcat | atcaatcgta | agcatgcacg | cactcctcat | gatctgctac  | acgaatgact  | 480 |
| tgccccctga | tattagcac  |            |            |             |             | 499 |

## (2) INFORMATION FOR SEQ ID NO:436

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tcatttcctt  | ttcggttgga | ggacatccaa | gaggcatatc | gacattcatg | ccatgttcaa | 60  |
| gatcnatcgt  | ttccattggc | acctgacaga | ggatcaggat | ggcgtatcga | aatcaagaaa | 120 |
| taccacacgac | tgacgaagtg | gggtctaaag | gacggaaggg | gacggtacgc | agtactccgg | 180 |

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| tttctacacg  | caggagaagt | acgggatatt | gtacaatacg  | catcggatcg | tttcattacg  | 240  |
| gtgatcccg   | gatcgaaatg | cccggacatg | ccatggctgc  | cctcgctgct | tatcgagtt   | 300  |
| ggcttgcttc  | ccacgcgaat | tcaagccncg | gattatctgg  | ggatggagca | ggatgtttat  | 360  |
| tgtgccggta  | aggacagcgt | cttccgtttt | attctgatgt  | tatcgacgag | gtagcaccct  | 420  |
| ttttccccgg  | cacatacttc | ctatcggagg | ggacgaatgc  | cctaaagatc | gatggaaggc  | 480  |
| ttgttcgctt  | gtcagaagcg | tatgcgtgac | aatgggttga  | aagacgaaca | cgagctgcaa  | 540  |
| gttatttcat  | caaacaagct | gaaaaggctt | tacaaaagca  | cggcaagaac | tgatcggttg  | 600  |
| ggatgaaatc  | ctcgaaggcg | ggcttgacc  | ttctgccccg  | ttatgagctg | gcgtggagag  | 660  |
| gatggtggca  | tgcgagcggc | taatataatc | acgatgtgat  | catgactccg | ggtagcggag  | 720  |
| gtctctactt  | ggatcttatc | aggagatcc  | gaccgtcgag  | cctgttgcca | tcggagggtta | 780  |
| tgctcatttg  | agcaagtgt  | tgcttacaat | cctttgcccga | aagaattgcc | ggcgataaagc | 840  |
| atcgctacgt  | gctcggagca | caggccaatc | tgtgggcaga  | atcctctata | cttccgaacg  | 900  |
| atacgactat  | caggcctatc | caaggctact | gctgtggcag  | agcttacctg | gacaccgttg  | 960  |
| gccaaagaaag | attttgccga | ttctgtcgcc | gtttggataa  | tgcttgcgtt | cgtctggaca  | 1020 |
| tgcattggtac | aattaccaca | ttccgctgcc | cgaacaaccg  | ggtggctctt | ccgactttta  | 1080 |
| gccttttacgg | acaaggctaa | gctgaccttc | acgacatcgc  | gtccgataaa | atgggtctata | 1140 |
| cgctggacga  | aaccgaaccg | accctcacat | cgactcttac  | acggtccctc | ttgaattttgc | 1200 |
| acaaacgggc  | cttctgaaga | ttcgtccgtc | acggccgggtg | ggaagatgag | tcccgtacgc  | 1260 |
| gcgattcgtg  | tggaaaacaa | cccttcaata | tgtcaatgga  | agtaccggca | ccgaaaccgg  | 1320 |
| gacgaccatt  | cgtacggctt | acggtgactt | atatgatgtg  | cctgatctgc | agaggtagcc  | 1380 |
| tcatgggaag  | tagggaccgt | tagctctttg | gaggaaatca  | tcacgggaaa | gagaagataa  | 1440 |
| cttctcctga  | agtactggag | cgcagagttg | agaggctacc  | ggttatgtgc | ttattccgga  | 1500 |
| ggatggggta  | tatgagttcc | tcggaaaaca | aacgaagttt  | tggattgata | atgggaaagc  | 1560 |
| ttgatcgaaa  | tgtgggcgaa | gttaagaaat | tctcccgctc  | gcaatagcag | tcgttccctt  | 1620 |
| cag         |            |            |             |            |             | 1623 |

## (2) INFORMATION FOR SEQ ID NO:437

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...542

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| ccgacaatcg  | taccttcaag | gccaaactga | tcggtagcga  | tgccacgacg | acatagcctt | 60  |
| gctgaaagta  | gatgccaagg | ggctgcccgc | aattccttcg  | gcgactctga | caagcttcgt | 120 |
| gtgggagagt  | gggtattggc | cgtaggcatc | cttttaatct  | tacttccacg | gtaacggccg | 180 |
| gcacgcgtcag | cgcaaaggtc | gctccactca | tcagggtggcc | agaggcgggt | cgctccagat | 240 |
| agaatttttta | ttcagacgga | tgctgcccgc | aattcaggca  | acagcggcgg | tgctgggtga | 300 |
| atgatcgtgg  | cgaactgatc | ggtatcaata | cgatgatcta  | cagcaaaccg | gcaactatgc | 360 |
| cggctactca  | tttgccgnac | ctatttccat | agggcgaaag  | tggtagccga | catcaagcag | 420 |
| tacggaaccg  | tacagcgcgc | ctgctgggca | ttgccggcgg  | agatatatcg | gacgaagcac | 480 |
| gtcaaagaat  | cgatctgaag | tgcgcaaggg | tgctctcgtg  | gcagactttg | ccgaagtcac | 540 |
| gc          |            |            |             |            |            | 542 |

## (2) INFORMATION FOR SEQ ID NO:438

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| ggatgatacg  | atcgccggcc | gcccattcct  | ttatcccggc | cagtacaata | tcaagagaaa | 60  |
| aattttcagt  | cttttcattg | ctctaaattc  | tttattatat | tagttgtgta | taacaaagaa | 120 |
| cctatatgaa  | tctgaaaaga | atctgaatga  | caaaagattt | tgaaaaaatt | ttttccgacc | 180 |
| ggctgatcga  | gcacttccta | tgcttccttg  | ccgatggaaa | aagtgtgttt | ccattctctg | 240 |
| aagcgttaagt | cagtcggagt | ccgtacagct  | ggcatataga | gcgtgcaatg | ggaaccccaa | 300 |
| gccggaagaa  | tgagcctgtt | tcatatcgtg  | atagaaacgt | tcgatatcaa | ggtctcgtcc | 360 |
| aaagcgttct  | tcacccccgt | attcgcctatg | ctcaatgcat | agaggtaaga | tcgatatgga | 420 |
| tctctccatc  | tctttcaaga | atgtgcaaga  | gtatgccgtt | cttaagcagg | ttgcttagca | 480 |
| agactttggc  | aaagtcgggt | tcattgatag  | aaccattggt | tcacttctgc | tccatacaag | 540 |
| cgaatacgtc  | gattggcgaa | aatcgcttca  | tactcctccg | ccaaattagc | aatagctcat | 600 |
| tcacatctat  | gctttcctcc | tcagggaatt  | gatggtttcg | attttgctat | agaggaggag | 660 |
| ggttttattg  | agctgtacaa | tatggtgatg  | gactgtatag | ccttataaat | ctgttcgagc | 720 |
| tgctgtcatt  | caaagaggga | tcttgacagta | gcatttccag | tttattgcgg | cttatggcca | 780 |
| gagggg      |            |             |            |            |            | 786 |

(2) INFORMATION FOR SEQ ID NO:439

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| cggtcgattg | cgtacttcgc  | cgaattcgtc | ttggccggtc | atgatcggaa | aatggcttgg | 60  |
| atcttaaatg | ccacatcgct  | attggtcggg | gtgaagtaca | ttcttccttt | acgtagtagg | 120 |
| ctttgacttc | tgccgagggg  | atgtcgcata | tgccaccttg | aagagctccg | cattcttggt | 180 |
| cgtactcggg | tggtaaaagat | gccaaacctg | tccagaaact | cttggaactt | gatcttgtag | 240 |
| tggtcgtgaa | ggcttcgaat  | ccatccagat | attcgtacac | gtcgaggctg | ttggattgat | 300 |
| gagtcgcaat | atcgtgctga  | agagattcct | gcgatcacca | atcgccgggg | aggataatag | 360 |
| agtaccgcat | tggtactctc  | catcagggtc | accgtcggta | cacgactcgc | ctccaggggg | 420 |
| cgttgtcggt | cttctgtgtc  | aacgtctgtt | gaattcctga | gcacgattgg | atagagtagt | 480 |
| cgtttgttcc | cctcgggtatt | gcgcgggtgc | cgaccacctt | gcggagagcg | gttgttcggt | 540 |
| tttctgcgc  | aacggacgag  | atactgacgg | tcgctgcaag | gatcgctcta | tgactgcttt | 600 |
| gaatactttc | ataaacacta  | ttagttcaca | attacttaat | ggccggaatc | ttacgttcga | 660 |
| taccatccgg | accgcgtgca  | attactctgt | tacgtagaaa | cgcttgccct | tgccagatt  | 720 |



|            |             |             |            |             |            |      |
|------------|-------------|-------------|------------|-------------|------------|------|
| ctgtatttgt | cgttttgtct  | ctcagagaat  | gaagctccgt | cggaaacttc  | gggaatcgag | 780  |
| ttgccatcga | atcatagaat  | acgagttgga  | acttcaccac | tgtgtagttt  | actccagcaa | 840  |
| atcatcgtca | agagcggctt  | taatgccgcc  | tgctgccagg | attcacgctt  | acccaaacgg | 900  |
| ccacccttga | agcgtttcgt  | gttccccctg  | aatccttata | ttcgatatag  | ggaagaggat | 960  |
| cggggagagc | tctgacacgt  | aggtagtctt  | tgccatttgg | atggtagcgg  | ctcctgattg | 1020 |
| agctgtgacg | aaataatggc  | ttcgctgcct  | actttcgtcg | gccgtgctat  | ccagagatgc | 1080 |
| cacggcgagt | gagcgtaacca | ttgttgatcg  | ttgcagaaac | gtttttgcgag | ccacaccctg | 1140 |
| tacggcgata | ttgatcggtt  | tgtctatacc  | ggcataagta | cgttcatcat  | cgtcggagca | 1200 |
| acggaggcca | ttggttccgt  | aacgagtatt  | cgctttcaaa | gtcacggcga  | atcttaaccc | 1260 |
| catcgttacc | catctttcga  | tatatccttt  | gaccggatat | gtgcccgggtg | cacctgccgt | 1320 |
| agcgtaaata | ggcccatggt  | ctcgggagaa  | aggagcttac | cgtttataaa  | tagtccggtc | 1380 |
| tttgcggtgt | atctacactg  | gagaggacga  | tattggcctt | aatgtatcgc  | ccgacatgac | 1440 |
| gatttggtct | tgtggaatca  | cttgtgccgt  | atactgttca | cacgataatc  | ccccacatcc | 1500 |
| acgctcttta | ccagatcgga  | agtacttcgc  | cctgagcata | acgcacatcg  | ctttggagct | 1560 |
| tggtcagggt | gtaatggctg  | ctacagtagg  | catattctcg | aacaaagaac  | tttcccagat | 1620 |
| ttgccttttg | tgccggattc  | tgtgttaagg  | gcttgttcta | tgagttcaac  | ttcgccctgt | 1680 |
| cggtcatgag | tgtagcgacc  | agctcgcgga  | acttgccacc | tccttgcgaa  | gtgtgctgcc | 1740 |
| tttaccgttg | atcggattca  | gcatattacg  | gaagaagcat | cgagattgtc  | ctttcgtctg | 1800 |
| atatcattga | ctttgcatct  | ttcccatccg  | actcacgggc | aatggccaac  | ttcagatcat | 1860 |
| cttaaaggta | cagagcgaat  | ctgcctcttt  | ctgtaagaca | aggctacgct  | ctaccatact | 1920 |
| ttcacctttt | cgggattggt  | gcgataagcc  | gtattcagct | ggacagcacc  | agattggtgc | 1980 |
| gcttatcgga | gccgtcgatg  | gaagaggcta  | gctcttatcc | actttgtcga  | aaccatccag | 2040 |
| tacctcactc | gatacgtaa   | agccatcatg  | gcgatgaaca | cgaggtaacat | caggttgatc | 2100 |
| atcttttctc | attggcattc  | ccattagaac  | ctactgccat | ggcttataag  | ggtgagtgcc | 2160 |
| ggatgatgaa | ggattagaag  | caccaaattt  | ccggggcata | ccgggagacc  | tacattcgtt | 2220 |
| gtcaaggctt | ggagcaagcg  | agcatacacc  | tcgtgagttg | tgtagttgg   | cgtgccatac | 2280 |
| gctcgttttc | gttgcggaat  | gaaaactgtc  | gatgacacta | ttgtcataca  | tatctcggat | 2340 |
| atgagccaat | cccggttgat  | gcgatcgatg  | gtgtcgatct | gggagctgat  | gcccttgagc | 2400 |
| ttatttcgta | tatggtattc  | aggccggaga  | tattgcgact | gaggctttcc  | tctgctggat | 2460 |
| atacgattgc | gaattgagac  | gcaggccctc  | ctgatccgct | gcatctgctc  | gtagctctcc | 2520 |
| gtcatggcgg | ctgcagtcgg  | gccgatacgg  | caagctgttc | gcctgcttca  | gccagtttgt | 2580 |
| ctatgccttc | gctcagggtt  | ggatctgctc  | ttccggcagt | attccgggtca | gttgggactg | 2640 |
| gaaaggggtg | caggcttggtg | ctgttcttgc  | ggttgcgtag | ccaaagaggc  | agaggaaggc | 2700 |
| gcacagaaga | tggtctttcc  | gcgtatgcag  | ctgcttcttt | ggcctttcac  | gaagatactc | 2760 |
| ccgacgctgc | tccatctccc  | gacggctccat | cggttcttcg | agtccagttc  | ggggaagacc | 2820 |
| tcttcccagt | gatattccat  | tgggggtttt  | caaatccgga | gataaaaaac  | accagaatt  | 2880 |
| ctgtgatcat | ccacgaaaag  | catctcattg  | gccatcggca | aatggagcaa  | cttgaagaga | 2940 |
| cgccaaaatc | accact      |             |            |             |            | 2956 |

## (2) INFORMATION FOR SEQ ID NO:440

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...432

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cagcaaatat | aacacttgga | gtgtaggaac | tcaatctcac | cctgagcatt | cgtagataaa | 60  |
| tacgtatttg | tattttgcta | gactcgcagt | gcttgagcat | agtttgatga | cttgcatata | 120 |
| ctctcatgg  | agctctagat | tgtgtattca | gtacgaataa | aatcgtgagg | aaaagatgcg | 180 |
| tcttgatact | tggattttg  | agtaaagagg | agtatacata | cggatcctta | cctatgagga | 240 |
| tctgcacata | gttccctctc | tctctagaaa | ggcagatagt | tcctttatca | caaggccata | 300 |

```

cctgggacat cccaatatcc cgtggctatt cgaactcgat tgaccaatcc aatctaaaac 360
attgtttcag acaggaactc atagaaagtt cggcgaagaa ttatcaatta agggattgcg 420
taatagcata gt 432

```

## (2) INFORMATION FOR SEQ ID NO:441

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...698

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

```

gcagagtgat ttcctcagaa aagcgaatcg gatcctggat gaaacggcaa gggaaaacta 60
cagttttcgg cattattccc tgagatycgc caccgattat ccctccacag aatccgaaga 120
gcaaagaccg gagggaaaag gctgaaagac tttggagaaa tacaagcagg agataaaggg 180
gaggaaagac aagctcatag ccaactgctg tcggcattcg atatgaatca gagacaactg 240
ccctccgtct tctggatgaa tggatgaata tcaggcctgc aagccattca gtcagcttcg 300
tacttatgtc aagcagctca atgaagactg ccgactacgc ctgggaagtt tcggaaggat 360
ggcgatggga aagctcgtgc catacctctc gtggtgaaat ggctacctc ctctctcagg 420
acatcgtccg catgatcata acgaagagac gaagaagctg atcacctccg cttactacaa 480
tgagatgcaa gctctctggc acaatatgcc ggagaagaga atcgccgcca attcagggca 540
tcgtggcaga actgcacctt cttgaccctt cttccggaca tccgttcctt ccgcgaccat 600
ggagacagct catcggtata cggaagactt ctacaaagct atctcgagaa gaaacgggaa 660
tggttggtcaa aaactttcta tcggccggtg ccgagctg 698

```

## (2) INFORMATION FOR SEQ ID NO:442

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...826

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

```

ccctggacag gtaccacaca tgcgaggttc atagaagcct tgggacgttg cgcaagaaag 60
gggctacgag ccttatactc gatctgcgag aaaatcgggc ggtttgctgg agccggctat 120
tgccatggcc aatgaatttt tgggtaaaat ctccccattc ttcagatcga aggcaaagcg 180

```

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| tatccgcgtg | aggagattcg  | tccgatgggc | aaaaggtatc  | ttgcagcaaa  | ttcctctggt  | 240 |
| agtgcggtgg | atgagttctc  | ggcaagcagc | agcgagggtat | ttaccggtgc  | catgaagacc  | 300 |
| atgaccgcgc | tcaaatacatc | ggtcgcccga | cgttccggcaa | gggctggtgc  | aactgccggt  | 360 |
| cgatttggca | gatggttctg  | ccatccgcct | gacgtagcac  | gctattatac  | gccatcgga   | 420 |
| cgctccattc | agaagccgta  | tcttccggcg | tagatgaaaa  | ttactatcag  | gatctgagga  | 480 |
| atcgcttcaa | cacggagagc  | tatactcggc | cgacagcata  | ccttccactgg | gaggaaagaa  | 540 |
| ttcaagacag | ccggtggccg  | cgaagtctat | ggtggcgggtg | gcatacatag  | gatattttta  | 600 |
| tcccactgga | tacagccggt  | cttaattcct | atatgataaa  | gtggaggatt  | cggatttggat | 660 |
| cctcgcctat | gctttcctgt  | acagcgtgcg | aacagggttt  | ccttgagtcg  | ttttaagaca  | 720 |
| gtcgaggagt | tgggacttat  | ctggatcgta | cttatctgat  | tttcgacttt  | gcttcttttg  | 780 |
| ccaggtagcg | gatccccgatg | ccgtactttt | tttaatcaac  | gaagct      |             | 826 |

## (2) INFORMATION FOR SEQ ID NO:443

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| ccaggattgg  | caaaggcatt  | gcgccaagg  | atgaagcgct | ggggatcatt  | gataatcaca | 60  |
| tatcccgtag  | ccccgggctg  | atcgcgcaaa | tatacatcgc | aagagcaacg  | acttcgcgga | 120 |
| caattacatc  | agaaggaaga  | ccgaccacac | accatgtcct | tcatatgcca  | aatcgtagac | 180 |
| atgcctacgc  | atttctccgg  | catatcggcc | gtgtattcat | tatcgacacg  | cttatcagga | 240 |
| ttgggttcacg | taaataatct  | tgccactcca | tcctgcgaca | atgctcctgg  | gtcaatcaaa | 300 |
| tacatcttca  | taacaacgga  | atgaagcagc | tatatccttg | gcccatacaca | aatctgcggt | 360 |
| aagaagctgt  | agttctcagg  | aggcaaagtg | ccgattcatc | gaaaaagcga  | gcacgcaagg | 420 |
| cctcgaagcg  | tgcggtctct  | ttcgtccaac | acgcatcttg | atgctccgtc  | cgcctttata | 480 |
| gcttacatag  | tggagctata  | ctcaggcgta | tagtcaaatt | cgccccaaagg | ataaccggga | 540 |
| cctgatcttg  | aagaaagagt  | gttactgcct | cgatatgctt | gcatgttcaa  | gccatttcgt | 600 |
| tctaaaaatcg | agacaagaac  | aataattccg | ttcgtcggaa | caccacggaa  | tgcaactcgg | 660 |
| tatcggttgc  | ggccggtttgc | gaccaataat | cgccccatat | ccgattctca  | tccaaatggt | 720 |
| caacatcgaa  | aggatctgtt  | cagcaaattc | tcttcttaat | cctacttgcc  | actcttctac | 780 |
| ggtctgcctt  | ccggacaaaa  | ccgattagac | aatttctggt | ctttcattga  | ataaccttct | 840 |
| tttactttac  | attatatatt  | gtctgcagaa | ttcatgtgta | catatcaatc  | cggccttttt | 900 |
| cgagttccggc | tttcac      |            |            |             |            | 916 |

## (2) INFORMATION FOR SEQ ID NO:444

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1873

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

```

tttgagtctt ccaaaaagat gttgtagaaa gatttaccat agcgcgaaaa gttatttttag 60
tttccacttg agtggattta cctttcatac tttattcacc tttttaataa aaatcatctg 120
taagaatat actatgcaat ggcaagactt taccgtcagc gcgtttgctc tgcagacgaa 180
gctgtcgtgg actctctaaa ccgggaacga aagttgtatt cggtcacgct gctgctgcgc 240
ctgtcgtttc tctcaggcta tgtaccgcca gcgtgaaaag ttggagaata tcacgttttc 300
cacatgttgt atttcggcga cgcgcgcgac cttgctcccg aaagcgttcg catgtacacc 360
cgactctcaa ctcccttgag ggcaactccc gtccggcaagc cgtgaccgtc gtgtcgattt 420
cattccctgc cacttccacg agtaccggaa ctgtttcgtc agggattctt tccattggat 480
gtagccgtag gcaggtatct actcctaacg aagaggggta ttgctctttc ggagtttccg 540
cgactacaca aaggctgccg ccgagtgccg tccggtagta gtagccgagt gaacaagcaa 600
atgccattca tcgggtggtga aaacctgatt cacatctcaa actgacccat atcatcgaag 660
tggacgagcc gattgcagaa gtattgctcc tgctatcagc gacctgaac tgaggatagg 720
tcagaattgt gcctcctgat caaagacggc gataccctcc agttgggtat cggcgggtatc 780
cccgcgctgt gttgcgtgca ttggaagggc ataaagatct cgggtattcac acgaaatggt 840
taccgacggg gtgatgcgta tgattcgcaa ggggattatc aagggaagaa aaaaacattg 900
catcccgaia aagtcgttac ctgcctaata tcggatcgaa agaattgtac gattttgtca 960
ataacaatcc ggtgatagaa gctatccggt ggattatata aacaaccccg atgttatcgg 1020
taagaatgac gcatggtttc tatcaattcc tgcttgagga tggatctcat ggggcaggag 1080
cttctgagtc gatcgggtac gaacagttca gtggatccgg aggtcaatcg atttccttcg 1140
tggggccaag cgttccaagg gaggaatctc cattatgctt tccccagtac ggccaagaaa 1200
gggactgaga gtccgcatcg tcccatctga aagaggggtc ttgtgtcacg accggccgta 1260
acgaagtgga ctattggtga cggaatatgg cgtagcgcgt ctgcgtggcg caacgccttcg 1320
tcacgtgctg aagccttgac tgctatagca catcccgatt tccgaccggc cctgaggagg 1380
aaatccgccc acgcttcgaa taagtcggaa ggaatttagg cttatataaa cggattcgaa 1440
gccatgtaca actacattgt gtacatggct cgtatgttta acgtgagttc aatgtaagcg 1500
atatggtgcc gattctctct gatgggatat tgactataac cgaatcagaa aatgaaaggg 1560
aaaaagttga cgtctcatcg gacgtcggag cctctcgaag ctgaaacctc tcaacagcaa 1620
atgaaataca ttgacaaaca gcatattgca tgtttttctt ggatcgatcc gcattgtttt 1680
atagccgttc ggaacatacg ccgaaagggg gtccgactac ccctacagcg actcgggcta 1740
cgccgtagag cgtaccgagc tgcgtctacg gctcttcgag ctacgctgta gagcgtacct 1800
cgccgagctc tacgcgtagc tcgaagagcc gtacgggata gctcgtcatc ctctatgggtg 1860
tacgccatct tgc

```

## (2) INFORMATION FOR SEQ ID NO:445

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...3285

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

agggtacgga ttttcagtcg acncatcggg aggtccggat gagtccgacc accagagaag 60
atatttcggg acgtttcatg cgctattttt gtgttgagga ctcccaatag cctatcgaca 120

```

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| aatactttttt | cctgatcgaa  | catcagttta  | cttccaccgg | caggtaataa | aatcttttct  | 180  |
| gcatctcttg  | cggaaagaag  | attgtcgtag  | ggccagtcgc | atggcatctt | tctcgggtaca | 240  |
| taccatatgg  | cattggcatc  | tttccgatgc  | agttcgtgcc | aatcttggat | gagcaacaga  | 300  |
| tctctctgtc  | ggtaaactca  | tgatgatccg  | gatagatgcg | atcgttccgg | aggggaatcg  | 360  |
| ggtgcgtatt  | tctcgggaag  | acagtttcgg  | actgctattc | cggcgatagc | cagcgccagag | 420  |
| cgtactttctg | ccgaaggaga  | cgatcggaaa  | acaaaggctt | cagtccctgt | ccgtacagaa  | 480  |
| atttggagaa  | aacagcttct  | gatgcgggta  | taaggccaag | tcgcgtttgg | ctgctctaaa  | 540  |
| tctatgggag  | caagatcatc  | ggggcattht  | gtcaggatta | ccatatcgca | cgctgtatag  | 600  |
| agccggcagg  | ttctctcaga  | cgaccggccg  | gaagcagtag | tctttgggtc | gaatacgggt  | 660  |
| gtagtctgtg  | agtactatgt  | tcagggttgc  | ttcaccttac | ggtgttgga  | gccatcgctc  | 720  |
| agaacgatga  | gctgtgcctt  | tgtctttctg  | ccagatcgca | tagatagccg | atggctctgc  | 780  |
| tccgtcagca  | tccacgatga  | cggtcaggtc  | cggatattht | cgtttgatct | gacaggttcg  | 840  |
| tctcctatat  | cctatgcagt  | cgatccttcg  | gttgcaacga | tctccctttg | gttttccgct  | 900  |
| tatagccgag  | gctaaccact  | gctacacgat  | acgtggatgc | aggagccgaa | tcaggatttc  | 960  |
| tacgtggggg  | gtcttaccgg  | gccgccgatg  | gtgatattgc | ctacacagac | gataggggatg | 1020 |
| tcgaaagagt  | cgaaatcagg  | acgttcttgt  | cgaagaggta | gttgccgaac | ctcacgccac  | 1080 |
| cccgtagagg  | gcggaagcgg  | gtttgagcca  | cttgttgata | cggggcgatc | catctcttca  | 1140 |
| gcaattacgg  | ttgtctcatt  | tatcagtagc  | gcatgagtaa | taggggagac | gtgcctgtat  | 1200 |
| gcccgaagga  | cggggcgagg  | tggaggaggt  | tcgcgcagaa | cttctatttc | cggatcggag  | 1260 |
| agaatgggtac | tcagatggca  | gacttcatat  | ccgctgctga | tgaggagagc | aactcttcga  | 1320 |
| agagttgctg  | ttggtcttgc  | catactctat  | gctgtagtgt | ccaccgagct | gaccagcttc  | 1380 |
| gcggcccgtt  | tgatagctgt  | gtccaaacct  | ccaagctcat | caccaaaccg | agtgcgaagag | 1440 |
| ctttgtcgcc  | gagccatata  | cggccttgag  | gatgctgtcg | atctgtgcct | tgggtgcggt  | 1500 |
| gcggccttcc  | gatacgcgat  | gaggaagagg  | tcgtagccct | gctctatgta | gcgttggtatg | 1560 |
| agggcacgtc  | ttcgaccgtc  | atcggagcga  | aggtgttgcc | caagtctgca | tacttgggtg  | 1620 |
| ctgtacgacg  | tccatattca  | ctcctatctt  | cttggctacg | cccgcgagtt | cgggaacatg  | 1680 |
| ccgaatatgc  | cgatggagcc  | ggtcagagtc  | gtatgtctgc | cacgatactg | ttggctgcgc  | 1740 |
| aggctatgta  | gtatccgccc  | gaggtgctac  | gtcgcctcat | gagaccacga | taggcttttt  | 1800 |
| ggccttgaga  | tcgctacctg  | cttccatata  | tgttcggaag | tgaaagcaat | acctcccggg  | 1860 |
| gattgacacg  | aagtactacg  | gctttgatata | catcgctcat | ggctgtctgc | tgatttcttt  | 1920 |
| ggcgagttct  | tgtgtgatgg  | agctaccgtc  | agtgtcgaa  | gcttctttat | tatttcttcc  | 1980 |
| gttatttccac | cttcggcaaa  | gagaacggca  | ttcgactgcc | tttcgttttg | ttcatcgggc  | 2040 |
| cattggccag  | aacctgagaa  | gcgatacgaa  | ccgaagttca | tctttctctc | cgcgttgagg  | 2100 |
| catcttttga  | gttctttctc  | cacatcggtg  | cggtaagcca | gctcatccac | gagcttatct  | 2160 |
| ccaccgcttt  | ctcggcaaga  | ccgaacattt  | cgcctttgtc | ggcaacattt | tcacggaatc  | 2220 |
| cattgccgtc  | ttgcgcgact  | ctgcaatata  | ggattgatct | tgtcccaaag | cccgtttatg  | 2280 |
| tatgtggtga  | tttgttcgcg  | attgcacgcg  | tcactctgtt | gagcatgaat | ggctctacgg  | 2340 |
| ctgccttgta  | gggcctacct  | tgaagatctc  | catcttcacg | ccgaatttgt | caggggcatc  | 2400 |
| ttgtagaaca  | ttgtttgggt  | cgcaatcccg  | ataagcccca | acattccttt | ggattgaggt  | 2460 |
| agagtttgtc  | tgcaatactg  | gagaggtagt  | aacctttttg | gtgtatctgt | cggcatagga  | 2520 |
| tacgacgaac  | ttgcccagca  | tcttgaaacc  | tgcaacgcgc | gacgcaattc | ctctgccgat  | 2580 |
| gccataccga  | cggaaagtgt  | tccagatcga  | ggaagatacc | ggttatgttg | ggattattht  | 2640 |
| tggcttgccg  | atggcttcga  | ctgcctgtga  | gagcgatacg | gactcgtctt | tgccttgagc  | 2700 |
| atgctccagg  | gattggccga  | tacgatctca  | gggaagaag  | aatttctata | tgtaggatgg  | 2760 |
| agtttgcttc  | gatcttcgga  | atggttcctc  | ccgtgccttg | gaggcaatac | cggctacgat  | 2820 |
| gccgaaaaag  | ataaatagaa  | agtacagaac  | aagatgattc | ctgccgttat | aaccccgagg  | 2880 |
| atcgaggcga  | aaacattttg  | aaaaattctt  | tcatttcaga | tttgctatth | gtttctgtgc  | 2940 |
| ttattgtttt  | taatgtcact  | attgcaaagg  | taagtattta | atthacagtt | cgcacggggt  | 3000 |
| ttgcttgcca  | acctctgtca  | ttttcggcat  | gcaagaacaa | gaaagagcta | cctgctaaaa  | 3060 |
| tattccgact  | catthttcaag | cagcctthtc  | ttgatgatcg | attgtccatt | gccgtagaaa  | 3120 |
| gaagaacttg  | aattgtaagt  | agagacggcg  | atcgaaattt | gattcttgct | tttcaataaa  | 3180 |
| gaagagaata  | aaacctgatt  | catacagggg  | atgaagtgca | tatttcattg | cattcgtttg  | 3240 |
| atgggtgtcg  | agttgataga  | attgatttht  | cagaccgaga | ctttg      |             | 3285 |

## (2) INFORMATION FOR SEQ ID NO:446

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...719

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```

gcgaactcgt cgcattggga cgtagccctt ataccggatt ctggggcagt tgcagaaagg 60
agacagaaag ctcgtggcag aagccgtaga acgtgtggaa tcgctccgct gatcaatcgc 120
gaactaacta cgctcagcga tggagaggac aaaaagtagt catcgcaaaa gccctggcac 180
agcagacacc gatcatttcc tcgacgaacc gacggcttcc ctcgattatc ccagcaagat 240
ggaacgttgc acctcttgca cagcctggcc catgataccg gcaggactat cttctctcca 300
ctcatgatct ggatgccatt ttacccatgg ccgatcgcgt ttgctgctgg acaaggagcg 360
ttctttccgt gagggctcgc cggcatcttt ggctctgcgc ttgaagatta tttcggctat 420
atccatcctt ctccacatt aagccggtgt agcatgctcg ccggtgtata atccgatagc 480
tttgctcccc aatcaaagct atccggacag cccgatcggt ccccttctct ttctcttta 540
gttataatga gccgaagtat agctcctttc ggtataggaa tccatgcctt tgacctgccg 600
tcatgtatgc aaggccgact tataccataa gagctgttct gtaaaaacgg aaaaggagtg 660
tgccaaatgc agtgaaccct gaaagtcgat acaaaacatt cagggttcac ttcaaaacc 719

```

## (2) INFORMATION FOR SEQ ID NO:447

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 887 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...887

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

```

actctagagg atccccggca gtcgtatacg acatgcaggg ccgaatcgtg agaaagtttc 60
attttcaggg aaagaatata agctgaatgt gcagtatcgt ccaaaggtag gtacatgctg 120
aaagttagtg cggatacgga gtatttctgg aaaaaatcat tgtagagtaa gaaatcggca 180
cgaaaaaatct aagaacgaaa aagacacctg agtcttggag tgggaatgct tgtcgggaaga 240
gaatccccga cttctttccc gctttgaggc gatgaacagc gaactctccc gtccatctgc 300
gggaggggtt aagacccctt tatacacaag ggtctctaataaatgtgacc ggatccatga 360
gaggagagag cgtcctgaca aaccctcttg tgatctttct tttttctat cggcttgaat 420
ggtggcaaaa cgcaccggct cacattcagg atgttcgggc gtcggggata gctcaagggtc 480
ggtttgcgct caaaattttc gtgtttgtga cctctaaaaa cgtgggtgcgt aaactgtttg 540
ttttggcgtg ggaagtgaag aatttacgca ccacgacgaa aaaaatctgt tccgttttct 600
cggaaaacac agaccgcaat cggcagatgt ttggctcagg ttggccggag atcggatcac 660
cgaagcgagg ctgatgcacg ggtataatga gccaaaggat gtatctgtag gaattgacgt 720
acttttgtcc ggaacaagtc cgtttttagag tatgcgcttt gatgaattga atttaggaga 780
tgaatatagg atggtctcga tgccatgaat ttcacgcaga ccacacctgt gcaactgcaac 840
catccacca ttctggagggt cgcgatgtga tcgcttgtgc caacgca 887

```

## (2) INFORMATION FOR SEQ ID NO:448

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 674 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: UNKNOWN  
 (vi) ORIGINAL SOURCE:  
     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
     (A) NAME/KEY: misc feature  
     (B) LOCATION 1...674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| gccaaaaaaa | gttttttcat | aatgattttt | ctcattgggt  | attagcgacg  | caaagggtatc | 60  |
| ggccgcatc  | agacaggcca | atacctacct | tagggatatc  | tttcacttat  | ttggatggaa  | 120 |
| ttaggtattt | ctgacgatat | tcctaagtgt | tgctgttacc  | tcttgaggat  | attccttata  | 180 |
| ggtgtctcct | atatgggacc | tttgcccaac | aagcaggcat  | tttatccatt  | cattttattg  | 240 |
| tgtacggccg | attgttttgt | gtgtttatgg | tatgatcaat  | gacacaaaac  | gatgtacgac  | 300 |
| aaggaaaatc | atccgacgag | aagagggttc | attcaggggac | gtctgccagc  | gaatcgatac  | 360 |
| gggaaagcac | ggaatgtatt | tttgacccaa | gtgatacgct  | tatatgagag  | gatactatgg  | 420 |
| tctcctatga | gaggatacta | tgtctcacat | gagaggatac  | tatgggtctcc | tatgagagga  | 480 |
| tctatgggtc | ctatgagagg | atactatggt | ctcctatgag  | aggatactat  | gggtctcatag | 540 |
| agaggatact | atggtctcat | atgagaggat | actatgggtc  | cgcatagggg  | atactatggt  | 600 |
| ctcctatgag | aggatactat | gatctcgcat | gagaggggact | atggctattg  | atggaagatg  | 660 |
| ctatctgctc | tctg       |            |             |             |             | 674 |

(2) INFORMATION FOR SEQ ID NO:449

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 484 base pairs  
     (B) TYPE: nucleic acid  
     (C) STRANDEDNESS: double  
     (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: UNKNOWN  
 (vi) ORIGINAL SOURCE:  
     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
     (A) NAME/KEY: misc feature  
     (B) LOCATION 1...484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atccccgaaa | ctcttcttgc | gacaggctta | ctgttttcag | ttgacttnca | atctttttaca | 60  |
| ttcgaggaaa | cgtattttgt | ctgccaactc | cttacgagtt | cttctgtcag | ttcaaaagca  | 120 |
| ttccaaagca | tttttacttc | ttttctccat | acttttctgc | catctctggg | aaatagcaaa  | 180 |
| cctccaaaag | atgaagtatt | cttcgaattg | ggacaaaatt | ccttgctcaa | tatctatggg  | 240 |
| ctgtactctt | ttgaatgtat | gttttgcaag | agatgcctta | actcttgact | gggattgttt  | 300 |
| cgttcaggct | atctgtcatt | attcgggaaa | aaggaataga | agacaatgaa | aggcctgtac  | 360 |
| tgcagattct | ttatcattgt | tcaagaaggt | gttcattcct | aagtagtaat | aatctatagg  | 420 |
| agccggctct | ttttgagtcg | aactttgtct | atggcatctg | tgataatggg | tcttttgacc  | 480 |
| aaga       |            |            |            |            |             | 484 |

(2) INFORMATION FOR SEQ ID NO:450

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| ggctggtacc  | cgatagaact  | ggctgatggc | aaggaagget | ggcttcctgt  | accgtcctca  | 60   |
| ctcgattcca  | tgtctctccc  | gcagactgat | atttaccttc | ttgcatatat  | gtttttggaa  | 120  |
| tacattcttg  | aagtagaaag  | gaacctcttt | tgactctgaa | cggagtagac  | catcctttgt  | 180  |
| tggacggttt  | tttctattga  | tctcggccaa | atggacttgg | gtgataatgt  | ccatcgcggt  | 240  |
| tctgtcttcc  | ttttttataa  | gaaaccgaca | aaggaagctc | tcttcacgt   | aggacagtct  | 300  |
| tattgagcgt  | actcatctgc  | gatcaactct | cctcttcttt | tttaagcctt  | tcttcgcaag  | 360  |
| attccgacct  | tgcaccacc   | ctgattttat | cgctatgtga | agacgggtcta | cggctatcgg  | 420  |
| ggaggaaagt  | acggatttat  | ccagggcata | cgacgaacta | catatcgctg  | gcattattta  | 480  |
| cgagccgtat  | tttcggaata  | aattctacac | gtggacgata | tggagcgctg  | tgcactcgc   | 540  |
| atctatagcc  | gtattttatat | cggagtgcac | ttcatcaccg | atattatccg  | ggtatcgccg  | 600  |
| toggacttat  | cgtaggacac  | tttgtttata | aagtctactg | tatgcacgtt  | cccgttgggt  | 660  |
| gggagccctca | tgccttgccc  | atccgtggca | gtctatgccg | gcgattccat  | tccgctttgg  | 720  |
| acacttagcc  | tcatcgcttt  | gtctttggca | tgctgtgtat | gtcccgccag  | ttgacggaga  | 780  |
| tactcagtac  | tatgtcttcc  | tgctcttctg | aggaaattcc | tccgtatcaa  | tctcgaggag  | 840  |
| gagctgtagt  | tccgtccgtg  | tgatatccct | atgaatctcc | cccggtaggc  | gaacgaaatc  | 900  |
| cgccctctct  | cttcgctgat  | aataatgata | tggcatccgt | ctcctgcgag  | agaccagag   | 960  |
| cgatccggtg  | gcgcaatccc  | aatccttggt | cgatccgcta | ttgtatgcga  | ccggcaggat  | 1020 |
| acagccggcg  | caatgatgct  | attgtccgca | atcaccatgg | caccgtcgtg  | cagcggacgt  | 1080 |
| ttttgaagaa  | aatgttttcg  | accagacggg | catttacttc | ggcgcggaca  | cttcgcccgt  | 1140 |
| atgggcaaac  | ggagttaggt  | ctattccctg | ctggatgcga | tgagagcgcc  | ggtcttcttg  | 1200 |
| cgagccatgt  | tcatacaggg  | aagcagagcg | gagctatgat | acggcgctcg  | tcctgcaaat  | 1260 |
| cctgttcgcg  | ctttccttat  | tgagaagacg | cttgagcgaa | cgccatcggc  | gcgtagagcc  | 1320 |
| tatgcccgtg  | gcactttgcg  | cagctctccc | tgaaaaagaa | tgaccagtag  | gagaacccca  | 1380 |
| agctgacgaa  | atggttcgca  | tgagacgcag | cggaaatatc | gcgatacgat  |             | 1440 |
| gatccaaatg  | acgaagaagg  | tgagaatccc | tgaaaaagag | ccttgctgcc  | cgagtgcctt  | 1500 |
| aaagtgggat  | aaacggcatg  | atgaataaag | ccacgagcag | gatgtctatt  | acatccttga  | 1560 |
| tggtaaacgg  | agaaacatga  | gattgagatg | tttttttgtg | gagtgagaat  | ttctgttccg  | 1620 |
| atagagaggg  | gttgccctta  | cttgacgacg | ccgagtttgt | cggctaaccg  | catacttcca  | 1680 |
| ccgcttcccg  | cacatcgtgc  | acccgaagaa | tgtcccccca | tgcatacac   | tgtacatatt  | 1740 |
| cagtgcggcg  | gtaccggtga  | gagctcctcc | ggagtgggtg | cgaatagttt  | gtagatcata  | 1800 |
| ctcttgccgc  | agacccgacc  | aggatgggaa | gctccagctc | gccgaaagcc  | tcctcctgcc  | 1860 |
| gcatagcaat  | tcgtaattct  | gctccagcgt | cttgctgaaa | ccataaccgg  | gtcagaggata | 1920 |
| atgtcgtgca  | gacccaatcc  | gcccagctct | ccgacacgct | cacgaagtaa  | tcagtatata  | 1980 |
| ctaccgcaat  | gtcttcgtag  | tccgtgaggt | ctgcacgtga | gccgggtgtg  | cgcgcatgtg  | 2040 |
| catcaggata  | tagggcactg  | caaagccggc | accgtgcgga | acatatcgcc  | gtcagagctgt | 2100 |
| ccgcccgaat  | atcgttgacg  | atgggctacc | ccgtactcct | ctacgcacat  | cttcgcacat  | 2160 |
| cggcagcgaa  | ggtatccacc  | gataccggca | tgtccgaaaa | ctcatccgca  | atactttcag  | 2220 |
| tgccggggcg  | agtcgctcca  | tttctctcgt | tgccgaatat | gatccgcatt  | aggacgtgag  | 2280 |
| gaataagcac  | cgacgtcgat  | caagcccttc | cttcttcgac | gatttcgcgt  | gcccgaactcc | 2340 |
| gcacactgtc  | cagctcgaga  | ggcggctgcc | ggagtaaaaa | gaatcggggg  | tgatattcat  | 2400 |
| atgcccattha | cgacgggctt  | ttccaggctg | aaaagcctgc | cgcgaggggt  | agagtccttc  | 2460 |
| gtttcatctg  | cttgatgctt  | tcttttgaga | ccccaaaaat | agccaattcg  | atccataccg  | 2520 |
| aggtcgtaag  | attttcacac  | acattggagc | acattccggt | ctcagtgca   | acgtgaccga  | 2580 |
| ttgggtttta  | tagccggtac  | ggcagtgtag | gggtgcagaa | gttctgttcg  | actttttagg  | 2640 |
| ttccggattt  | tctcgtttta  | cagtcagcaa | aacgtgggtc | gagaaaaatt  | ttgtttggcg  | 2700 |
| tggaaaaaat  | aatttatcga  | acaaaaacga | aaaaaattac | gcgcagtttt  | cccgttttca  | 2760 |



|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ggaacggcaa | tttcatcatt | tttggttcca | aaacgggagg | cactcctatc | gaatcacctt | 2820 |
| aaaagagcct | cgatattgcc | cagaagtgtg | aagaatcctt | ggcagataaa | tattcagttg | 2880 |
| gattaaactc | ctgtgaaagc | agatttaatt | ctctgtattt | ttttgttggt | ttttatctaa | 2940 |
| gtttatgtgt | acattttgtt | ttcaaaactt | caaaaatcaa | ttcgtatggt | tttaaagaca | 3000 |
| tcttgaggca | actttcagag | agaatcgaaa | aacttagaac | aatttgcaaa | cagaggaggc | 3060 |
| aacgaagaat | gcacttatca | tgccattatt | caggcgatgg | gatatgacgt | gtttaatccg | 3120 |
| ttggaagtta | ttccggattt | acttgcgata | taggcacaaa | aaagggagag | aagattgatt | 3180 |
| atgcattatg | cgtgataatg | aacccatcat | tttgattgag | tgcaaacatt | ggcggatacc | 3240 |
| cttactcttg | ccgataatca | actattaagg | tactttcatg | tttgtctgca | aaattcggga | 3300 |
| tgctaactaa | cggtatcatc | tatcgcttct | atcagacttg | gatcaagcta | ataaaatgga | 3360 |
| tgaaaac    |            |            |            |            |            | 3367 |

## (2) INFORMATION FOR SEQ ID NO:451

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| tcagatagcg | ccattttcca | cggggcagat  | tcttcttggt | cagtccggca | aataaacgcg  | 60  |
| atccagtttg | acaacacgat | agccaagggtg | ttcaaacaac | ggcgcacaat | acgatttcgt  | 120 |
| ccgctatgaa | tctctattcc | cacctgcaaa  | gacgtctctc | ttttacgtaa | ctgatggcat  | 180 |
| cggcatgtat | ctcacctcat | ccaattccac  | gccgtcggct | attttctgca | tgtcttcaat  | 240 |
| gcttaatctt | tattgagcca | cacgtggtag  | atcttcttct | tcttgaaaga | cggaggggtca | 300 |
| gcttagaggc | aagatcgcca | tcatttgtaa  | tcagaagtac | accgtagtat | tccgatccaa  | 360 |
| acgtcctacc | ggatatattc | tctcaggaca  | ggatatcgta | ctatatccat | tactgtggta  | 420 |
| cggcattcgg | ggtcatcaga | atggtcacac  | aatttttagg | cttattgagc | agtacataaa  | 480 |
| ctttactctc | atttccactc | tcttatcctt  | gtagattacc | tcatcctgac | gtgtaaattt  | 540 |
| tctaccgagt | tcggtcacga | cttcttcatt  | gacccgtgat | ctcttccttt | tcgatcagca  | 600 |
| gaatccggtt | tcctttcgcg | agcaaaccac  | cgggcatg   |            |             | 638 |

## (2) INFORMATION FOR SEQ ID NO:452

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| ggcattacct  | cggtgttcac | tctgagaaaag | gggaattgac  | tgccgaagga  | atgtcatatc | 60   |
| cggctatcgc  | tatcttcagg | acagtacgcg  | agtatttgct  | atatggagac  | ggagcagcag | 120  |
| cctgtgacgt  | acgctcgccg | ttcggaaaag  | gcgagtacat  | ctggaataag  | ggcaaggtaa | 180  |
| cgggcaaaac  | tctcgtctga | actacgatct  | ggccggaacg  | gatctcttcc  | ttcgctatgg | 240  |
| tattttctata | tcagtgtggc | acaagccaaa  | aagaatcttc  | gtcaggaaat  | acagcttaca | 300  |
| acgtggaagt  | ggtgtccaag | atgggacgga  | acgaatggaa  | caaacactgg  | gcaaagtgca | 360  |
| gatcgaggga  | ggtacgattc | ttcagcgaca  | ggattctaca  | ccagccttta  | tcgtacatat | 420  |
| gaacggatga  | tcaatatctc | gaggatggtc  | atcttctacag | tgccgaagat  | catgctgtgc | 480  |
| atccggatag  | ggcattcctt | tctatacaga  | cgattgggtg  | tgggacacct  | atcgggctga | 540  |
| catccctgcg  | tattcttttg | gagccggaga  | tggaaatccga | catggtcatt  | cctacattcg | 600  |
| tatggctttg  | cttagcaggg | agaaatggtt  | gcctacctcc  | cggaaagtgc  | aggcgacagc | 660  |
| catcgatatga | atggcaatca | tgctatgcca  | tgcttgccga  | tgccatgccc  | aaaggtctta | 720  |
| cgggttttcaa | tttgatgagg | cgtatacggg  | agccaaaaaa  | gtgatggccg  | agaagacgta | 780  |
| cgcacttggc  | ggcgtatgcc | caaaggcaca  | ctcgatcaat  | ttttcgatga  | gaaggctact | 840  |
| accccgcat   | gccacaggac | caaaaaggaaa | ccgaccctac  | caacactctt  | gggagaagcg | 900  |
| gcaggcagta  | gccgttacgc | ttgctattgc  | tacgattatt  | ggtgccttag  | ccgattggca | 960  |
| cagttctccg  | gccacgagca | gaagcgcgtg  | aatttctgcg  | taggagctac  | gactaccgac | 1020 |
| atctttacat  | tcggagacgg | gattctttca  | tcccaaggat  | gagaaggggac | gcttcataag | 1080 |
| cccttcgatt  | acgaatttga | tggaggcccg  | ggtgcacgag  | actattagac  | gagaacaatg | 1140 |
| cttacactta  | tcgctgggat | gtacagcaca  | acctcctgat  | ctgattgcct  | tgatggatgg | 1200 |
| gccggaacag  | tttgtcagtt | tcttgatcag  | actttccgca  | caccgatgag  | tacatgggaa | 1260 |
| gttcaatttt  | tattcaagct | gcccgaccag  | acaggcaatg  | taggacagtt  | ttccatggcc | 1320 |
| aataagccga  | gccttgcata | tacctatatt  | atatgtctat  | gccggtcagc  | caggcgaacg | 1380 |
| cagaagttga  | tccatgagct | t           |             |             |            | 1401 |

(2) INFORMATION FOR SEQ ID NO:453

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3010 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...3010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| gggaggatgg | ttttaccctg | ctcttttgcca | gtgatcgacc  | tgatggaatg  | gcggatatga  | 60  |
| tctgtatatg | accgctcggt | atcttgaggga | tggcattttc  | tggaaaccaac | tttgctcggt  | 120 |
| atgcctttca | attcccttta | caacgatata  | tgctgggtgta | cgacgaatta  | cgtgggatcg  | 180 |
| gcttctttgc | cagtgcaggt | tttgtcctgc  | ggatggtgtc  | actgtctata  | ccttcgttat  | 240 |
| caatgagaag | ggcgccctgt | ggctactgac  | gatattggcc  | tcaaaagagc  | gtatcatccc  | 300 |
| tcaagagcat | aagagcgacg | caagaccctg  | agcgagacta  | cagcgtctga  | tcgcatcggc  | 360 |
| tcgggacaac | cgcaccgatg | cagagaagaa  | ggttccgaac  | gtcagattta  | tttccctatg  | 420 |
| caggggatgc | gtatctatac | ggctggagcg  | acttccaaag  | cagcgaagcc  | aagtcgctct  | 480 |
| atcaggatgt | atggctcgga | aaagaaaatt  | ggaacaggcg  | gctaccctgc  | tggaaagagta | 540 |
| cgactcttgt | atggaagagc | atcggctttg  | gagcgaagcg  | gtatgaagag  | gaaattcttc  | 600 |
| gtctcgaaaa | tgccattcct | ccactggaag  | aagaagtggc  | cgaatggaaa  | aggaagtgcg  | 660 |
| aaacatggag | ttacaagccg | tgcaagcttt  | tagaccaagg  | ccgacctttt  | cgagagccat  | 720 |
| cttacgattg | atctgctcac | ctcttaaaac  | attaatgaac  | ttatgaaaac  | caaaagaacg  | 780 |
| attccccctc | cgagctgatc | atcaatacgg  | acggttcggg  | cttbcacatc  | catttcgtcc  | 840 |
| cgaacaattg | gccgataagg | tcatattggt  | aggtgatcct  | gccgagtggg  | tcgagtcgcc  | 900 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tctcgttttcg | agcgtattga  | atgcaatgta  | tcaataggga  | gtttcatacc  | gtcacggggg  | 960  |
| ggatattggcg | caagcgtatc  | cggtgcagag  | ccacggcatc  | ggctctgata  | atatagatat  | 1020 |
| agtcttgaag  | aactggatgc  | tctggccaat  | atagacttcg  | ataccgcga   | ggtgaaggtc  | 1080 |
| ggctacgcaa  | actcacactc  | gtaagggttg  | ggacttcggg  | cggattgagg  | acaatacgcc  | 1140 |
| cataggatct  | tatgtggctg  | cagagcgaag  | catcggttcg  | atggagtcac  | gtattttctat | 1200 |
| agcgatacgg  | agaagatacg  | ggatgggcct  | tcgaagcagc  | acttcaggat  | caactggagt  | 1260 |
| ggaaaatcga  | agggtgaaac  | cctacgtgat  | accggctgac  | aagacgctgt  | cggatcgaat  | 1320 |
| atgcggggagg | acatcctgcg  | agggtgtgact | attgcagcca  | atggcttcta  | cgaccgcagg  | 1380 |
| ggcgctcgctt | gcgcttacct  | ctcaaagacg  | aggatctgaa  | cggaagatac  | aggctttcga  | 1440 |
| cttcaatggc  | agccgtatta  | cgaactatga  | atggaaagct  | cctctttggc  | cggctctggct | 1500 |
| gccctgatgg  | ggcacgaagc  | atcacgggtct | gttgtatcat  | cgcaggcagg  | aaatccgaaa  | 1560 |
| agatgaatcc  | tcctatcagg  | gaagtataga  | gggccttatc  | gatttggttc  | tggaacgatac | 1620 |
| tgatagaaat  | aagttacctt  | tgtgaaccaa  | ggtttttccc  | cctcggcgaa  | tggtctccgat | 1680 |
| cgtgtcgggt  | atgcagcaga  | gcaagcaagt  | tgctgagggg  | gaatataaat  | tagaagtttt  | 1740 |
| tgcatgaaca  | tactcgaact  | ttcgaacaag  | aagtcgtacg  | ccgtaacagc  | ttagagcaac  | 1800 |
| tgcgtaattt  | gggatcgatc  | catatcctgc  | agcggaaatg  | accgtcaatg  | cctattccgc  | 1860 |
| cggatcaaaa  | ggaatttcaa  | tggcgatgag  | aatgctcgca  | aacgtcaagt  | agcattgccg  | 1920 |
| gacgtattat  | gagccgcccgt | atcatgggga  | aagctacatt  | atggagctgc  | aagatgctga  | 1980 |
| ggggcggtatc | cagatctata  | ttactcgggc  | gatatttgtc  | cgggtgagga  | taaggagttc  | 2040 |
| tacaatacgg  | tggtcaagag  | tgtacggata  | taggtgattt  | tatcggagtg  | aaagggtacg  | 2100 |
| tattccgact  | cagatgggag  | aaatatcggt  | gcattgtgcag | gagatgactt  | tcttgtgaaa  | 2160 |
| gctatccgcc  | cccttcctgt  | ggtaaaagaa  | aaagatgggg  | aggctctgat  | ggcttcacgg  | 2220 |
| atccggagca  | gcgttatcgt  | cagcgatacg  | tggactgggtc | gtcaatagtc  | atgtcaaaga  | 2280 |
| cattttcctc  | aagcgtacga  | tggattcaat  | tcgatgcgca  | gtttcttcaa  | tgagtgcgga  | 2340 |
| tacatcgaag  | tgatacacct  | gtactccaat  | cgatcccggg  | agggtgcagct | gcgcgtcctt  | 2400 |
| tatcacgcat  | cataacgctc  | tggacattcc  | gctctatctg  | agaatcgcta  | cgaattgtat  | 2460 |
| ctgaagcgtc  | tgatcgtggg  | cggtttctgat | gggtgtgtata | attcagccgc  | aatttccgaa  | 2520 |
| atgaggggat  | ggaccgcacg  | cataatccga  | gttcacggcc  | atggagatct  | atgtggcgta  | 2580 |
| taaggattac  | aactggagat  | gaactttacg  | gagcagatgc  | tcgaacgcat  | ctgtatggat  | 2640 |
| gtgctggtag  | tactcagatg  | aagggtggcg  | ggaaattgat  | cgacttcaag  | gcccctacaa  | 2700 |
| gcgagtgacc  | atgatcgaag  | ccatccatga  | gcatacgggt  | atcgcatcag  | cggaatgaac  | 2760 |
| gaggccgagc  | tgcgctcagg  | atgcgacaag  | ctggcgtaga  | gcacaatgaa  | acgatgggca  | 2820 |
| aaggcaagct  | catcgatgag  | atttcggcga  | gaagtgcgag  | aagaactata  | tccagcctac  | 2880 |
| tttcatcaca  | gctatccgaa  | agaaatgtcg  | cctctgacga  | aggagcaccg  | caccaatccg  | 2940 |
| agctgacaga  | gcgattcgag  | ctgatgggtca | atggcaaggga | gttggccaag  | cctactcgga  | 3000 |
| gctgaacgac  |             |             |             |             |             | 3010 |

## (2) INFORMATION FOR SEQ ID NO:454

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...671

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| ccccgctcta | tttcaatgca  | gcgaggctga  | acggttttgag | cttcaggcat | ctgctccggt  | 60  |
| tgcttctctt | ggcagttctca | tgtgggagct  | gcttatggaa  | acgagccacc | gagtatcaac  | 120 |
| gacctctgtg | ccaccaccat  | aggcggttag  | ctttggggga  | gatggggcac | aggctgtcgg  | 180 |
| acctgtcat  | cgacaacgta  | ccacagggtg  | ggaacgtatg  | gggcgcgagg | tggtatcgcg  | 240 |
| tctgacaatc | cgatgcgctt  | tctcaaccgt  | ctgacagcag  | gagaggtgac | ttcttcggga  | 300 |
| gtcgcagcgg | acagatatct  | cagtcctgtcc | ccataaacat  | agtgtcgatg | ccggcttttcg | 360 |
| ctttttggca | gacaagcggc  | atgcccgaac  | cgtgccacgg  | ctctgaccct | gaatctgaga  | 420 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttcgactacg | gcgatccatt | cgaagcgaga | ctttctctcc | atacgatttc | ttccaattca | 480 |
| aagccggatt | agtttctccg | aatcgcaacc | tctgctgagc | cagatcaatc | tgatcggaac | 540 |
| ctaagcggat | gccaactgct | cgcacacgaa | cgaacggttt | tggtgggagg | tctctttcag | 600 |
| cacttcgact | actacaattc | ggaaaaacga | ataagcaaaa | ttcgaggagg | gtactcgtca | 660 |
| cccataccgg | a          |            |            |            |            | 671 |

## (2) INFORMATION FOR SEQ ID NO:455

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...590

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gcatcagccg | gaacataacc | taaggagttg | taccactccc | aacctttgca | cccgtggagg  | 60  |
| agattttcgg | atggacggct | ttcgtagcat | gcaagagtcg | ttcatcagtg | tacgggtatc  | 120 |
| ttctacccga | acacccttga | gtaggctcc  | gccagaacag | aagcagagtt | gttgccctatc | 180 |
| atacaatccc | gatggccgga | ctggcccatt | cggggaaaaa | gccactctcg | cgatatacat  | 240 |
| tcagcgacct | tcctgaattt | taatgttttc | atcgggatac | agcagattga | gcaggggaaa  | 300 |
| agggctcgaa | aagtgtccca | aaatccggtg | tcggtataga | gataccggga | agtacctctc  | 360 |
| cattgtaggg | gctgtaatgc | acaaaattgc | cgaagcatcc | tcctcataga | agcgacgggg  | 420 |
| aaaaagcaga | cagcgataga | ggcggaatag | aatgtagtgc | gctcatcctt | cgntcctcct  | 480 |
| tcnacatgna | gcgtccgagc | accttattcc | agcttcgcga | cggcaagtct | gatccgggtca | 540 |
| aactctgccc | tttgacttnc | gcagatttct | ttcggtctgt | cgacactgta |             | 590 |

## (2) INFORMATION FOR SEQ ID NO:456

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...997

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tgcggtctgta | tctcttccaa | tagagccatg | atgatgcgca | cgtcttctct | cccaaaggat | 60  |
| ttttcttgat  | caatcccgtc | tcatagaaag | gcagatcggg | aaatgaacat | gatacctcgg | 120 |
| caatcccaag  | tatctgcatg | ccgtccggct | tcttcgcgtc | gtatggttcc | tttcataaac | 180 |

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| ctgatatacct | cctgctggga | tccccctcta | tctttttgtg  | catgagatag | tgccgcacct | 240 |
| cttcccccttg | gccagaatgg | ggctgctctc | atgaccgtat  | tggcggcata | cattctgagg | 300 |
| tacgacacat  | atcgaatcac | ttcttcatcc | cccacggcta  | tatgccggag | gtctggtagg | 360 |
| ctacatgtac  | atcgtggccc | tgattgacca | attgtggaat  | gttcctccca | tcgaaatgac | 420 |
| atcgtcatcg  | gggtggggac | taagataacc | accctcttgg  | gatagggtag | tgccctctca | 480 |
| ggcctgctgc  | gtcatcggca | ttgggttttc | cgccccggcca | gccggtgatg | gtgtgctggg | 540 |
| gtcgttgaag  | agcttgatgt | tcacctcgta | ggccgagccg  | tatttggcag | caattcgccc | 600 |
| aatccgttct  | ccgtatagtc | cttgttcgtc | agcttcagat  | gggcttgccg | gtcagtcgcg | 660 |
| acagccatac  | cacagccctg | cgtatggctg | tttggtccag  | atacagctcg | tcaccagcca | 720 |
| aggacgactg  | atcctgtgag | acaagacgat | gccgatagat  | ccagcacgat | ggaggcattg | 780 |
| cgatcaattg  | cagggacgaa | gccggagaag | cctcgcaaat  | ctttccttcg | atacttgggc | 840 |
| tattacctct  | gccttactct | ctccccatgc | cagcagggtc  | acttgtgagc | tttttggatg | 900 |
| gtagccagtc  | ccatactgat | agccgatggg | ggatggtgtc  | gtgggagctg | aatatcgtea | 960 |
| gagcatcgtt  | gtgctccgta | ggccgagtac | gacgagt     |            |            | 997 |

## (2) INFORMATION FOR SEQ ID NO:457

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| cggcctggcg  | cagcagatag  | gaacgggtcag | cgatgatgag | cagcaccacc | gaatatcttc  | 60  |
| ggcgatggag  | aggaggaagt  | gctcgaagtt  | ggccgtatga | tagccgtatt | ggcgatgtag  | 120 |
| atctccgatg  | ttttcagcag  | gaggtcgtea  | ggcgagccac | atcttcgccc | atgagctcgg  | 180 |
| ctatctcctc  | cggtctgtca  | gcccccttcat | cgccggacga | tagaagagga | gtgctccgat  | 240 |
| ggccttatcc  | ccagcccgat  | ctcacaggag  | gctatgcgtg | ccacttccat | gttggcaaaa  | 300 |
| gtccgtgcat  | accgtttttg  | tgcgatacga  | aacatcccaa | ctcgtaaaac | ggctcagcag  | 360 |
| actgcgtact  | ttcttcacga  | gctgccgata  | ggagctagt  | tacgaatcaa | actcgcgtat  | 420 |
| gaggagagga  | agcgactccg  | ccatcgggcg  | agaaaagagt | attgtcgtgt | attgtcatga  | 480 |
| gggatacagg  | tgggataatg  | aatagtggac  | gatggatcat | acttgtagtc | ggaaagcatt  | 540 |
| cgggttagagc | agaggagaga  | aaaggcgaac  | aaaggattcg | ctgaattttt | tatccggcctt | 600 |
| ctctttcgcc  | agcgttttgag | atcgagcggt  | tcgctctcaa | caagtcctcg | aagaagatgg  | 660 |
| cttccaatcg  | gtggacagta  | ggctcgcata  | gatgatacca | ttgaattcga | agttattttc  | 720 |
| caagctgcgg  | aagtcataat  | cgtagagccg  | atcgaagcca | cctgactata | caccattatc  | 780 |
| agctggaatg  | gagaaagccg  | ttggtataga  | ggtgtacatg | tacaccggcc | tgagagatc   | 840 |
| ctccacatag  | gagaaggccg  | ccacttgtgg  | cagacgggca | tccttcgttt | gggcaccagc  | 900 |
| aggtgtacat  | cgatgccggc  | caaagctgcc  | ggatgagagc | attattcagt | ccttcgggtcg | 960 |
| gaaggaagta  | aggagtctcg  | tatagacatg  | ttcgcagg   |            |             | 998 |

## (2) INFORMATION FOR SEQ ID NO:458

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| ccgctccttg  | aagactgtgt | tcacgcgcaa | cttcacacaa | tctaccggct | ccccgtacag | 60   |
| ctgtataccg  | tatagccttc | ctctctgtgc | cgaagcttag | cttgatgggg | agagtagagg | 120  |
| taatggcagc  | cgaagccccg | gatcgtgccc | gtcgggagct | acgatcgtga | cattccctaa | 180  |
| tgggcgcagg  | gcttctccag | ctcgcggata | cctgtgtctc | gaaaaccatc | gtcattcgaa | 240  |
| actaaatttc  | aatcggatcg | gctttcattt | cttgtcttct | tcaggaataa | tgcccttagt | 300  |
| tttacgataa  | aacgtagtgc | ggaataggag | gggatgggta | cgaatttgcg | ctcgatgcag | 360  |
| ggacgccttt  | gcttccatag | gctaaatacc | agggacgatg | aactcacact | cgtctccgat | 420  |
| aaccatattc  | tgcaaagcaa | tcggaagccg | gtgatcgact | tatccttctc | attcctgtaa | 480  |
| agtggtgatac | tgccggcttt | tcggagttat | agtttccatc | taccatgata | tttcttacta | 540  |
| acgatacgtt  | tggtagtggg | cctccacacg | ggaggtggcg | atcggatgtc | tgtacccgta | 600  |
| ccgtttggtta | tccagcgcgt | gtaaacgtat | gcggtcgtcc | atcaacagat | actttcttga | 660  |
| agttggtgct  | gtccgcatag | gcgttgaggc | cacttcgttg | tcgtgacgac | gctgtttttc | 720  |
| ctcattcggt  | ctttttcgca | cgaggagaaa | acaaggaaga | tgtttaccag | catcagccca | 780  |
| agggcatgat  | gatattcttt | ttcgttttca | taggtctatc | tttttgagca | agccttgagg | 840  |
| cttacatatt  | ccgagataat | agcattcaaa | cggctgatct | cccacgctcc | tgctccatcg | 900  |
| tgtcacgata  | gcggatggtc | acggtattgt | ctcgagcgat | tggtgatcta | ccgtgataca | 960  |
| gaaaggggta  | ccgattgcgt | ctgacggcgg | tagcgtttgc | cgatagaatc | cttttcacgc | 1020 |
| tattggcagc  | gaagtcgaaa | cggaggtcgt | gaacaatctc | ccgagccttc | gcatcaagcc | 1080 |
| atccttccga  | accagagggg | gtacggccag | cttcacggga | gccaatgtgc | gggcagcttc | 1140 |
| agcactacgc  | gcatctcgcc | ggttgaagtc | tcttctcgca | atacgatccg | aagagaatcg | 1200 |
| tcaggaacat  | ccgatccagt | ccgatgaggt | ttccactaca | tacggcacgt | agctcttggt | 1260 |
| ctgttcggga  | tcgaatactg | cagtt      |            |            |            | 1285 |

(2) INFORMATION FOR SEQ ID NO:459

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1116 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| accgttgctt | gaacgcgctn  | nctagagnat | cccctatgcc | gatggatacc  | ttcgccctta | 60  |
| tcacgcgcag | atcgggggtct | tctatcctct | tcagacatca | gccgcgaacg  | tcgtgtggac | 120 |
| tattcttcca | tacctatata  | tatagaagta | acgacgaatc | cgtgggtacga | ctactggaat | 180 |
| ccgtcgctcg | tcttatagca  | ggaacgttct | ccgctgtaca | tcggagcagc  | gactctatct | 240 |
| gcactggctg | ctgtattttg  | ctgcaatttc | acgaatcatc | tctatgcctt  | gagtagcaaa | 300 |
| tgctggccgc | acatggnctg  | ccgccacgct | ctctggctcc | tctatcgcat  | agactgcggc | 360 |
| caaggtgcag | gagatgtccg  | ccaccgaagc | tcgaccgggc | cggcctaaaag | agacgacaca | 420 |
| aacactctgc | aaaaacatct  | cgtctgctca | acccatatcc | ggattggcag  | gagatctatc | 480 |

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| ggatacttag | gatagcattc | ggaagatgta | cggaccgaaa  | gaacaataaa | ccccatttta | 540  |
| tctcatgagt | agtattccat | tcgacctgaa | gtccatacgg  | ggattcggtt | cgatgtggac | 600  |
| ggagtgatca | gccataccgt | ttcggctatg | gatgccgagg  | ccagcctatg | cgaacgatga | 660  |
| atgtaaaaga | cggttatgcc | atgcaaatgc | cgtcaagcaa  | ggcttcttgc | tggccatcat | 720  |
| cacaggcgga | tacagccggn | catagccnaa | acgggcagaa  | tatctcggca | tcaaacatgt | 780  |
| ctattgcgtt | cgtccaacaa | ggtggagcag | ctcgaacacc  | tcctgcagga | gacgggttga | 840  |
| aagccgaaga | gatagtttat | ataggggacg | atatacccgga | tcgccggtga | tgcaagaggg | 900  |
| tggctttgcc | cgttgccccg | gcggatgcag | tccggagatc  | aaacaggtgg | ccaaatacat | 960  |
| atcgactgc  | cggggaggag | gggcgtcgtc | cgcgatgtca  | tcgagcaaac | gctgaaagca | 1020 |
| caaggccgcg | ggcacagggg | aatgggttcg | gatggtagcg  | gacggaagtc | ttcttgatga | 1080 |
| aaaatcttgt | ggtttatgct | ggacaatctg | aagaaa      |            |            | 1116 |

## (2) INFORMATION FOR SEQ ID NO:460

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| agaagcncac | tcgggtagcc  | gaagtttgcg | ccatgttgcc  | gaatcccatg  | cctgtacgtt  | 60   |
| cacagccgta | ccccattctg  | cggggatacc | ttccatgcac  | ggtagaggat  | ggcacgctcg  | 120  |
| ttcatccaag | agtcgaacnc  | ggccatgtag | caccccaaag  | ctgctcttcg  | gcagagaaaag | 180  |
| ggaagtcctt | acccgttgag  | cctttacggc | tgccctgaaa  | cgggatacna  | ggtctttgag  | 240  |
| gtttttacgg | agagttcgtt  | gtccaagtgc | acaccattct  | cttccttgac  | cttccgatta  | 300  |
| tttcttcgaa | cggatctata  | tcttccttat | tcgtgggctt  | catccgagta  | ccacgtcgcc  | 360  |
| gtacatctgc | acgaagcgac  | gataagagtc | cgggcaaadc  | gttcggttgc  | ggtcttgctg  | 420  |
| acgataccgg | ccaccacttc  | gcgttcagac | cgaggttgag  | gatcgtatcc  | atcataccgg  | 480  |
| gcatggaagc | cgtgctcccg  | aacgtacgga | tacgagaaga  | gggttctcgg  | tgtcgccgat  | 540  |
| ttcgacttca | tcagtccttc  | gatatttctg | atcgcatcgt  | ttacttcgca  | cgcagcagct  | 600  |
| ccactacttt | gtctcggccc  | aatgtatagt | attcctgcaa  | acctctgtcg  | tgatcgtaaa  | 660  |
| accgggaggc | accggcacac  | cgataaattc | atttcggcca  | aattggcacc  | cttacctccg  | 720  |
| agcaggttct | tcatacctgct | tctccctcgg | ccttcccat   | gccgaagggtg | tagactcttt  | 780  |
| tctttccatt | tagattagtc  | cgttcgttat | tattatgatt  | tgatagtttc  | ttattatgac  | 840  |
| aaaaagcgat | aaccgactcc  | ttctccgagc | ttccggaagg  | ggcgtttttt  | gttgtaaact  | 900  |
| gcaaattaac | gaaaaaagag  | caagatacgc | tctttccacc  | acccctcaaa  | cccatgaacc  | 960  |
| tcaaggagta | tgggacagaa  | agtaggcgaa | gcattgctata | tcacaggaga  | aaaagac     | 1017 |

## (2) INFORMATION FOR SEQ ID NO:461

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2408

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```

cctgtgtagt ttgggtggata gacctttgtt gatagagatt cgggtggcac tttcgtctcg 60
tatgtgtcgt taaagaaccc atcgatcttg gatatcgaag atccggctcg aataccactt 120
cgggtacggt cggacgggtt ccattgctcn taaatcgcg ctagaccattg tgagagaaaag 180
agcgttccaa tatatttcgt ccatataagt attcccttcg gcgaggatat tttccacgcg 240
tttggcgtct ctatggcctt gtcgtttgat ccgtagcggt catcgccctcc tgtataaggg 300
cagaggagaa ttcgacactg aagttgccgc ccagcatcga cgagacgtaa cacctccact 360
attgccgaag ccgcgtcgac caccgccttg ggagagaaga aggtcatgga tcccatctcg 420
ctgtccatct cgctaaagcc ctattgttcg tattgttcgc actaccgatc aatgtccatt 480
gcttatttcc tcgaaccgat tgacgttccc tccggccata tagcgtttgt cggtagccgtg 540
ccggcctgaa gcgttccgaa gaggccttcc tttttttcgg gcttcacctc aggttgatta 600
cggctctctc ttctccatca tcgaaaccgc tcatccggag agctcgctca gttgttcag 660
tacctgtact ttattgacca tatcggcgga agattcttta ttgccacctg tggatctttg 720
gagaaaaact ctttgcacgc acaaggatct tgctaattgtc cttgccgttg atggtgatct 780
tccctcggat ccgatctctg ctccgggtag cttcttgatc agttcctcga tagagctccc 840
tgtgctacgg tataggatcc ggcattgaat tcgagcgtat cgtgcgtacc acgacctctg 900
ccgcttttagc ctgcaccgtc acactctgta gagacgggca tcttcgttca tggatatatc 960
tttgagcgta atggtttgcc gtttctaaga gatatttttt cgtcgtgggt agtgtaacct 1020
acatatgaac gcgcagaatg tagtcacctc cctgtgacgt tttcaggctg aacaacctt 1080
ttcattagtg gcacctgcgg caacggctac ttggccggta ctctgtaaag ctgtacgttg 1140
gcttgaatca tgggggttgc ttcttcgtcc aatacttacc tgctactccg gcttggttggg 1200
cttcacgccc gacgaaacca agagagcaag gagtattgac aacagtaatt gataaatcga 1260
tcgcataaga aaagttgaaa agaaaaatag gtgctatcgt tccattctc cgaaatgga 1320
tttacgattt accctacaa tcgaaatagag aggaaaagag aaataagttt aaagaccatg 1380
tcgattttcc acattcggac ctccccgcaa ctgtcgggaa aggcgacaag tatcaaggag 1440
caagtcggat ggcattcttc tttggtatta ttgcctcaag ggagcaaaca tgtatctatt 1500
ctatatattt ccgctcatga aaaaggtgaa gaaattccgt cgaaaagtag tcgcttacag 1560
agaaatcaga acgaaaaatg atgagattgc ggtgcgattt ttggggaaaa tacgcgctaa 1620
attttttcgt tttggttcgt aattttttga cttctcgcgc caaaacaaaa atttctcgcg 1680
ccacgttttt acgatccacg ccgcagcatt ttttcgacgt aaaaacgtcg gagaggaaa 1740
tgccctccat ctgctgtttt ttctcccgcc agtggaggaa aagctcggat ggaagagcct 1800
tcgggacaca gaccggggag ccgtctttct caaaaaacac gtatctttcg gagattttag 1860
ctcaaccgcc cgattattat gaagcatttt ttcagtgcga tacgccgttt ctgccaccct 1920
ataagaagta tgtggcatgg agcgtggtgg ccaatacgtc agtgcactgc tcaacctatt 1980
gtctttctct ctgatcatgc ccactctgct atcctcttca ggatagaccg gcaggtgacc 2040
acttacatct cgatggatgt atagactggg gtagcatgga tggctggaaa gctgccggag 2100
ccgctctagc aataatttca gctggtagct aagccaactt atagaggtag gtggagatcg 2160
tttacgctta tcatgctggg gatttatctg gtggtgatga ccttttgaaa gtggcttcga 2220
tgtacctcgg attctacagc atgattccgc tgcgacggga gtggtgcggg acattcgcaa 2280
tcagatcaac gataagatcc tcgactcccc ctttcctttt tcagcgaaga gcgcaagggc 2340
gatatcatgg cagcatttcg ggggatgtga atgagataga gacttcggtc atcagttcgc 2400
tgatatgt

```

## (2) INFORMATION FOR SEQ ID NO:462

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:



## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...487

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

```

actgctgctg tagcacacac aagcctatac cgatcagaat gccgatggcg cccccgtcat 60
ggagacgagc agtccttcta tccgaaagat acgagagagg tttgggatgt tgctcccatt 120
gagtgaagcg tatagatgtc ttccttcttt ctataaggag catggagagg ctgctgacta 180
tattaaatgt agcaagacaa ggataaacag gaggatcagg tagctcatcc acttctccat 240
cgctacaagt gagtgatttc gggatgctgt ccggccaaat cgagtacttg gtagtgctcc 300
ccagagtctc ttttaggcgg agagctatct gctctgcac gctcccgttc gtagctgtat 360
ggccacggct tctgcttcat gatccgaata ataagcagat tgcgcagact gtctatggaa 420
aggatgatgg aattgtctc tgttgccaggc cggatgcaaa taccgatgcc acttgccctg 480
gagcgac 487

```

## (2) INFORMATION FOR SEQ ID NO:463

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...483

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```

tttactgccg tatcagtatc cgcggaggat tcgtttgatg tcgttcagct attgagggcc 60
tccaaggggg tgaggttgtc gatgttcaga tcgaggattc ctctctgatt tgggacaaga 120
cgggatcatc gagctgaaag aagctaactg ataaccgtcg atgctcctgc ctttttcgtc 180
ccgaggaagc gtgggcacgc atttttcacc ttttcggaag ggcctcgttt ggtgtctttg 240
gttttgctc ctcttctct attttctccc tttcttggtc gagacgatgc aggagtctgt 300
ggctcgctgt acgatatggt gtggcatacc gccgagacgg gctcttgaat accgaagctg 360
tgtgcactgc cgcccggtc caatttgcca agaagagcat cttgccgtcc acttcgcgag 420
ccgatacatt gaagttgggt accganncca gttgcccttt ccagctcgtc agttcgggat 480
aat 483

```

## (2) INFORMATION FOR SEQ ID NO:464

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...726

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

```

tttttattac aactttggag cgaatttttt caagggcaga ctcgggagct tgttttccac 60
gacctttcaa cgtagagccg actgcttaat cttatttttaa acaggaacag aaatatgtcg 120
aaaaaatcga tcctttctgct ttgctgtcgc tgtgcttcat ttctgctacg aaggctgtga 180
cccccgtcag aaatgtcgca atagccaagt gaacagcaaaa gcaaagaccg aacgtacaaa 240
gccctggact ctgtacggta cattagcaac atgattgcag atcggtgga gttcgcaaca 300
agattttcttc cgaaaaagag gtaagaaaag ccgaatatga aaacggctgg cgatggaagc 360
actcaattac cctgccatag atttatatgg tgagattctt ggagcgagta tgtaaaccct 420
ttcgtgggtg caggaaccga ttcgaaattc cgaactccta tgacattgat tgctcttcgt 480
tcgtgatgcc gtcgaagata agcagggtcac ctctcaattt ggctaccgtc ggcgtttcga 540
cggatgcact atgggtattga tctttcagtg aatcgtggcg atacgataga gcagcctttg 600
acgggaaagt tcgtgtacgc agctatgaag cgcgtggtat ggctactaca tagtcttgcg 660
ccatccgaac ggactggaga ctgtgtccga cacatgagtc gccaatgggt agacgagaat 720
cagatc

```

## (2) INFORMATION FOR SEQ ID NO:465

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...591

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

```

tcgaacaaaa agtcaaagaa tattttctgca acatcaatgg atataatgaa gcaatatttt 60
ctgggttgcac aacacactat ttaggcaata atagcctatt attagttgcc ttggggctgc 120
tattcctgta attgcaggaa aattcatgag aatgagactt cttccgaaga aatgagctat 180
gaagaattca aaaaacgctc tttgagtgcg gcgaggtaga tgacctcatc aaacttatta 240
ataaacgggt tattgccgtc cgataaaaagt tgtttgattg ctcaccagct tttgtgatat 300
aaaaaagcag gtatcgatcc tccaggatcg atacctgctt catcaaatta aatatcatct 360
tatcccatata ttgaactatg acgagggact aactcttgct tcttggtgaa gttaaaagtg 420
atttggtgca ccttgccgaa gtatcttcta tatatacgtc taaagatatt ggtgccggca 480
tttcatecccc ttcgtcgcca ttttccctcc gattggattc ggtgccggca gaagtttttc 540
ttccgtttgt aacaaatgga tccttttgca tcttcatata tacagggtt c

```

## (2) INFORMATION FOR SEQ ID NO:466

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgaatatagc | cgctgccgta | ggctcgctgg | cagtaatggg | gctgatcggt | ttgtcagcac | 60  |
| caaggtgcmc | agccacgta  | cgctgctcat | tatcggcgta | tgatcggata | tgtagccact | 120 |
| gccgtcatcg | gggtattcaa | gtttttcgta | tcgaagaaga | tattcgggca | tacgtaattt | 180 |
| gggggttggg | cagctttccc | gtgccacgga | ttcgcaactg | agtttctttg | ccattctgat | 240 |
| gttgacttta | ttccggccgg | tatgctcctt | gtcaagcagt | tgaatctctt | attgtgggag | 300 |
| aaagctacgc | acgtaatctg | ggactgaata | ctcgtcgggc | acgctgctcg | tgatctcttc | 360 |
| cgccggtttg | ctcatcgcta | ccggaacggc | ctttgcggcc | catcggtttt | ttgggg     | 416 |

(2) INFORMATION FOR SEQ ID NO:467

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 664 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tagaggatcc  | ccgcaaaatt | cattcataaa | atggaaattt | tattgtttgt | gaagccttat | 60  |
| tatatattgac | taaagttaca | gaactatata | tgaatattgt | tacatacagc | cagatatgaa | 120 |
| tagactcaac  | tggacgcttt | ctgcactatt | gaattatcca | cttttagaga | ggatgatttg | 180 |
| ttttctatgg  | aattaacaat | ttgcatgaaa | ctgtcaagaa | agaaatcttg | gaataactga | 240 |
| gtgattagaa  | aaaggaccaa | tctttacttc | taaaattcga | gagataaaat | caaatttgaa | 300 |
| aattcttttg  | tcgatattga | ggagcataag | gataatttgt | tatagaagca | aaggaaatac | 360 |
| ataaaagcac  | cttggttcga | tttgagaaa  | ataaatgttt | gtgattgact | ttagaaatgg | 420 |
| aaatctcgaa  | ctttattcat | caatgaccaa | tgaccatggc | gaatgagtta | tgtatggctt | 480 |
| ctgttttttt  | tcatatcggt | tttagttgaa | actacagaga | aaaatgaatg | aagtacctgg | 540 |
| attaagaaaa  | ggacgcttga | agtcttattg | gaatacagct | tttaaagggc | ttttttctcg | 600 |
| gatattcggtg | gtcctggctg | cattgacaag | cagaactgtg | gactcttgct | cttcggctga | 660 |
| tgat        |            |            |            |            |            | 664 |

(2) INFORMATION FOR SEQ ID NO:468

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| attctaactt | ccaagattga | tcatgggctc | aatccagata  | cacatgccat  | tttcagcaaa  | 60   |
| ggccctgtac | ccggctcgtc | ataatttggc | acctccggga  | ttcatgcac   | tgccgaccga  | 120  |
| ttccatgtcc | gaccaactct | cgaacgaaga | gtatccacga  | ctttcgcagt  | acttctgtac  | 180  |
| tgcactgccg | atatccctat | tcgatagcct | tctatggcaa  | cagcaattcc  | ttcgtacaac  | 240  |
| gactcttcgt | cgttttcaat | agtcgaatta | cttccggagc  | aactttctct  | acagaaacgt  | 300  |
| ataggcagaa | tctcctgtaa | atccattcaa | ggatgtaccg  | cagcgactga  | tacaatatcg  | 360  |
| ccttctttga | tgatagcttt | agcagaaggg | atccatgaac  | cacattctca  | ttgaccgata  | 420  |
| cgcaaatact | attggggaaa | caccataacc | aaggaaagcc  | ggctcagctc  | catgggtcacg | 480  |
| aataaattcc | ctgcgacctt | atcaagcacc | aagggtcgaa  | caccggcgcc  | aataatttttg | 540  |
| caacttcggc | cagagtcttt | ccaaccaact | gatttgcttc  | gcgcacacg   | cgatttcttc  | 600  |
| atctgtcttt | aggtaaatac | tcaatatgcy | gaacaggccc  | aactctacct  | ttaatacgcc  | 660  |
| cgctcttcaa | caagccatcg | taatgttcat | caagagatgg  | ctttcgatct  | gttgcaacgt  | 720  |
| atccaaaaca | actccacca  | aatcagcaga | gaagttcctc  | cgaagaattg  | cgaaaagct   | 780  |
| gaacaactcc | gaacatctcc | gcaaaagcag | gcaggatggc  | aactatagcc  | aaaacaatgc  | 840  |
| tccaggaagc | gttatccggg | ccattatcgc | atcaatataa  | tcttcgtttg  | ttttccgggc  | 900  |
| ttaataccgg | gaataaaacc | gttggttctc | tcagggtcac  | ggccatctgc  | ttaggattga  | 960  |
| tcgtaatcgc | cgtatagaaa | tacgtaaaaa | gaatgatcaa  | aatagcaaat  | acaagattat  | 1020 |
| accaaactcc | gtgtgtgtag | acatagcact | cagaaacccc  | gaagactgat  | ctacattgcy  | 1080 |
| aatcccaaaa | tagagatcgg | aatgaacatc | agcgccctgag | caaagatata  | ggcatcacat  | 1140 |
| tggcagcatt | taccttcaag | gggatataat | ggcggtgtccc | ccatactgct  | tattaccgac  | 1200 |
| aaccgccttc | gcataattga | caggtctttt | cttggttctt  | gtacaaaaag  | gattgcacct  | 1260 |
| gctatgacaa | aaagaggaat | acaatctcag | caagaaaagc  | aaccaaactc  | ccaacagcac  | 1320 |
| tcgtgtgcga | gatgtgaact | cagctacaaa | tgcatggggt  | aaacgagcaa  | tataccgatg  | 1380 |
| agaatgatca | acgaaatacc | attaccgata | cccttggtctg | tatacgctct  | cctaaccaca  | 1440 |
| gaacaaacat | actaccaccg | gtaagaatag | aaccgcaact  | atctggaacc  | aaaggccacc  | 1500 |
| gggcatcgat | gtcctacaaa | ctgcatttgc | actcgcaagt  | tcaccaaata  | ggtaagagac  | 1560 |
| tgtaaaataa | aatagcaaca | gtcagataac | gagtcactcg  | attgatcttc  | atagccact   | 1620 |
| ctcaccttct | cgctgcaact | tttgcatgac | aggtacagca  | atcgctccaa  | ctgcataaca  | 1680 |
| atcgaagcag | agatataagg | cataataccc | aaagcaaaa   | agatgcatgg  | gagaaagccc  | 1740 |
| ccccggaaaa | catatccaag | agagcatcag | tcctccagca  | gtctgggtctt | tgagtgtctga | 1800 |
| caacgatgcy | gggcaatacc | ggggatcacg | gaccaaataa  | acccaaagcg  | ataaacgacg  | 1860 |
| gaggaacaat | aatggtcgtg | agaatgcgtt | gacgcaaaa   | cctcaatctt  | catatattct  | 1920 |
| tgattgtttc | taccgcacgc | attaagctta | tagttttaca  | cagatcctcc  | tgctcttaca  | 1980 |
| atagcttctt | ctgctgtctt | tgagaaagct | gagcttctac  | tgtcaaagcc  | gtagtcaactg | 2040 |
| taccattagc | caatatctaa | ctaaagagtt | tcgagaaaac  | agccctgcag  | caatcaagtc  | 2100 |
| ctctacaaa  | tcttggtcag | agagtttagc | tcagacaaag  | tttgaagcac  | agacagttga  | 2160 |
| taggcttgta | ttctactcga | tttatattct | ttaaagccg   |             |             | 2198 |

(2) INFORMATION FOR SEQ ID NO:469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1129

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

```

gctttcttac aaggaaaagg ttgtatctcc ttgtctaata tgctctcgtc ctcttcggtc 60
agcagagacc aaacatctct aagcaagtgt cccaatcctt atccgaagct gtcttcacac 120
tataagtgtt cagagaatgt ctatttgtca aatccgtaca acgaggaaga aaggccgtag 180
aactattatt atgagaccgg cgaagaatcg aggggaaagt gcttctctat caatatcttc 240
catcctgtat attgcaaaaa taagtctgaa agtcggaata accacaaaat aaggggttac 300
ttatccggaa atcagtaaaa aataaaataa tcagagcagt gtcaaggaga aaacctccga 360
cacagccctg attatatcgt ttgaggctat ttccctgtgg aactattccg atgggtgcttc 420
ttccattgcc gggtcggctg tggcacggaa aggaaactct tacgctcggc tgtcgccctt 480
tcgtaatcgt acgatgcata acgacgagct tctcgtaatc gcgcaaacca gtaccggccg 540
aatgagggtga ccgcagataa cgttttccct cagtccttcc aggtagtcgt cttaccacag 600
atagctgctt cattcagcac cttgggtgtc tcttggaaga ggccgcggac atgaagctct 660
tggtctgcag tgccgcacgg gtaatacttg gagtatctgg ctggcagtag ctgacttggc 720
atcgcgcaat ttcacatctt gagatcctta cgcttgagca tactgttctc atcacggagc 780
ttgctgcctg aacaatctgt ccggctttca gcacttggct atctccggca tcataactac 840
cttcttaccg cagatgcgat cgttctcttc cattacttcg aattatcgac tacctgctgt 900
tcgaggaaga ggggtgtcac ccgatcgaca attcaacctt gcgcatcatc tggcgaacaa 960
taacttcgaa gtgcttatca tgatcttcac accctgaagc ctatacacgt cttgtacttc 1020
attgacgatt actcctgtac tgccgtggga cctttgattg ccagaatata agccggagaa 1080
tagcttccgt cagaaaagcg gtgttcctgc acgaaacgaa gtcgtttct 1129

```

## (2) INFORMATION FOR SEQ ID NO:470

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2443

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

```

ccatactttg tcacttgcta tatatcggtg ccgccgcaat cctcacgggt gcaactcaag 60
caatgcagcc cttcagtcgg gagcggagnt aaaacacgac atcaggaaga ttacgacat 120
gatggagata aagcagagaa aaaatcccat cggccaatga gattcacttc tcatgccggc 180
aggctgaagc agtaggttgc aggtagagga agtggcacct gcctctttca actatgtgat 240
caaaaaagcg gacagatcct ctccgcccaa ggcgatgaag ccaccatagc agctcggcca 300
acggcatcgt ttcgtttgcc gggtcggcct ttacagaagg agctccgtac gagcaggaga 360
gtgcatcgta cgcactctct ccaaaaatct gcggatggag atcccgtaac caaggcaaag 420
atcgcttacg aatcggctca aaggaaacac ggccggctga aaagctggta aaagatcaga 480
tcatttcgaa aaggaatacg aacagacttg caggactat cagacagcca agaccatata 540
gaagcccaag catccggcac cgggtcggga ggggtcagcg tggcgtctct atgagcggat 600
atatcaaaaa ccgcattggtc aaccagggcg aatacgttcc gtaggccaac ccatagccac 660
cgtgtcacia aaccgccggg tgcagcacgg gcggaggtat cggagagcca tttcaagaat 720
gtccgcaatg tctccgtgcc aacttccaga cttcatacga caacaagctc tacgagctgt 780
ccgactgaac ggaaggctgc tctcgttcgg gcgtgcatac acacagtcac cctcatcccc 840
gttacattcg aattcgacaa tgtggcgcaa gtcgtaccgg gcttttcgtc actgtgtatc 900
tgctctccaa tactcaggaa gaagttctct cgttcccgtg tcggccatta ccgaagagca 960

```

```

gggattgcac ttcgtctatc gcggttgccc gaagaggagt atcagaaaca agaggttacc 1020
ctcggggcagg caacggacgt cgtgtgcgaa tcctgtccgg actgaaagcc ggagacaagt 1080
tgtgactcat ggagtatatc aggtgaaact ggccgctact tcgtccgaat gcctgaaggt 1140
catactcact aaagagagag gatattcgat catgctaaca agatcattcg gttctctctg 1200
aacaaccggc tgaccatatt ggtagatccg tactgctgat gctggtcggc acctatacgg 1260
cctccaatat ggagtggacg tattccctga cttgaacgct cctaccgtcg tagtgatgac 1320
ggagntaccg gtatggcacc cgaggaagtg gaacgcctcg taaccttccc cgcgagacgg 1380
ccgtcaatgg agctaccgac gtgcgtcgcg tgcgtcgtc tccactacgg gcttctctat 1440
cgtttgggtg gaattcgact gggggacgga atttatcgtg ctgcgtcagat cgtgtcggaa 1500
aagctggcca tggtcgggtgc gatctgccgg acaatgtggg caaacctacg ctcgcccccc 1560
aatcctcctc ctccggcgaag tcatgattat cggacttacg gccgacagca cctctctcaa 1620
gacctccgta ctttggccga ctggacgata cgtccgcgct tgctctgata ggaggtgtgg 1680
cacaggtgac agtactcggg ggcgacatca aggaaatcag atactgctca atcccgaag 1740
gatgaagcac tacggtatca cgtgcgcgaa gtacgtgctg ccgtcgcacca aatgaaccgc 1800
aatgcatcgg gtgcgtactg tatgaatacg gcaacgaata tatcatttgc ggactcctct 1860
cccgaacgat gctgccgcat tgggtaagac actggtaaaa agtctcgatg aattcccatc 1920
atgctcgaaa cgtgtggcaga ggtaagggtg ggcaataagg accgaagttg ggccttgctt 1980
ccgagcggag acaatctgcc gtactcgtgc catcaccaaa cagccggcga cgagtacact 2040
ggagctgacc gaaaggttga tcgctctctg gccgatctgc aaaaggctct cccctccgat 2100
gtgaaaggag tacagacata ttccgtcaag agcgtttcat cgaaaattct atcagcacgt 2160
acgaaaagct ctgtacgaag gaggcattat ccgtcgtcat cgtatattca ttttctctgat 2220
gaatgctcgt gccacgaatc atttcgctgg tcacattccc ctttcgctgg ttgcatcctt 2280
tttgacactc aaactgatgg gacgaccatc aatacgatga gtctcggagg tatggctatc 2340
gccatcggtc gcggtggacg atgccatcgg gacgtggaga atgtatacaa acgcctgcgc 2400
gaaccgtatg aagcctgcga agaacaggac acggtgctca acg 2443

```

## (2) INFORMATION FOR SEQ ID NO:471

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2971

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

```

gactaaggaa ctgctcgtcg acttttagagg atcccccggt catgcccgtc tgccccattt 60
tggcgatcat gatacgcggc tgacggcctt ctttctttca aacttctctg ccaattcttt 120
ggcatgggcg aagtctttat cttctccgat tcggatgagt acacgcctga aatagttctg 180
attactgctt tatatctccc acaaccttct cacatgcgtc cgagatctca cccaaagagg 240
cacgcgccct gcagctttga ccgcaaggtc gagcagggtt cctcttttcg tctcacgcat 300
ttggtgatag cctcaagggc ttcttgacac gctttctcat cacgtgagag cggagatcgt 360
tgaggcgctc tatctgctgc ttacgaacag cctattgtcg atctcaagaa tatctatagg 420
atcctcctta ggcagacgat attgtttacc cccacgataa cctgctggtg cgagtcgata 480
cgagcctgtg acgggcagca gcttcttcga tacgcagctt gggtagtcgg gtctcgatgc 540
ttttgccatt ccgcccattc cctgtaactt cttgatgagt gtccacgctt gtgtacgagt 600
tcgttggtca ggctttccac atagtaggag ccaccccggg atcgatttcc ttgcagacga 660
gagtttcttc ctggatatag atttgggtatt acgggcaata cgtgccgaga agtccgtcgg 720
cagggcgata gcctctcgag agcattgggtg tgcagcgact gggatatgcc caaagcggct 780
gccaaagctt gatacaggtg cgtccgacat tgttgaacgg atcctgctcc gtcgcgacca 840
gcctgacgct tggctgtgtg tgcgcagagc caatgacttg ggttcttcgc cccgaagctc 900
ttcacgatct tggcccatag gaggcgtgcc gacgcattct ggcgatctcc atgaagtgat 960
tgacgccgat ggcccagaag atgagagacg aggagcaaaa gcatccacat cgataccggc 1020
atcgataccg ctttgagata ctgcataccg tctgccagcg tataggccat ttcgatgtgg 1080

```

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| cggtggctcc  | tgcctcttgc  | atgtggtaac  | cggagatcga  | gatcgaatga | acttggggcat | 1140 |
| attctgagag  | gtgtactcga  | agatgtcggc  | aatgatcgca  | tcgagaattc | gggcggatag  | 1200 |
| atataagtgt  | tgcgcacat   | gaacttttga  | ggatgtcggt  | ctggatcggt | ccggccatct  | 1260 |
| cttcgagctt  | tgtccttgct  | ccagtcgggc  | attgatgtag  | aaagccagga | tgggcaaaac  | 1320 |
| agcccgttca  | tgcgtcatgga | aacggacatc  | ttgctcaatg  | gaataccgtc | gaaaggactt  | 1380 |
| tcatactctt  | cagcgagcaa  | atggaaacac  | cggccttgcc  | gcacgcgcca | ccacgcgcga  | 1440 |
| atgatccgcg  | tcatagccgc  | ggtgcgtggc  | aaatcgaatg  | ccacggacag | acccttctga  | 1500 |
| ccggaggcca  | gattgcgaca  | tagaaagcgt  | tcgactcttc  | cgcgtagag  | aatccggcat  | 1560 |
| actggcgata  | gtccacggac  | gcatgggata  | catgccgcta  | taggggacct | gcaggaagga  | 1620 |
| ggcagaccgg  | atacatagtc  | gagatgctcc  | atgccttcaa  | ggtcgtcttc | gtatagaggg  | 1680 |
| gctttaccat  | gatttgctcc  | ggagtacgcc  | agtcaccacg  | atgccctttt | cttcgcgcca  | 1740 |
| gcgcgtagca  | tccttagcca  | cgaaccggcg  | gacttaatat  | cgatgtcttt | ataattaggt  | 1800 |
| ttcatctttg  | atttttgctt  | tagggatgga  | tactaccgaa  | taccgaattt | gtcgttgaag  | 1860 |
| gccgaagcgt  | ttcgaggaca  | ttggacttca  | catgcacata  | attccggatg | ctttggacct  | 1920 |
| aagatccgcc  | atacaagccg  | gtgcaccggc  | cactacgaac  | cggcacggcc | ggcaaggata  | 1980 |
| gtcgaatgca  | gccggagcgt  | actcggcatt  | tcatcgtcac  | tggagcagag | caccacgata  | 2040 |
| tcggcttttg  | gtcccaatcc  | gcatccacac  | cttcctccac  | ggacttaaag | cccaaattgt  | 2100 |
| cgatcagttg  | tagccggcac  | agccgaagaa  | gttgcttgag  | aactgagagc | gtgccaacgc  | 2160 |
| atggccagat  | tgccgatagt  | gagcatgaag  | acgacgggcg  | ttttgcgctc | ttttccggtg  | 2220 |
| cgagacggag  | agcttcgaat  | tcggatgctc  | ctcgctgaag  | ttcaggggtt | cgatggattt  | 2280 |
| gacacagtta  | cagtcatgct  | ctcctgagca  | agagtgatct  | tgtcgccggc | aacttcctgt  | 2340 |
| aaattgggga  | acggttggtc  | ccgaggaaga  | tctcgcgggc  | agtcgccacc | gactggtggc  | 2400 |
| gttgatattg  | cttgcatgga  | cagccttctg  | aatgcttgct  | gtctcagcag | ctgagtgaag  | 2460 |
| ccgcccgcac  | cctctacgga  | gaggaacagc  | ttccacgctc  | ctctccaatg | gagttggtca  | 2520 |
| gcgtctcgat  | ataataagat  | ccggccgagg  | gtcgataacc  | ttgtcgaagt | ggcattcctc  | 2580 |
| tttgagcaaaa | agctgctggt  | gcgagcgata  | cgctccgaga  | agtcacgctc | ctgctgatag  | 2640 |
| gtgacacgaa  | aggcaatacg  | gttatggagt  | ccactccggc  | tatcgctgca | gacatgtttc  | 2700 |
| ggctctgtgt  | cgcaggaggt  | ttacgtgtgc  | atcgaaaacg  | gtctgttcca | catggacgtc  | 2760 |
| gtagcatgct  | ggtggatctt  | ggccgtttcg  | ttctgtactg  | atcgccatac | gagcccacga  | 2820 |
| tctgagccca  | cagccagcga  | gcgcacggaa  | cttggtctatc | tccatgaagt | agttggatcc  | 2880 |
| tataccgaag  | tgaacttgat  | acgtgaagcg  | atttcctccn  | gcttgtagcc | ggcatcggtc  | 2940 |
| gcttgtccaa  | cagctctgcg  | ccccaaagcca | a           |            |             | 2971 |

## (2) INFORMATION FOR SEQ ID NO:472

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| ctgccgtcga | ctttagagga  | tccccggcag  | cgctcgcaaac | tgccggaaag | tcaaagtgc   | 60  |
| ctctcccca  | aaaccgagtt  | tcagccttgg  | gaaagttgaa  | tatcggttcg | accgagcatg  | 120 |
| caaaaagcaa | agaacgatta  | cggcacatag  | tcagtgtttt  | gaaagaagac | ttccatggct  | 180 |
| ttgcgacagg | ctcgatgggtg | cgcctgatct  | gaatacggta  | cttacctatg | ccttcccggtg | 240 |
| cgaatcgaat | atccctggat  | taacttcaaa  | ccgggttata  | cccagcaaca | gggtgggggtg | 300 |
| gagccaatgt | atggcaggcc  | ggtggtactg  | tttgcttcaa  | tgcgatggag | agaattttctc | 360 |
| tcacctgaat | acgcctatgc  | tcaacgtttc  | cgctatcaga  | acattgccat | cgttcgcttc  | 420 |
| gatggagtat | ctgattctct  | ctctcctgct  | tgattcggga  | aatcagaaca | ttgcctatcg  | 480 |
| tcgcttcgat | cccgtagcgc  | ggaaggaaatg | gccaatcaga  | ttatgataga | agcggccgaa  | 540 |
| cgttcaatat | gaagtcctac  | atgggaatct  | gctcgtgctt  | ttcctttact | tccggttact  | 600 |
|            |             |             |             |            |             | 601 |

## (2) INFORMATION FOR SEQ ID NO:473

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...970

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| cggggtcacca | accagcgcgga | acgattgctt  | tcgggcgaga  | actttccac  | ttcatatact  | 60  |
| cttgctgcac  | cagtaccatg  | accatacaaa  | tggcaaagcc  | gtaccgataa | tgccgataac  | 120 |
| gctgagcacc  | ggattctgcc  | ggatgattgc  | cacgattgtc  | tgatatactt | tttcattgtt  | 180 |
| tctgtctctt  | gtgcgggtatt | tcatgggatg  | cggaaggcgt  | ccgaatggga | agggggagaac | 240 |
| ctctgcccga  | gcctccggca  | ccatctttgc  | gatatgcttt  | ttctatcctt | ttggaggggcc | 300 |
| gaatcaaact  | atatactttg  | gtctgactaa  | actatatagt  | ttgtctgacc | gaactatata  | 360 |
| ctttgggtga  | accaaactat  | atactttggt  | ttgtcaaact  | atatagtttg | gttttagcccc | 420 |
| cttttgaggt  | cgattcgggc  | actctcaaga  | ctggtcatta  | aaaccctgta | tttcaattga  | 480 |
| ttaacctacc  | gatgcccgtc  | gaacattcgg  | atgggtccggc | tcgtctcccc | ggcttgcaat  | 540 |
| cgttgtgagt  | gaccatgacg  | atggtaagtt  | ccgtcctctg  | tattgagcga | tgaaggatac  | 600 |
| tcattacttc  | cgccccatt   | ttggaatcga  | ggttaccgta  | ggttcgtctg | cgaggataat  | 660 |
| ctcgggattg  | cctacaatgg  | cgcggggaatg | gccacgcgtt  | ggcattgacc | tccggagagc  | 720 |
| tgttggggat  | aatgggcagc  | cgatgcgtca  | tttccatgcg  | ctcgaggact | tcgtacgccg  | 780 |
| ccttctcctt  | ttactttcgc  | tcattgcggc  | atagaggagc  | ggcagcatgg | cgtgtccagc  | 840 |
| acgttgagcg  | tattgacgag  | atgaaaactc  | tgaaatacga  | atccagcttt | tcattgcgga  | 900 |
| aagcggccaa  | agccttgctg  | ttcatggagt  | gaccgtttgt  | ccgaggattt | gcaccgtccc  | 960 |
| cgtggttagga |             |             |             |            |             | 970 |

## (2) INFORMATION FOR SEQ ID NO:474

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...764

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| ttctataaaa | ccaagccacc | tttcatagaa | tatagcaagg | tctggctctt | atgatcagaa | 60 |
|------------|------------|------------|------------|------------|------------|----|



|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| ctagaaatga | ctttatctga  | tgctatatat  | tgggtaaatt | aaatctttca | tcaagtaacc | 120 |
| atagattatg | atcctcatat  | cggatttcct  | atcatcctta | atcataggaa | atattagggt | 180 |
| atgcatttca | ctttcttatg  | tgattttcca  | ccatctattc | ttttacgcaa | atcatcaaac | 240 |
| aattcattat | tctacgtctc  | tggaacaacat | aatgagccaa | atcattctta | gctgttctgt | 300 |
| tacatttttc | aagattttat  | ttgcttcac   | ttctagtgcg | ctacgcaact | ttcgtctccc | 360 |
| gatgagtatt | tatcttgcaa  | ttcctttaat  | gcacccctgc | attttgctct | ttgtcaaac  | 420 |
| ttattttttg | gaagcgcatt  | tcaaatcaaa  | ttctgaaact | cctattggaa | tagattccat | 480 |
| atctacgtct | tttaacaaagt | cttattccaa  | gggtgctgtg | tatatacata | atgttcgact | 540 |
| tttgcttctt | atcatttatat | cggttttcta  | tgtcttcgga | aaaatacgtt | taatggatta | 600 |
| atgaagtgtg | tttcattatt  | ggttctcaga  | taaatcaaat | aaaatgtcat | cttctttttc | 660 |
| caaaaatgga | aacccatctt  | ctttctgtgg  | tacnattttc | atctagatat | ttacccttgg | 720 |
| aacataccgc | ttttatcatg  | gtagtccttc  | tggagtcca  | tggt       |            | 764 |

## (2) INFORMATION FOR SEQ ID NO:475

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...598

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| caattctttg | atagctaaca | atgcgttcaa | atcatagaaa | tggcggattt  | agacgataag | 60  |
| gatgccaaag | gacctcgtc  | tatagagaat | cgaatgagga | aacagttttc  | tcgcacaagg | 120 |
| tttgtctaag | ggacaacaca | ttcaactaaa | aggttcaagg | tggtattgag  | tcaccacatc | 180 |
| ctccatattt | cgtttttcag | gtatgtgggt | acaaatggct | ctatcattct  | tttttcataa | 240 |
| ggaaaggatt | ggcaaagtcg | ctgatttcca | caacaattct | cgaaggaata  | ggattacaga | 300 |
| cacatctaaa | cccacctgag | catcatagga | gaaggcttgc | ttctatatatt | tgagcctttg | 360 |
| gatatatctg | aaaaggattt | atcctccgtc | aactggctgt | tacctctttc  | atcaagttgg | 420 |
| ataaaagcat | cttaacttga | tgccactcat | attctcactg | atgacagcaa  | agtccacatc | 480 |
| ctcagaaaac | gatcaatcaa | tagataagcc | ttggataaag | acgttccgcc  | cttaaatata | 540 |
| tttgctgact | ataagagctc | ttggataatg | cacgaagtat | ttctgagaat  | aatagtct   | 598 |

## (2) INFORMATION FOR SEQ ID NO:476

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

## (B) LOCATION 1...445

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gcgtagcccg | agtcgctgta | ggcgtagct  | cgacccccct | tcggcatatt | tccgaacggc | 60  |
| tataaaacaa | tgcgatttca | atccaggaaa | aatatgcata | tgctgtttat | cagcatattd | 120 |
| catttctcag | ttgaaagatt | tcagcttgag | aggcttcgac | atccgatgag | acttcaaact | 180 |
| ttttcccttt | catttttgat | cggttatagt | caatgcccc  | acaagagctt | gatcgataag | 240 |
| gcggccttat | gagaatcggc | accgtatcgc | ttacatcgaa | cacacgtaga | tttacgagga | 300 |
| taaatccgtc | aaattcttcg | aaaggtattg | gtcggaaaa  | aatgttttga | tggattctgt | 360 |
| tcttaaacga | cattgacagg | gtgaccggaa | ataaagcccg | aagattctcc | ttgatcgtcc | 420 |
| cgagaaaggc | gcaagcgccg | cgcaa      |            |            |            | 445 |

## (2) INFORMATION FOR SEQ ID NO:477

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...6819

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| cgagacggag  | agagactttc  | gaagaagttg  | ctgcagttcg  | tgcgtgacac  | cggttcgac   | 60   |
| gggtgggagc  | attcacctat  | tcgcacgaga  | gcggcaccac  | tgcgacaaga  | actatcaaga  | 120  |
| cgatataccc  | gaatccgtca  | aacaggacgt  | cttggcggaac | tgatggccgt  | gcaggaaacgt | 180  |
| atatccgccg  | ctcatcacgag | gcgaagatcg  | gcagccgcct  | gcattgtggtc | atagaccgtg  | 240  |
| cggaataggc  | ttctatgttg  | ggcgtagcga  | atagactctc  | cctgagggtcg | atccgaggta  | 300  |
| ctgatcccg   | tcgtctcccg  | tcaggagttg  | aatcccgggc  | ggtttatatg  | gcggaagtga  | 360  |
| ccggtgcaga  | gcctttcgat  | ctctatgcac  | gttagtggac  | tgataaacacc | cttcctaccg  | 420  |
| aaacccaaag  | cagaaccgga  | tatacaacag  | gaacttttga  | ttgcacagtt  | ggctacggct  | 480  |
| tcaggtgtcg  | tgtatcgacc  | tcgaacgaac  | tatggtctca  | ttactgtcgt  | ttgatgggga  | 540  |
| gttcctcacc  | aaaggagacg  | ctgtacggca  | agatggtatc  | ggcttgtgca  | ggctgtaaaa  | 600  |
| gcggatgaat  | atgtaggaat  | ccgtccggac  | ggctcactgt  | gctggtaccg  | ccgaggatag  | 660  |
| aactccggct  | cactctctcg  | ggcgccggc   | catccgagag  | acgatccctc  | atgctcttat  | 720  |
| agacttggtg  | ccctaacgga  | ggaagtccgtg | atgcgctggg  | ggaaggctat  | ccccgaactg  | 780  |
| ctttggagct  | tctccgaaga  | ggacaccccg  | tatcctggtc  | gcagttcgga  | cgctcgagcc  | 840  |
| gggtgaaagaa | ggcgatgctc  | tgacaggata  | ccgcttcac   | gcgaaggaga  | gttgtcggag  | 900  |
| ttgctcaaca  | gacctttctc  | catgttcccc  | cagtcgattt  | gttgccgacc  | ggagagatac  | 960  |
| ccgataccat  | tacccaaccg  | ttgtcgaaga  | aggggtttcg  | ttcgtttcat  | tgacgaaga   | 1020 |
| gagccaagag  | aagtcgcaga  | gcctcaagag  | atccccgtcc  | cagccgaaa   | cgataccgta  | 1080 |
| catcggtaga  | gacggaagat  | gatatacttc  | ctacacctgc  | cgaggagaag  | ccttgacgga  | 1140 |
| ggagccgctt  | cccgatacgg  | aggaggtatc  | acagccgcag  | cgaggagacc  | tttcgtcccg  | 1200 |
| atcgaagagc  | cggcagagaa  | gaaagaagga  | agcgaagag   | agcaggagac  | accgctattg  | 1260 |
| tcttcttagc  | agtctgatac  | tgggtgctac  | tgccgcatac  | ttgctactgt  | atcggatgcc  | 1320 |
| tgtctctcga  | caaaagagcc  | ggccccgaaa  | gaacctttcg  | gccggatgtc  | ttacccgtgg  | 1380 |
| atacgatcgn  | caagacggtc  | gatacggtaa  | agaccgtacc  | tccgcgacgg  | atctcggccg  | 1440 |
| gatcgttatc  | cgcaaggggg  | acatttttag  | cgtatcgctc  | tggagaagta  | tggcgaccgc  | 1500 |
| gtattctggg  | tctatatatt  | gaagagaaca  | aagagaaaa   | cgagatccc   | aacaacattc  | 1560 |
| ctttgggtcg  | gagctggtac  | ttcctttacc  | tgagaagtat  | gggatagatg  | cggccgaacg  | 1620 |
| gcttcgttga  | gaagagcttt  | ggctcttcag  | ttccgaatag  | gaatgggaaa  | gaacggcagt  | 1680 |
| agcgttgggg  | tttttcta    | tttgtggcca  | tgagcccaat  | atagatgtac  | aacagatcaa  | 1740 |
| acagcgtttc  | ggcatcatcg  | gtagagtccg  | ctgatggaa   | atgtcatacg  | agtggcagca  | 1800 |
| caggtggctc  | ctacgacatg  | tccgtcctcg  | tgacggggga  | gagcggttcg  | gggaaagagt  | 1860 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tctcccacag  | ataatccact  | actacagcgc  | cggaaacat   | catagctaca  | tgagtcfaat  | 1920 |
| tgccgagcca  | tcccgaagg   | aaccatcgat  | tccgagctgt  | cggacaccgc  | aaaggttcct  | 1980 |
| ttaccggagc  | cgtatcggat  | cgcaagggga  | cttcgaagaa  | gcatccggcg  | gcacgatctt  | 2040 |
| tctggacgaa  | gtgggcgact  | gcctttgccc  | acgcaggcga  | ggctgctgag  | ggtgctggag  | 2100 |
| acgggcggtt  | catccccgta  | ggagccagcc  | agtcgcagaa  | gacggatgtc  | cgtatctagc  | 2160 |
| ggcgacgaat  | gtgaacctca  | aggaggcggt  | agcgaacggg  | aagttcggga  | agacctcttc  | 2220 |
| ttccggctca  | atacgggtacc | gacgcaggtg  | cctggctgcg  | tatgcgaccg  | gacgacgtgc  | 2280 |
| ccttgctttt  | tcgccgattc  | gccccgacag  | cgccgagaag  | tatcggtatgc | ctccgctgcg  | 2340 |
| cctatcggac  | gagcccgtag  | catattaatg  | cgttaccgct  | ggcccgcaaa  | tgtgcgagag  | 2400 |
| cgcgcaatat  | aaccgacagg  | ctgagcatcc  | tggaggagga  | gcggacggta  | cggcagagac  | 2460 |
| catcactcgc  | tacctggacg  | ctgaggggat  | gcaagacctc  | accccgctcgt | gatccgacgg  | 2520 |
| aacgaaacga  | ccgaagcggg  | caaacaaacc  | cccattacga  | gcgcgaaatc  | atctaccagg  | 2580 |
| tgctatacga  | tatgaagaag  | agatagccga  | tttgaagggg  | atgatgaacc  | gcctgcgcga  | 2640 |
| ccacgcagcg  | cctcatggcc  | tgtagggtcg  | gacgtctggg  | gcaacgacga  | caagccaccg  | 2700 |
| cagatccgaa  | gtggggcgctc | agcacgcaca  | aggcccccac  | cgcgacgcgg  | cagaaccctg  | 2760 |
| ggagccgata  | caggaagcca  | gcgaatacac  | cgagatccgg  | tttcgctgga  | ggaggtagag  | 2820 |
| aagaaaatga  | tttcccttgc  | atggaacgcc  | acggcggaag  | gcgcaagcag  | acagccgagg  | 2880 |
| aactgaagat  | tcggagcggg  | cactataaccg | taaaatcaag  | gagtatggac  | tggaatagaa  | 2940 |
| cctcggggcg  | tacagccttt  | ccgctcttgc  | ggcgggtgct  | atcgtcctgt  | gacctgctcg  | 3000 |
| gcatgcagca  | tctcctacag  | cttcaacggg  | ggtgctctga  | ctatagccgc  | atcaaaacgc  | 3060 |
| tttatatgcc  | ggatgtgacc  | aatcaggcac  | ccgcgtatat  | cccccgcttg  | cgcagactat  | 3120 |
| gaccgaagcc  | ctccaaacca  | ttttacgcgc  | cgtaccaagc  | tcgaaatggc  | acgaaccaac  | 3180 |
| gatgcgacat  | gatcatcgag  | gtggtcatca  | ctaattacga  | cttcgctccc  | ctcgcgtaca  | 3240 |
| ggacaacgat  | ctggccgcac  | gcaccaaggt  | aaccttatcc  | ataaggtgca  | ctacgagaac  | 3300 |
| aaggcctccc  | gaacagaact  | tcgatcggga  | cttacgtctt  | ccacggactt  | cgacagcagc  | 3360 |
| gagcagctgg  | tggagctaca  | aacgccttgc  | tggccaatat  | ggtcgacgac  | ttggtgaagc  | 3420 |
| aggtgtataa  | gctacggtag  | agaactggta  | atcctccccc  | accatgacga  | ctaacgatcg  | 3480 |
| tacgcctaca  | tggagcacc   | ctcgcygtt   | tcggctgaca  | cgctgccag   | atgaaagccc  | 3540 |
| tgtacgaggc  | ctatccctac  | tgtctccact  | tcgtcttcta  | tacctatata  | atatgtatgt  | 3600 |
| ggtgcaggac  | gtgcgctatg  | cttcgggctg  | cgccggctgg  | cacctatct   | gccggacagg  | 3660 |
| cgcaagctgt  | acctgtcgtg  | gagcaatata  | cgcattccgga | gcagctgcaa  | cccgcctcgg  | 3720 |
| ccgaaaggag  | ccggagccct  | tctcgtctat  | cgatgacttc  | ctcgacgaaa  | tgaccgaagc  | 3780 |
| ggagccgacc  | tgccctcggg  | gattttcttac | ggagggagcga | gcgtatcccc  | tcggcttcgg  | 3840 |
| actacttcgc  | cgccacgtca  | ccggccgatc  | agccgaaccg  | tccgcagca   | tgccggtctt  | 3900 |
| gtccgtgcag  | gcagccggca  | accggccgag  | agcgcacctc  | cggcagcgaa  | agatccggcc  | 3960 |
| ccgatcggcc  | ggcgagcag   | ctggacgaag  | ggctcttcac  | cgagaccctc  | gcacgtatta  | 4020 |
| catcaagcag  | ggacgttacg  | ataaggcact  | gaggataata  | aagaccacag  | tttgaattat  | 4080 |
| ccggaaaaaa  | acctttactt  | tgcggatcaa  | attcgatctt  | agaaaagtgt  | attattaacg  | 4140 |
| acaaaaacaa  | aatataaaga  | tgtactcgta  | ctgactattc  | tcattcctgct | catatcgctc  | 4200 |
| ttccttattc  | tgggtgtagt  | gtacagaact  | ccaaaggggg  | cggcttgga   | gcccggcttcg | 4260 |
| catcagcaat  | cagatcatgg  | gcgtccgcaa  | gactaccgat  | ttcctcgaga  | agccacttgg  | 4320 |
| tggtcggccg  | gtatcattgc  | cgttctggcc  | atcgtttcta  | ccacttcctc  | cacacgggaa  | 4380 |
| aggtcgatga  | gagccaaaac  | gtcctgaagg  | aaccctggac  | aagaagggtga | aggaagaaaa  | 4440 |
| gaactctgca  | gtgatcaact  | cgggtggagat | gccgctgcta  | cggaaatctgc | ccggcccgcg  | 4500 |
| accggagagc  | catcccgag   | gaggggcagg  | cacaataagg  | aggaccggcc  | ccttccaatc  | 4560 |
| ccttgacgga  | gatacgggga  | tcgacagacg  | tctttgtctt  | tgagccaggc  | ttgagggcaa  | 4620 |
| agacgttttg  | tttggcaggg  | tgccgctcgc  | cgcacccccg  | ggacaaggct  | caaggggcgg  | 4680 |
| aacggacaga  | gcctccgagg  | gggtcgacaa  | gcccttgcca  | acggaacgga  | cggacgtacc  | 4740 |
| cgaaaaaacg  | tctgacgttc  | cgacaaaaac  | gtctagacgt  | tttgactgaa  | acgtctagac  | 4800 |
| gttcgaagca  | aacgtctaga  | cgtttttcgc  | gaaaggtcta  | gacgttttga  | cgaccgcacc  | 4860 |
| ttttggcaga  | agacaagaga  | gatgacaaag  | agactattcc  | gcccgaatgg  | gcaccgcaag  | 4920 |
| aggccgtaca  | attgacctgg  | cctcacgacg  | aaccgactgg  | gcttatatgc  | tcgacgaggt  | 4980 |
| ggaaacctgc  | ttcgtccgat  | agccaccgcc  | atactccgcc  | acgagcgact  | gatagtcggt  | 5040 |
| tgccccgctg  | caagcgggtg  | ttcggcctgc  | tgccctccga  | gctgcaccac  | cggctcactg  | 5100 |
| cttcgagctg  | ccctcgaaac  | atacatgggc  | gcgcgaccac  | ggaggatttc  | cctcctcgcc  | 5160 |
| gacggccgctc | cgatgatagc  | cgacttcgcc  | ttcacggctg  | gggcatgaag  | tttgccgccc  | 5220 |
| atcacgacaa  | cctcatcacg  | agaggtccca  | cgccttgggc  | ctggttcgcg  | aaggagttac  | 5280 |
| cctggacaat  | cgtctgcctt  | cgctctcgaa  | ggaggagcac  | tggagacgga  | tggcgaaggt  | 5340 |
| atttgctgac  | cacggacagc  | tgccctcttc  | agccgaaccg  | caatgccggc  | tgagccgcac  | 5400 |
| ggccattatc  | gacacgctga  | aagagagcct  | cggcgtcagc  | gcgtactctc  | cctccgccac  | 5460 |
| ggagcccttg  | ccggcgacga  | caccgacggc  | acatcgacac  | gttgccgcgg  | ttcgtcgaca  | 5520 |
| cccgtaccat  | cgtctatttc  | gctcggaaga  | tccttcggac  | gagcactact  | ccgacctcac  | 5580 |
| ggccatgagc  | aggagctgaa  | ggagctgcgc  | cgcccgagac  | gacagccgta  | ccggccgtgc  | 5640 |
| cgctgccccat | ggcggaagct  | ctgtacgacg  | gagcggacag  | gctgccgcca  | cctatgccaa  | 5700 |
| cttcctcatc  | atcaacgggg  | cagtactcgt  | gccacctacg  | attcgcacct  | cgatgccgtc  | 5760 |
| gccctctcgg  | tgatgcaggg  | gcgtttcccg  | atagagaggt  | catcggcac   | gactgccgtc  | 5820 |
| cgctcgtcaa  | gagcatggca  | gtctccactg  | cgtcacgatg  | oagtaacccc  | aaggattcat  | 5880 |
| cgctaattcc  | acagcaaaga  | actatgaaag  | tagcactcat  | tcagcaagca  | acacggcgga  | 5940 |

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| cgtctgctcg | aaccgggagc  | ggctggcagc | gaagatcccc  | aagccgcccc  | acgcggtgcc  | 6000 |
| gagctggctg | tactccccga  | actgcacacg | ggctttatth  | ctgccagacg  | gaagacgtgc  | 6060 |
| aggtgttcga | ccgggcgaga  | ccatccccgg | accgagtacc  | gatttcttcg  | gcaccatcgc  | 6120 |
| ccgcgagccg | gcgtcgtgct  | ggtgctctcc | ctcttcgaga  | agcgcgctcc  | cgggtttacc  | 6180 |
| acaatacggc | cgctcgtgctg | gagcgggacg | gcactatcgc  | aggaagtatc  | gcaagatgca  | 6240 |
| catccccgat | gaccctgcct  | attacgaaaa | gtctatthca  | cacccgccga  | cttgggctth  | 6300 |
| acccccatcc | cgacgtccgt  | cgatgcctcg | gcgtactggt  | ttgctgggat  | cagtgggtatc | 6360 |
| ccgaagcggc | cgactgatgg  | ccatgcaggg | tgccgatata  | ctcattthacc | ccacggccac  | 6420 |
| ggtaccgaga | gtacggacct  | gcctgccgag | cagctccgcc  | aacgtcagcg  | tggcagatcg  | 6480 |
| tacagcgcg  | acatgccgtg  | gccaacggta | ttccccgtgtg | gcggtgaaca  | gggtcggcca  | 6540 |
| cgaggcagac | ccttcaggcc  | gcaccgtggc | atcacgttct  | ggggctccgg  | attcgtagcc  | 6600 |
| ggaccgcagg | gcgaatgctg  | gccgagctga | gcgcaacgga  | agaggcggtg  | gaggtagtgg  | 6660 |
| atatgatccc | tcccgaaccg  | agcaggtgcg | ccgctggtgg  | ccgtcttccg  | ggacggcgga  | 6720 |
| tcgacgctth | ctccggcctt  | acgganagtt | tccttcgctg  | ctaccatcat  | ggcgagaggg  | 6780 |
| gggatggcgt | tccgtccctt  | ccccctccga | caggagccg   |             |             | 6819 |

## (2) INFORMATION FOR SEQ ID NO:478

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...724

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| ggtgccttga | tttccgtttc  | ggcaacgccg | ccatgcaatt  | tgagcgcgcc | agcgtggcca  | 60  |
| cgaggacggt | aagcttgggt  | gcgacaccca | tttcccgaa   | ttgatgtcaa | ggaatttttc  | 120 |
| tgcacccaga | tctgcaccga  | aaccggctcg | gtgacggcat  | attcgccgaa | agagagagcc  | 180 |
| atctttgttg | ccaagaggag  | ttacagccat | gtgcgatatt  | ggcaaagggg | cctccatgta  | 240 |
| caaataccga | gtgtgctctg  | tggctgttac | cagattagcc  | tttatggcat | cttttagcaag | 300 |
| acggcaatgg | atcctgctat  | gccgaggtct | ttgaccgtaa  | aggagcacct | tctttggtat  | 360 |
| agccgagaag | aataattttca | agacggctgc | gggggtcttca | aagtcttttg | ccagacagag  | 420 |
| gatagccatg | atctcggaag  | cggcgtaatg | tcaaaacccg  | tctggcgagg | tattccgtcc  | 480 |
| gagatggtac | caaccccgta  | acggcattgc | gcaaagagcg  | gtcgtaaacg | tccagtacag  | 540 |
| cttccaaagt | atttcggaga  | ggccgtcgca | agtattgcg   | ttctgataat | atagttctcc  | 600 |
| aaaagagccg | taatcatggt  | gtgagccgaa | atgacagatg  | gaaatcaccg | gtgaagtggg  | 660 |
| ggttgatggt | ctccatgggc  | agtaccgtgc | atagccacct  | tcggcagccc | ccctttcata  | 720 |
| ccga       |             |            |             |            |             | 724 |

## (2) INFORMATION FOR SEQ ID NO:479

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...390

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gcatccaaaa | taattttaat | caaaagtaaa | agatgaaatg | cttctttatg | ccctgattgg | 60  |
| gctgttggtc | agtctgaata | catatgctca | gcttccggcg | ttagtgtgaa | aaatatcgaa | 120 |
| ggaaaaacgg | tacagaccaa | caagttgaga | atgccggaaa | gccgatgac  | atcagctttt | 180 |
| ttgctacgaa | ctgcaacctt | gtttgcgcga | gctgaaagcc | attcaggagg | tatatgcaga | 240 |
| ttggcggacg | agacgggcgt | aaggcttata | gctgtatcta | tcgatgaggg | gcaaatgcac | 300 |
| agaaggtgaa | acctctggct | gacggcaacg | gctgggaata | cgagtgtctc | tcgacagcaa | 360 |
| cggtgatttc | aaacgtgcca | tgaacgtgac |            |            |            | 390 |

## (2) INFORMATION FOR SEQ ID NO:480

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 882 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...882

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gcggacattt | gcttctggct | gcggtggata | cggcttttta | tttggtagag | agcgcaaaca  | 60  |
| ggccgatcgt | actccgatca | atgaccgctt | gcacaggcca | ataccgaatt | ggaggctttt  | 120 |
| ctaagtcgct | attagtcggg | agagaggcta | ctatcgtttt | ttcttctcat | tcctttccatc | 180 |
| ctttgtttct | ttcctttctt | cgaggctctt | gccgtgatcg | gccttggaca | cgtgtgttgt  | 240 |
| aatacgctac | ttactaattt | caaagaatac | aaacagaaat | gggaatagga | acactttatt  | 300 |
| atttactttt | ttggggcttg | tagccggtgc | cactgccgta | tggtagtcac | gcggacactg  | 360 |
| ctcaagcaaa | ggacagaggg | gattctcgcc | gagctcgccg | tgaagccgag | gtaatcaagc  | 420 |
| agaagaagct | cctcgaagtg | aagagaaatt | tctccaactg | aaaggcgacc | tggaaaagca  | 480 |
| ggtggcacag | gcaatagcaa | gctccaatcg | gtggagagca | aactcaaaag | ccgcgaacaa  | 540 |
| ccctcaacca | acgtcaggaa | gatataacga | agaaggggca | ggaaatggtt | tgatgccgtg  | 600 |
| agaatctgac | tgctcaactc | tctgtgattg | aaaagaaaag | acggaactcg | acgagctgaa  | 660 |
| aactcgcgaa | caggetcatc | tggagtcttg | agcggactct | ccgctgccga | ggctaaagac  | 720 |
| agactggtgg | aaagctcaaa | gatgaagcca | aaggacaagc | ctctgcatac | gtcaatgaga  | 780 |
| ttatgaagag | gccaaagatg | ctgccaacaa | agaggccaag | cgaatcgta  | tccatccatc  | 840 |
| cagcgcgtgg | ctacggaaac | ggctatcgaa | aactccgtga | cc         |             | 882 |

## (2) INFORMATION FOR SEQ ID NO:481

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ggcttcaagt  | cgcgatcaga | catgatggct | ccttcgagtg | caaatgccca | tcgaagattt | 60  |
| tgatgcggca  | gcgatcatat | tcgcccaca  | aagtcttgct | tcatccaacg | tagctttgtg | 120 |
| ctcgggaaaag | tgggacataa | gtccgggacc | cttcgatcgt | accggtagcg | tatgtacttg | 180 |
| gaccaatcct  | tacgctgctc | ttgatttcga | tcggttgccg | cacaagagaa | agagaattat | 240 |
| caccccttca  | ccctctttct | ccaagacctt | agcatggaca | gccagcgaga | attgttctcc | 300 |
| tcatccaata  | tgctgctatg | tttttcaagt | ccgggcagaa | tatctcttct | ctatcgggtc | 360 |
| atcatcttgt  | ntgatggcca | tcagcatagc | cgctcgtctc | ttgcacgagg | cggagcataa | 420 |
| nttcacggt   | tcattgcggc | tcggtgaaag | ctccgttgga | tgtcggcagc | caagtcagga | 480 |
| gggacaggc   |            |            |            |            |            | 489 |

(2) INFORMATION FOR SEQ ID NO:482

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| agtattctcc | gcaggaacaa | gtatttttag | gggcacccct | gaaaagggtga | agcaccgctt | 60  |
| atgtatggag | atcgtgaggt | atggggtatg | gctcgtgcag | cgaggatttc  | ttttttatac | 120 |
| ttcccgttac | ggatgacctc | actcccggct | tttctataac | cgtcttacaa  | acgaaccctg | 180 |
| ctttgtgtca | gaccaagaat | aactgagtat | ttcaaattcg | ctcaagaagg  | tgattacatt | 240 |
| gaagtgaagg | aagctctgta | ttcatggcga | atcttttgta | ctatcgtttt  | ttccgacaag | 300 |
| aattacctnc | tataatgctc | ccattgaagg | tgttgcgagc | aagcgggaaa  |            | 350 |

(2) INFORMATION FOR SEQ ID NO:483

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ggaaaaaattt | ctgacgaatt | tgagttggag | tccggacgaa | aatatcttga | tgtagctgag | 60  |
| gtgaatcgtg  | ctcaaaacga | atgtgaggta | aatgcctaga | cgctgagacc | ggtagattcg | 120 |
| tccgtacgct  | ttttgttgaa | accgataaca | ttatgtagag | ccgttacatc | ccctgacatt | 180 |
| ccttccggga  | agtaacatca | gttcatttgg | cagagccgtc | gcgacggatg | gaaccatctc | 240 |
| tatcttatga  | tactacaggt | cgtctgatcc | gtcaggtgac | aaaaggggag | tgggggttac | 300 |
| aaactttgca  | ggcttcgac  | ccaagggaac | acggctctat | ttcaaagtac | cgaagccagc | 360 |
| cctctcgaac  | gccattttta | ct         |            |            |            | 382 |

(2) INFORMATION FOR SEQ ID NO:484

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| ttttccaaag | agcggttcga | atacaccgcc | ggtggcatcg | aagcatgccc  | atagaggata | 60  |
| gtatcttcgg | tgtggaagta | ttcggcaatg | gctttctcaa | ttctttgtgg  | atgtcttgcg | 120 |
| ttccgcaaat | gaagcgtacg | gagctcacc  | gaatccacgc | tcattccatcg | catccttggc | 180 |
| agcctgtatc | agccgaggtg | atcggacaga | ccgagatagt | tgttggcaca  | aaagttcaat | 240 |
| acctctggcc | ttcgtttacg | cggatgtcag | cacgctgggg | ggtgatgatg  | atccttcttt | 300 |
| cttgtacaga | ccggcttctt | cgatactctt | gagttcggca | gccagtagtc  | tttcattcct | 360 |
| ttgtacatag | cactggagtt | ttttaggt   |            |             |            | 388 |

(2) INFORMATION FOR SEQ ID NO:485

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 651 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| atggaatata | tgatagcctc  | gatgctcttg | aaggcatcgt  | cgtctatgtg  | atataccttga | 60  |
| tggcctttcc | cactcccggg  | atcatggatg | caagctcttg  | aggttaccca  | tctttttgat  | 120 |
| ctgatgtatc | tgggcaagga  | agtcattaag | tcgaactgat  | tcttggctat  | tttctcctcc  | 180 |
| agtttgcgag | cttcccttcg  | tcgtattgct | cctgagcacg  | ctccacaagc  | gatacgaatg  | 240 |
| ccccctgcc  | aggatacggg  | cggccatacg | ctcgggggtga | aaagcatcga  | ttgctccatc  | 300 |
| ttctccccc  | taccgacgaa  | cttgatgggc | ttgtttacga  | ccgacggatc  | gagagggcgg  | 360 |
| caccgcccc  | ggatatctcca | tcgagcttgg | taggacaaca  | ccgtcgaaat  | ccaagcgtgt  | 420 |
| attgaactcc | ttggctgtat  | tacggcgctc | tgaccgggtca | tcgagtccac  | cacgaaaagg  | 480 |
| acttcgttcg | ctggatggca  | gccttgatgg | cctctatctc  | gcgcatcatt  | tcttcgtcgt  | 540 |
| ggccaaacga | cccgcgggtg  | cgatgatgac | aacgtcgttc  | cccttggttt  | ggcttcggct  | 600 |
| atggcgtgtc | gggctattct  | cggaccggct | ttttgctgcc  | cggttcgtctg | t           | 651 |

## (2) INFORMATION FOR SEQ ID NO:486

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2626 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2626

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| gtcaaacctt  | ccttgatctt  | cgtaccatca  | cgatacaccg | tgtaggtata  | tcggtcgggg  | 60   |
| tggggctgcc  | acccatggtg  | aactgaatat  | catccaaaga | atgtagttca  | aatccgagca  | 120  |
| attgtagtga  | cggaaagcaa  | catacttggtg | cccgaggga  | aatctaccgt  | acgctcgatc  | 180  |
| catacacttt  | gaggttggcg  | ccattggctt  | ccgtggaaag | accgaatctt  | gctccgccct  | 240  |
| tattttttccg | ttaggcggtt  | cttcgaaaaac | gaccgtgaag | tctccggcgt  | tcgtcccgtc  | 300  |
| ttggagatca  | tcaccgcata  | gtgatccccg  | ggaaaaccgt | cgtgactgca  | tagtagtact  | 360  |
| ttaccttcgt  | tgcgcctgta  | acatcctttg  | agtgaagatg | ttatcaggat  | tcaaagccat  | 420  |
| tccattccat  | gagaaagagg  | cactacgttg  | gtgccgccat | gagctgtcag  | ccatcccaat  | 480  |
| tgtccggaag  | cagacagagc  | caaccctgac  | catcgccatc | ggcatcgata  | gtagtccatc  | 540  |
| cgctggtgcc  | tctccatgag  | tagaagactc  | gaacgtttcc | gtgaagtcgc  | gcgcttgccg  | 600  |
| ttggccttga  | tctcaacatc  | atcgaggttg  | atccagagaa | gtccgtacag  | ccgaagtgac  | 660  |
| ggaaggcaac  | atacttagta  | cccgcagcaa  | ctgtaccgtc | ttttgatacc  | agggtgccctg | 720  |
| aacacgagtg  | ccacgatggc  | ttccggtgcc  | gtaacaactg | tcttggccgt  | cagcacttct  | 780  |
| tccacaaagc  | ttggcggaag  | ttggaagcgt  | cgttaccctg | agaagatgca  | taccggcata  | 840  |
| gtgctctgat  | gcataattgg  | catcttgctg  | acatacccag | aagtaagcgt  | tcctccgtta  | 900  |
| ggaagagaaa  | gctccggtgt  | aaccagatag  | tatcagggtt | ctgagggcct  | tcaaagttaga | 960  |
| tataagaagc  | cgaagagaca  | agatcgact   | gttgtagcct | gcaaaagagg  | agcctccggg  | 1020 |
| aggaggggtg  | tcgtccaatt  | gttgccgtca  | ccgtctgcat | cgatcgctct  | ccatgaggag  | 1080 |
| gaataccatt  | ttcgaaggat  | tcgttcagaa  | cttcgcgacg | cttagatccg  | gtgcattcca  | 1140 |
| tttaaggatt  | gcattccatg  | tgttaggagc  | ttgttcgccg | tcagggttctg | tacaggattg  | 1200 |
| aactgtgtcg  | gattaatatg  | tacgttacgc  | actctttcgg | agatacgccg  | gctgtgtact  | 1260 |
| tcacttccac  | gcaaaactcat | gattgcccgt  | agctacgccg | tcttcttcga  | aggtcgtttc  | 1320 |
| ggtaaaccctt | ccttgatctt  | cgtaccatca  | cgatacaccg | tgtaggtata  | atggtcgggg  | 1380 |
| tggggctgcc  | acccatggtg  | aactgaatat  | catccaaag  | atgtagttca  | aatccgagca  | 1440 |
| attgtagtga  | cggaaagcaa  | catacttcgt  | cccgaggga  | aatctaccgt  | acgctcgatc  | 1500 |



|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| catacacttt  | gaggtttggg  | ccattggcctt | ccgtggaaag  | accgaatctt | gctccgcctt | 1560 |
| tattttattcg | ttaggcgttt  | cttcgaaaac  | aaccgtgaag  | tctccggcgt | tctgtccgtc | 1620 |
| ttggagatca  | tcaccgcata  | gtgatccccg  | ggaaaaccgt  | cgttgatgca | tagtagtact | 1680 |
| ttacccttcgt | tgcgcctgta  | acatcccttg  | agatggatag  | ttatcaggat | tcaaagccat | 1740 |
| tccattccat  | gagaaagagc  | ttacacgttg  | gtgccgccat  | gagctgtcag | ccagtccaat | 1800 |
| tgctccggaag | acaacagagc  | caaccctgac  | catcgccatc  | ggcatcgata | gtagtccatt | 1860 |
| ccctggtgcc  | tctccatgag  | tagaagactc  | gaacgtttcc  | gtgaagtctg | ccgcttgcca | 1920 |
| ttggccttga  | tctcaacctc  | atcaaggctc  | atgtagaaca  | atccgtgctt | tggaagtgc  | 1980 |
| ggaaagcaac  | atatttcgta  | cctgcgggag  | gtctaccgtc  | ttctggcgcc | aagtaccctg | 2040 |
| tatacgacca  | cgaatagctc  | cggcgagcga  | acaccttttg  | ccgtaatcgt | ctcttccaac | 2100 |
| aaagcatcgt  | ggaagtggat  | gcatcgttac  | cggctcgaaga | tgcatacacc | gcataggctc | 2160 |
| ggatgcataa  | ttagcatcct  | gtgcgcatac  | ccagaaagtc  | aacttcctcc | gttaggcaaa | 2220 |
| tccaatgccg  | gtgttatcag  | atagttgtca  | ggggaagaac  | tcctatacca | ccaagaccga | 2280 |
| atgactctga  | atatacacia  | ccatgctatt  | gtagccagcg  | attccgggag | catttccagg | 2340 |
| cttccagcca  | tgccgtcacc  | gtctgcatcg  | atcgtcttcc  | atgaggcagg | aataccattt | 2400 |
| tgaatgattc  | ggaaagtgtg  | gttgttccgg  | gattcggatt  | tggtatcgga | ttggatttgg | 2460 |
| attcgggggt  | ccattagggtg | catcccactt  | aagcgttact  | tctggccgac | tgactaccg  | 2520 |
| gtcagggttct | gtacaggagc  | aaattcatgg  | atccttctac  | cgtaacgtct | ttacatacct | 2580 |
| tcggagatac  | gccggccttg  | acttaacttc  | cacgcaatac  | tcatga     |            | 2626 |

## (2) INFORMATION FOR SEQ ID NO:487

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| atataaatgt  | ttcgtccaaa | cctaagaggg | ctgcagtacg | ggcacggttc | gctgtagtgtg | 60  |
| ttcgtagcgg  | agattctgaa | ccacagccag | attgtgcttt | ttttgaacaa | acctatctcg  | 120 |
| tatgccactt  | gcatccgcgg | agctagcatt | ccactatact | ctcatctatc | tgatcaatct  | 180 |
| gcatgcgcca  | agagatagct | cttcgtcttg | cttttcggat | tgccgccttg | ggatacgcag  | 240 |
| tcgccgagga  | tttgggcaag | tacagtaggt | gttatctgct | ggcttgcatc | gcttgagcct  | 300 |
| tatccgggca  | gcaatgcgac | tcgataatta | gcccgtcgaa | attatttcca | tggttggctg  | 360 |
| gctgacggat  | tcgatccgat | ctctctgtcc | cgaatatgac | tcggatcaca | aaggatggtt  | 420 |
| aacgaaggaa  | aacgtctttt | caatcgaagg | gaatctgcca | atgtggagga | ttgcgaaacg  | 480 |
| tcttggtcgc  | taggtactga | atcctctatg | gatggctccg | atctgtcgaa | ctccggactc  | 540 |
| cgaagccgtt  | ctagggtctc | tgtccacaga | tccaaatcgg | gactgatcga | ttcttgacga  | 600 |
| ggacaatcac  | cgattcgtcc | ttgcctatcg | tatcggcatt | tcttgtacag | caaagggatt  | 660 |
| ggatgtggtt  | cgtgcaccta | accagatatt | ctgataccgg | cttgcatggc | ttgctctacg  | 720 |
| tggttcgcgag | tagcccttcc | gtggtagcaa | gcatatccaa | ttcatcctgt | acacgcacca  | 780 |
| accaggtagc  | cctgtttctn | ctactncttc | gaagcacecc | ggcaaggtag | gag         | 833 |

## (2) INFORMATION FOR SEQ ID NO:488

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

|            |             |            |            |             |             |      |
|------------|-------------|------------|------------|-------------|-------------|------|
| tgccaaagcg | atttcccatg  | gatttcggaa | acgatcgcg  | gattcgacga  | tttcgtgctt  | 60   |
| ggaatagttc | ggtggacagg  | aggcaaacca | ccggtaattc | accggctttt  | cccactgac   | 120  |
| gaggaatctt | cacccaaaatc | tgcgcaattt | gactgtgtcg | ccatcgctct  | tcacaacgtg  | 180  |
| ggcaccatc  | gggagatata  | gttcttgagc | atctctccat | tctcgtctat  | tattcgagca  | 240  |
| taggggccat | cgtcttatcc  | ttggattcga | tgataatctt | ttctttcaga  | ccggcgctct  | 300  |
| gtcgctttcc | atcttgaaag  | ttacattctc | cactacacct | tcgaagagag  | tgttcctgct  | 360  |
| acttccgata | cgatgaccgc  | attgaacgga | tccattcgat | gattttgtca  | cctttcttga  | 420  |
| ctgcatcacc | ttggcggaag  | acaattttgc | accgtagggg | atattgtgat  | tggccaaaat  | 480  |
| gataccggta | tccggtcggc  | aatacgcaat | tcagtcaccc | gactcactac  | gacctgatgg  | 540  |
| attcgtctgt | tacatccaca  | gcacgtagtt | cctcgaattc | caagatacat  | catatttgga  | 600  |
| gagcaagcta | ttctccgttg  | ccacattgga | tgcgatactc | cgacgtggaa  | tgttcggaga  | 660  |
| gtaagctgtg | tacccggttc  | tccaatgact | gagctgcaat | aacgcctacg  | acctcacccc  | 720  |
| gttgtagcat | gcggtggtag  | caagatttct | accatagcac | ttggcacata  | ctcctttctt  | 780  |
| ggatcgagc  | tgagaacaga  | acggatttca | acagcttcga | taggtgaatc  | ttcataatct  | 840  |
| gtgctgcctg | ctctctgac   | tcttctccag | ctctaacgat | taatccccctg | tagtaggatg  | 900  |
| gataatatcg | tgaacagaga  | cgcgcccagg | gtacgttcgt | acaaggaagc  | aacgacatct  | 960  |
| tctgttttgc | ttagctcgtg  | gtaagcagtc | cgcgtagcgt | gccacaatct  | tcctctgtga  | 1020 |
| taataacatg | tgagaaaacgt | ccacaagacg | acgggtgaga | taaccagcat  | ctgccgtttc  | 1080 |
| aatgcgggat | cggcaagccc  | cttacgtgca | ccatgagtag | aaataaatat  | tcaagtaccg  | 1140 |
| agagtccttc | cttgaagttt  | gaaagaatgg | ggttttaata | atctgacctc  | cttcggctcc  | 1200 |
| actcttttgg | ggcttgggcca | tcaatcacgc | atacctgaca | actgacgaat  | ctgttccttg  | 1260 |
| gaaccacgtg | ctccgaatcc  | atcatcatga | agacagagtt | gaatccgtca  | ttgtctgaac  | 1320 |
| tgattgcttg | atcagaacat  | ttgacaaacg | gccattgata | tggtgtccatg | tgcgataatc  | 1380 |
| tgattgtatc | gttcattaaa  | ggtgatgaat | cccatatcgt | atcttgcata  | atctgctcga  | 1440 |
| cggcagtgta | accttcttgg  | atcaattggt | tttctcatca | ggaataagca  | catctgccaa  | 1500 |
| gttgaaagac | aagccaccct  | aaaagccatg | tagtaaccca | aattcttgat  | atcatccaag  | 1560 |
| aatttggcgt | tgtagctact  | ccgcagatct | tgattacgct | accgataata  | tctcgtaagc  | 1620 |
| ttttttcccg | agtacttcat  | tgacatagcc | taccttcttc | ggtacaattc  | gtttaccatc  | 1680 |
| agtcgcccta | cggatgtctc  | taccatacga | cgaacagttc | tccgtttctg  | taatcctcta  | 1740 |
| catagacctt | aatcggcgca  | tgaaatcgac | ttaccctcg  | ttataggcta  | ttgtcgcttc  | 1800 |
| ttcagggcca | tagaaatcag  | gccgtgccc  | ttggtattgg | gacgtagctt  | ggtaataata  | 1860 |
| taagtcccaa | taccatatcc  | tgtgaaggaa | cggtaatcgg | tgctccattg  | gaggggttaag | 1920 |
| aatgttatgt | gaagccaaca  | taagcaattg | cgcctcaaga | tagcttcggt  | gctcagagga  | 1980 |
| aggtgtacag | ccatttggtc  | tccatcgaat | ccgcattaaa | tgagtagaaa  | ctcaatggat  | 2040 |
| gcaactgtat | tgcttttctt  | ctatcagttt | gggttggaat | gcttgaatac  | ctagtcgggtg | 2100 |
| aagagtcgtg | cacggttcag  | aaggac     |            |             |             | 2126 |

(2) INFORMATION FOR SEQ ID NO:489

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 940 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...940

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| acagcagttt | atgatcagcc | ggaagctgca | tgcttcgccc  | ttttctccgc  | cctcttccgt | 60  |
| ctgttggtc  | tcttcgccct | cctttttggt | gccaatgctt  | gataacctcat | gtcgattctc | 120 |
| cctggctcga | tataccctt  | cgttccaccc | catcgagta   | ggggcacttg  | tggcagtcta | 180 |
| tgccatgcgc | ctgtctccga | gttcaataga | gccatagaca  | aatatctccg  | tcgccgatga | 240 |
| gcctatacgt | cgattctctt | ctcgcttcta | tgccctccgc  | tcccaaaccg  | atgcgtatat | 300 |
| catcacagag | ggaaaacgac | gcctgcgcgc | cctaaccgta  | gagctcggct  | catttgcgaa | 360 |
| gcacagcagc | gcaacgatga | gctaaaaaag | aactatgcgg  | caaggaaacc  | atcaatgtcg | 420 |
| tattccttgc | cgtgtacgat | tcatgtggaa | atacgatgcc  | ctgtttgctg  | ccatgctccg | 480 |
| gcatccgcgt | ttcggcctgt | actcatcggt | tgncctgcgg  | gacaatctgc  | cgcccggcga | 540 |
| cggggcgaa  | tcctgcaaaa | gacgcttgct | cactttcagg  | ccaaaggctc  | gatccgcaac | 600 |
| cggcttgctg | ggacaatgga | gaggtgagag | acattcggct  | gaatttgcac  | cggattacat | 660 |
| tttctatacc | acaccttacg | acatccgttg | cctccgccccc | ttcgccagag  | gacctttccc | 720 |
| gatatactca | cctgcacagc | ctctatggct | atccctcga   | agaatatcct  | gactggtagc | 780 |
| acctctgttt | cacaatcttc | tggggtacta | cttttggttt  | cggaagaaga  | cctcgcatct | 840 |
| actcgcgact | cttctcgcgt | gaggggatgc | aacggagtgg  | tcgcggagca  | cctttgtcga | 900 |
| tgctttctcc | ttcgaaaatg | aggagtcgac | cgaaaaaat   |             |            | 940 |

## (2) INFORMATION FOR SEQ ID NO:490

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1920 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1920

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

|            |            |             |             |            |            |      |
|------------|------------|-------------|-------------|------------|------------|------|
| taccgtcttt | tggaggaatt | gcctaccgat  | ccttgggatc  | gcccgatggg | ggagtcatca | 60   |
| ccgaaagcga | aacactcttt | ctgctgaccg  | ttttttcctt  | tctgttgcc  | tcgtatgtag | 120  |
| ccgaaaggg  | cgaatgtatc | ggtgaaaagt  | tctctcgggg  | gattcctccg | ccggttggtc | 180  |
| ggggtggagc | caaatctggt | gtgggtctgt  | ttggatatgt  | cttcgggtgg | tagcttgctg | 240  |
| gttggtgaaa | agccctactt | ttgtaagaaa  | ccaataaata  | tatacacaat | gaagttgaag | 300  |
| tagccagcaa | cgctctgttg | caacacttgc  | aattgattgc  | ccggtcatag | cttcacgcag | 360  |
| tacacttcca | attttgaggt | ctgtactttt  | cggcttgagg  | gagatcaatt | acgtcttacc | 420  |
| gctgccgata | tggccaatcg | gtgagtacgg  | aacttaccgt  | gaacaacgta | gggggcgaaa | 480  |
| acggttcttt | gccgttcccg | agaggatctt  | acttgaacca  | ctgaaagaat | tgcccgatcg | 540  |
| ccgactctct | ttgagataaa | tatggaaacc  | aaagccgctg  | aaatagcaac | agcaacgggc | 600  |
| attacagttt | tgtggtacag | gatgtttcga  | cctatccgtg  | gcagcttctt | tgtctccgga | 660  |
| agcaatcggt | tctatcgttc | cggcggagcc  | ttgctcagtg  | gcctttcggc | tacgtctctt | 720  |
| gctaccagtc | aggacaacgc | cggccgatca  | tgacaggggt  | ctatctggat | ttcttcgagg | 780  |
| acaacttggt | ttcgtaggct | cggatggaca  | gatcttggtg  | aagcaggagg | atgtaatgtg | 840  |
| cagagccgtc | ggcgtagtgc | cttctgcctg  | cctaggaaaag | ccgtcttctg | ctgcgcaatg | 900  |
| ttctgccccg | actggaaggg | gatgtgacac  | tacgtatgac  | agcaactatc | tccatataga | 960  |
| acttggaat  | tatacgtca  | agcacggttg  | ctggaaggctc | gttatccgaa | ttataatagt | 1020 |
| gtaatacctc | cagcaatcct | ttctcgggtga | aagtggatcg  | tgctcaactc | ctatccgggc | 1080 |
| caagcgcgta | tctatcttct | ccaatccggc  | tacgagtatg  | ctgcgcagga | gtttaccctt | 1140 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| gcaggcatcc | gcttatcggc | taatgatata | gatttcctgt | ggctgctgaa | gaacatgtgc | 1200 |
| cggcagaatg | tccggccgac | atcaaagtcg | catcggattc | aagtcggatg | tctttcagac | 1260 |
| aattctgcaa | ggaagccatc | ggaagaagtg | ataatgactt | tggctgatca | gactcgtgcc | 1320 |
| ggttcatact | gccggcagag | aatgcaccgg | ggataagcct | gtgcaatttg | ctttgccgat | 1380 |
| gaagttgatc | ggcgaataaa | aacgaattcg | aatgaaattg | atctgaaaaa | cccgtctgac | 1440 |
| ttcttcgacc | tcgaaacgac | gggtgtggat | tggtagcgga | cagaatcgtc | gaaatctcca | 1500 |
| tactgaaagt | catgcccag  | gaagcgaaga | gtgtaaaaa  | aggcgtatca | atcccgaacg | 1560 |
| ccctattctc | ccgaatcgac | agccattcac | ggcattaggg | atgaggatgt | gaaggacgtc | 1620 |
| cgccattccg | ttcgggtggc | aaaagtcttg | cgcaatggat | agaagggtgt | atttggcagg | 1680 |
| cttcaattcg | acgcgattcg | atgtgccgat | gctggggagg | agttcctccg | tgcccggagt | 1740 |
| tggacatcga | cctccgccac | agaagctcat | agacgttcag | acgatttttc | ataagatgga | 1800 |
| acctcgaca  | ttgaggcagc | tactcgtttc | tattgnaata | gaacttttga | aatgcgcgat | 1860 |
| tcgctgaagc | cgatacgccg | tgctacatac | gatgtgttca | aggcccaatt | gatcgttatg |      |

1920

## (2) INFORMATION FOR SEQ ID NO:491

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...543

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| gacttttgtt | ggataatata | aaatgacata | cagaattatg  | aaagctaaac | tctattatta | 60  |
| gcacttgccg | gtctcgcatg | cacattcagt | gcaacagcca  | agaagctact | acacagaaca | 120 |
| aagcagggat | gcacaccgca | ttccaactga | taaggcctcc  | gatcattggg | tcattgacat | 180 |
| tgcagggtga | gcagggtggc | tctctcgga  | tggaataatg  | atgtagactt | tgtagatcgt | 240 |
| ctaagatcgt | tcctactttc | ggtatcggt  | aatggcatga  | gccttatttc | ggatcgtct  | 300 |
| ccaattcaca | ggattcgaca | tctatggatt | cccgcgaagg  | agcaggagcg | taaccacaat | 360 |
| tactttggaa | acgcccacct | tgacttcagt | ttgatctgac  | gaactatttc | ggtgtatacc | 420 |
| gtcccaatcg | tgtcttccat | acatcccatg | ggcagggtata | ggatttggtt | ataaattcca | 480 |
| tagcgaaaac | ccaatggtga | aaaagtagga | agtaaagatg  | atatgaccgg | aacagttaag | 540 |
| tcg        |            |            |             |            |            | 543 |

## (2) INFORMATION FOR SEQ ID NO:492

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...887

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

```

ccctcattaa aatncaggta aacggtaact gtctaatact gagaaaatca aatccaatag 60
cctttctctc ttagcagana agttcatcag gtactttctt gcagaaatac agtttgcccg 120
actctccgaa aagggaagt cgggcaattt atgaaaggac gaaaggtaat agccctgtaa 180
aagcctttat ccttcgcgtt cagcatttgg agtcgcttct ccagatcagg gaattggctt 240
tcgggaggag cgacgtacag atacgcatcg cttcgttgcg cttgctgcct gtcgttttag 300
cgtgatggca cacataccgt agcgcacaaa cttctcgatc aactgctgct atccatcccc 360
ttataaccga ctgtgaagta gaatccgtca gcagtggttc aatttgccgt ccttatcata 420
gacgatattg aagccgttgt caggaacatt ttcttcatga tccgagcctt ccggccatat 480
tcgattacag gtcgcggaag ttatatcttc catcattgca ggctttgagc atggcagcct 540
accccatgtg gcagagtggg tggctcccga agacagagca tacagagcga tgatgacaat 600
gcctcgccga aacgcagacg cccgaatgac tcttccagtc cggatactca cgctcgtaga 660
gcttgcccgga tatcatgagt actccgtgcg ctgaccggca tagctgaatg ccttggagct 720
ggagagagcc agtattaatt gtccgtgtag ttggctacgg aagggtgata gagcggctca 780
cccgatggga atagtcctta cggaaatcca tgccgaagta tgccaagtct tcttgacgat 840
aacatcatgt ttggtcgcca gctcaccgat gatgcgcagt tctcgtc 887

```

## (2) INFORMATION FOR SEQ ID NO:493

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...633

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

```

gctcgtgcct cttcgagcgc gatccgcatg tagcggatgt catccgtgga aaggtagggg 60
ctgtcatcgc atttcctcct ctcgaaaaag caanggaggt cgctttctaa ccggtgtatc 120
acttctttca tcagcgtttc tcggatcaac gggagcgggt ctctactttg aagcggctgc 180
aataggcttc gacggcttgt gctccgcttc gttcagtcgg atctgaatgg ctttctttcg 240
gagcacgtgg ctgcgaggag tacattgtgc cgatttttcc tgctcatatt cagtatgcaa 300
atatagtccc tttattctgt tgtcggccgg tctgcatcca ccatccacgg aaagtaagac 360
ggtgatgtgg cgaaactccg aaacgacgaa tacggatttg tgtgcagggt acggataacc 420
tttgttgccg tcccatccgt aatcggaag tccttattca gacggagcat cgagtcgtcc 480
cgataggttt ggccaaaatg gaagctgctg cgatggagcg atagcgggca tcgcctcccc 540
gatacagtgg tgagggattt gttcgaaagg atcgaaaccga ttgccgtcga tcagcaatct 600
ttcggggcga aaaggcaact gctctatggc gcg 633

```

## (2) INFORMATION FOR SEQ ID NO:494

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5572 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...5572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

|             |             |            |            |             |            |      |
|-------------|-------------|------------|------------|-------------|------------|------|
| cgagcagaaa  | ggtaaggtaa  | tagactgtgt | aaagacgggc | tatacgctca  | cgacaaagtg | 60   |
| atacgtcacg  | ctcatggggg  | ggtgggagaa | tgaatcccgt | caacgaatcg  | gagcagaacg | 120  |
| aacaaggata  | agacatggca  | gaaaaaaaga | ctattacgaa | gtccctcggtg | tatcgaagaa | 180  |
| tgccaccgac  | gatgaatgaa  | aaaagcatat | cgcaagaagg | ctatccaata  | ccatcctgat | 240  |
| aagaaccggg  | tgacaaggag  | gccgaaggag | acttcaaaga | ggtagctgaa  | gcctcgacgt | 300  |
| attgagcgat  | ccgcagaagc  | gcagtcataa | tgaccagttc | ggcatgccgg  | attgggcgga | 360  |
| gctgccgggtg | gaggttttcag | cggaggcggt | attccatgga | ggatattttc  | agtcgcttcg | 420  |
| gtgatctatt  | cggtgggttc  | gcggttcggc | ggattctccg | atatggccgg  | tggcagtcgc | 480  |
| agacgtgttc  | cagagggtct  | gacctgcgag | tacgagttaa | gctttctttg  | gccgatatag | 540  |
| taaagggtgtg | gagaagaaag  | tgaaggtaaa | aaagcaggta | gtgtgcagaa  | atgtcgtggc | 600  |
| gatggcacgg  | aagaagccaa  | tggcaagact | acctgccgac | ctgccatgga  | accggcgctg | 660  |
| ttacacgtgt  | gagcaacact  | ttccttgggc | catgcagacc | cagagcactt  | gtcccacttg | 720  |
| ccacggagag  | ggtgaatcat  | cacgaagcca | tgctccaagt | gtaagggcga  | aggtgtggag | 780  |
| atcgcgaaaga | ggtgatctca  | ttccacatcc | ctgccgggtg | agccgaagga  | atgaaatgtc | 840  |
| cgtgaacggc  | aagggaaatg  | ccgcgccccg | aggaggcggt | aaggcgactt  | gatagtcgtg | 900  |
| atcgccgagg  | aaccggatcc  | gaatctgac  | ccaatggcaa | cgatctgata  | tacaatctgc | 960  |
| ttatatccgt  | tccgttggct  | taaaaggagg | tagtgtggaa | gtgccgacga  | tagacggacg | 1020 |
| agccaagatc  | gcatcgaggc  | ggggacacaa | cccggaaga  | tgctgcgttt  | gcgcaatagg | 1080 |
| ggttgcccag  | cgtaaaccgg  | tatggcatgg | gagaccaact | ggtgaattca  | atgtctatat | 1140 |
| ccccgaatcg  | atcgatgcca  | aagatgagca | ggctatgcag | cgatggaaaa  | ctcggacagc | 1200 |
| ttcaaaccta  | ccgatgctgc  | tcgtaggata | tagacaagaa | atacagagag  | atgctggatt | 1260 |
| gaaagacaat  | gccatgtatg  | gtacttgacc | tgagaaaagc | tgccgggtac  | cggtatgcag | 1320 |
| tttacaacac  | agactttttt  | gagcgatgaa | caacgaattt | ttgcagacag  | aaaggatatt | 1380 |
| gtccgtatgc  | tgcgtagagt  | atacgacccc | gaaataccgg | taatgtgtac  | gatctggggg | 1440 |
| tgatatacaa  | tgtggacgta  | ggagccgacg | gttcgttacc | gtcaccatga  | cactgacggc | 1500 |
| accgaattgt  | cctgcagcaa  | cttcacata  | gaggatgttc | gcatgaaggt  | ggaagcggtg | 1560 |
| aaaggcgtaa  | gggggtaaag  | atagacctga | ccttcgaacc | cgaatggaat  | aaggacagat | 1620 |
| gacggaagaa  | gccatgctgg  | agcttggatt | ccctctaaaa | cctcggtccg  | aatcgaattt | 1680 |
| ccccatgcgt  | tcgaagatct  | actttaccag | cgatgccatc | tcggttccgc  | ccatcatgcc | 1740 |
| gacccatga   | cagtggagag  | gcgttggccg | cttgggttga | gcgtattcgc  | catgaggcca | 1800 |
| aggccatcta  | cttatgggcg  | acatgttcga | ctattgggtc | gagtatcggt  | atgtgggtgc | 1860 |
| tctggcttca  | cgcgtttcc   | cgggaaagta | gccgaattga | gcgatgaggg  | gtggagattc | 1920 |
| atttcttttc  | cggcaatcac  | gacgtatggc | tgacagatta | ttgaccaagg  | agctgggtgc | 1980 |
| tcgatgtccat | atgcatggca  | ttacggtggg | ttgtccggca | agctcttcgc  | cttggcacat | 2040 |
| ggagatgagg  | agtatcggt   | gtgaagcggt | cgtacgactg | catgtaccgc  | ctcttcgcga | 2100 |
| atccgttgca  | cgctctcttt  | atgcagccgt | gcacccctgc | tggacagtcg  | gtttggctat | 2160 |
| ggcatttcac  | tgaaaagcag  | acgcagcgga | gagaagcgaa | agacatccgg  | aatatcccc  | 2220 |
| acgcctacag  | caacgactac  | ttcgatatag | aaaagaatgg | ctgattccgt  | ttgccaaaga | 2280 |
| gcatagtgcc  | cgacatcccg  | aagggtatcc | tatatcttcg | gccatcgaca  | tctgctggtc | 2340 |
| gatattggcat | tggcgatgag  | aagcgtgtcc | tgatcccttg | cgattggatt  | cgttacaact | 2400 |
| ctatgccgtt  | tgggatggca  | cgacgcttgt | gctcgaatcc | atggaggaca  | ggaataagcc | 2460 |
| ttcggtacca  | agatcgggac  | agaccgcttg | ataaaataca | cttcacgccc  | gttcagggtg | 2520 |
| taaacgaaaa  | tagctctatg  | ggaaagatac | aatcacggta | ggcgatatta  | ctcgcttcga | 2580 |
| aggagatgcc  | attgtcatgc  | ggcgaatcat | acccttttgg | gtggaggggg  | agtggacgga | 2640 |
| gccattaccg  | agcagccggc  | cccgaactgc | ttggaggagt | gtcgcactct  | caacgttgcc | 2700 |
| ctacgggaga  | aagcaaaata  | acgggaggat | acaatctgcc | ggcgaatacg  | ttattcatac | 2760 |
| cgtaggccct  | gtgtggcatg  | gagggcaaca | ttggagccgg | agctattggc  | ttcctgctac | 2820 |
| cgtacatcgc  | tgtccatagc  | ttggacaagg | gactgaaatc | cattgccttc  | cctgcatcag | 2880 |
| taccggcggt  | tccgttatcc  | taaagatcag | gccgcccgcg | ttgctttggc  | cactatcggg | 2940 |
| agattattgc  | agatcgcccc  | attgacgtca | ctatcggtgt | cttctcggag  | cggataagga | 3000 |
| gttttatatc  | acacaggact  | gacgcgtaac | tccttggctt | ctcgcaagat  | ctctatcgaa | 3060 |
| aagccttgca  | gtataactcc  | ccttctttct | cttctctatt | cagttcgcct  | tcaccccccc | 3120 |
| aagggttccc  | ttccaaaccc  | cttagggatc | ccccctgaga | cccctaaggg  | gtcctacccg | 3180 |
| agactcttag  | gggtcccata  | ggagactcct | cgggggtctc | aacagggact  | cctagggatc | 3240 |

|              |             |             |              |             |             |      |
|--------------|-------------|-------------|--------------|-------------|-------------|------|
| gtccccatac   | ttcttgatgt  | cttcggagaa  | ggttttccaa   | agaacttttc  | ccctcctcct  | 3300 |
| ctctgcacgc   | ttgccctgaa  | tctgtgctgt  | cacgtcacgt   | ttttttttac  | at ttgtgcct | 3360 |
| aataagctaa   | ctctcgaggc  | tatgggaaaa  | ttgttacagg   | ataaattggc  | tcagtatacc  | 3420 |
| gagccgcaaa   | ggcacaagcc  | gcaggtat tt | acccttattt   | cagaaaaatc  | gaaagtgata  | 3480 |
| ggataccgag   | gtcgttatcg  | atggtcggaa  | agtccctcatg  | ttcggctcaa  | tgcatatctg  | 3540 |
| ggactgacga   | accacccgaa  | agtcaaggag  | gcagctacga   | agcgacaaag  | aagtacggta  | 3600 |
| cgggctgtgc   | cggctcccgc  | ttcctcacgg  | cacactcgat   | attcacctcg  | aactggaaaa  | 3660 |
| acggctggcc   | gagttgtcgg  | caaggaagat  | gccatcagct   | tctctaccgg  | cttccaagtg  | 3720 |
| aatcgggcgt   | tgtctcctgc  | atcaccggcc  | gcgaggatta   | tatcatctgg  | gacagttgga  | 3780 |
| tcatgcttcg   | atcatcgagg  | gtattcgctt  | ttcatttcagc  | acaagttaaa  | gtacaagcat  | 3840 |
| aatgatattg   | gttctctgga  | gaagcgggctc | cgcagtgcga   | cccggagaag  | atcaaactga  | 3900 |
| ttgtggtcga   | tggtgtcttc  | gtatggaggg  | tgatgtctgc   | aatctgccc   | aaatcgttcg  | 3960 |
| cctcgccaac   | gatacaagc   | caatgtgatg  | tggtgacgaag  | ctcacgggtat | cggcgtgagg  | 4020 |
| gcgaccacgg   | acgcggcgctc | tgcaatcact  | tcggtctgac   | cgacgaatgg  | acttgatcat  | 4080 |
| gggtactttc   | agcaaattctt | tcgcttcgct  | cggaggttta   | ttgcaggaga  | caagagcggt  | 4140 |
| atcaactacc   | tgcgccacca  | cgccccatcct | atat ttttcag | tgccagctgt  | acgcgggctt  | 4200 |
| ctacggcagc   | ggcacagctg  | ctctggacat  | tatgtttagc   | gaaccggagc  | gtttagccc   | 4260 |
| at ttggggagc | tgacgcacta  | ctcattgaac  | gcattccgca   | gtcttggtatt | cgaataggctc | 4320 |
| atacatcgac   | acctattatc  | cgcctttttta | tcgcgaacaa   | cagaagacat  | tccaaataac  | 4380 |
| ccgagacgct   | ttcgaagaag  | gggtatttcgt | aatccgggtgg  | tctctccggc  | ggtagctccg  | 4440 |
| tcgacaccct   | tattcgcttt  | cactcatggc  | tacgcatacg   | aaggagcaac  | tcgactttgc  | 4500 |
| catcgaaagc   | tgcataaggt  | attcaagcag  | aacgggtgtcc  | tgtaagtgt   | attaatgtaa  | 4560 |
| cagcgtgttg   | cggacacgct  | cctttggagg  | aggatggtaa   | tgaataaacg  | ataataggag  | 4620 |
| tagcaggcgg   | aagtgtctcc  | ggcaagagta  | cattgtgaaa   | aagctctgtg  | aggctttcgt  | 4680 |
| cgaagaagat   | gtgcttgtag  | tctgcacgat  | tactattaca   | aggccaatga  | ccacctctcc  | 4740 |
| cttgaggaaa   | gaagaagctg  | aactacgacc  | atcccaatgc   | tttcgacacg  | gatattgttcg | 4800 |
| tcgggatatt   | ctctctctga  | aggcaggcaa  | aacgatagag   | cgccgggtct  | atcttttcgta | 4860 |
| gagcacaatc   | gtttgcaaga  | aaaagtaacc  | gttcgtcctg   | caaagtgatc  | gtactggatg  | 4920 |
| gaatcctgat   | attcgagaac  | aaagagctgg  | ggatctgatg   | aatgtgaaag  | tattcgtcga  | 4980 |
| taccgatgcg   | gatattcgtt  | ggcgcgccgc  | cttgtgcgcg   | atgtccagga  | acggggacgc  | 5040 |
| aatatggttc   | ggtattggca  | caatacttca  | gtacggttcg   | gcctatgcac  | gaggatttgt  | 5100 |
| ggaaccatcc   | aagcggtagc  | ccgatctgat  | cattccggaa   | ggtgggtcaa  | ttcggtgccg  | 5160 |
| ctctcactcc   | ttgtcgaaaa  | aatccgatcg  | gtgatcgtaa   | ggaagaataa  | cagccggata  | 5220 |
| ctccgatctt   | tctctcaaaa  | ccaaacctta  | atgcgattaa   | aaccaaggct  | ttctttccaa  | 5280 |
| aacagcattc   | cttattgtgg  | tggatagctg  | ccatcgatc    | tgccattacg  | aaagctgctc  | 5340 |
| ccacaggcac   | aataactata  | ccatattccg  | ctcctctttc   | tatcattttc  | ccgacatcag  | 5400 |
| tcgctctatt   | cggcctatcc  | ggcagagcat  | cacgatgttt   | tctctacggc  | cctgtcttct  | 5460 |
| ctatcctttt   | cggccctttt  | gcccttttcc  | ttctttcata   | gggatgctgc  | tgtggctgtg  | 5520 |
| cttttcgggt   | gccggatcct  | ttgggctgtc  | agccaattac   | ccacgagcga  | aa          | 5572 |

## (2) INFORMATION FOR SEQ ID NO:495

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...495

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tcttgctccc | cggcaccaag | tgcatggctc | tcgcgaattg | agaggtagcg | cctttgccga | 60  |
| tattcttttt | tgatcttatt | ctacctgaga | ttcgatgtcc | ggcggaagta | tttttcgaaa | 120 |
| aataagatct | gataatctat | ggcattagcc | aataagctct | gttgtgcctt | ccggggcgga | 180 |
| tggtaaaatc | atgatcattt | gctttgccag | aagtgaggca | tgacgctctt | tgttgacatc | 240 |

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| cagaagaaat | cctccactcc | gcaatctatt  | aggatagcaa | gtgcgggnccc | tctcagctgt | 300 |
| cgagggtgtt | gatcacagtg | tactcgtccc  | catagcttcg | gatctcggcc  | aaagagccaa | 360 |
| gcccgtctgc | ttatctccca | gttggttcgga | aaggacgaat | atccgcacaa  | ccgctcattg | 420 |
| cttccacag  | gcttccgaac | gcgtcctgat  | gccgaaaggc | aatccataag  | gcgccgtgcc | 480 |
| cacccatgct | gagtc      |             |            |             |            | 495 |

## (2) INFORMATION FOR SEQ ID NO:496

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2487

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| gcagaacncc  | gatgacatct | atatgagcct | tatgcgcnag | tnggggctga | tgatcaggtg | 60   |
| tggcagnccg  | gagccatcct | gctgcgggtt | cggtcgggtg | cgtaatggnc | gacgagcgta | 120  |
| cctacgaata  | caccgtggca | ctgcgtgcgt | gacttctatg | gatgccatga | gtgccgattg | 180  |
| ggtgcatttg  | ccgtatatct | tctggccaag | gtgtcgaacg | aaataatcaa | taaagtgcgt | 240  |
| ggcgtaaccg  | cgtagtctac | gacatctcct | ccaaaccccc | cagcacaatc | gaatggaata | 300  |
| acaatgtcag  | cccatacagg | aatctgtaca | gcgaccaccg | atctattcac | tattataaaa | 360  |
| aactgctttc  | atgtccacgt | accaaccgga | agtactcgta | aggtaactac | acatcgcttc | 420  |
| atcgagatga  | agagccgtgg | gagaaaatct | ccatgctcac | agcttatgac | tactcaatgg | 480  |
| ctaagctggg  | gatgaggccg | gtatggatgt | cattcttgta | ggtgattcgg | cttcgaacgt | 540  |
| atggccggca  | atgtccaccg | cctgcccata | actctcgatc | agatgatcac | cacggcaagt | 600  |
| ctgtgggtcaa | ggccgtcaag | cgtagctctt | tggtcgtgat | cttcctttcg | gatcctatca | 660  |
| gggcaactcc  | aaagaagcct | tgtgctggcc | atccgtgtga | tgaaggagac | acatgccgac | 720  |
| tgtatcaaac  | tcgaagagga | gaagaggtgc | gcgagtcctc | tgtgcgaatc | ctctcgcccg | 780  |
| gtatcccatc  | atgggacacc | tcggactgat | gcctcagagc | atcaataaag | ttgcacctac | 840  |
| aatgtccgcg  | ccaaggaaga | ggccgaagcc | gagaagctgc | ttaggatgct | cacctcttgg | 900  |
| aagaactcgg  | atgcttcgct | ctcgctcctc | aaaaataacc | gccgaactgg | ctacacgtgt | 960  |
| agcttcggag  | ctgagcattc | ggttatcggc | atcggtgccg | gaggtggtgt | ggacggtcag | 1020 |
| gtgctgggtg  | gcacgacatg | ctcggtatca | cggaggggtt | cagtccccgt | ttcctgcgcg | 1080 |
| ttatgccaat  | ctggccaacg | agatagatcg | ggcactcaag | cattatacgc | tgatgtgaag | 1140 |
| agtatggact  | tcaccaataa | ggacgagcag | tactgacctg | ttttccctga | atcttacgtt | 1200 |
| ttcctcgcaa  | ttatcagcgg | tcgacatgca | tggaaataga | gaagggttta | ccgaatttat | 1260 |
| cacttggtgc  | gattcctcgg | aacctttgca | ttcgccatca | gtggtattcg | tttggctgca | 1320 |
| gccgacgctt  | cgattgggtc | ggagcctatg | tggtcgggtg | ggttacggct | gtggtgccgg | 1380 |
| tacgggtgcg  | gacatttttg | ttaatgtccc | gccgttttgg | agctccggcc | ttcctacctt | 1440 |
| tttatctcta  | tgctcgctct | catcttcacg | ttgtatttcc | gaagtatgta | gtacgactga | 1500 |
| atcatacggg  | tttcattttg | atactgtcgg | gataggcttg | ttcaccatag | tgggtgtggc | 1560 |
| taaaacttcg  | agtgcggata | tgcgtgggtg | ctggccattg | dgatgggtac | gattacaggt | 1620 |
| cgttcgggtg  | tatgattcgg | gatattctga | tcaatcagac | gccgctatct | tcgcgaagga | 1680 |
| tatatatgcc  | atggcgtgcc | tgatcggagg | agcggctatg | tgggactcat | gtacacgact | 1740 |
| ctcccgatcg  | aaatcataca | gttcttgctg | cctttattgt | cgtggctgtg | cgggttcgtc | 1800 |
| cggtgaaata  | ccaatcagca | tccccacttt | ccgcggggcc | gtataaaact | ttcccaaaac | 1860 |
| agagttctct  | tttggtggca | tcccccttga | ctatcatctt | attacgatag | cgtggagtga | 1920 |
| tattccgctc  | tctctttatc | gcgtttgcct | tcatatgcaa | ctgaaaaagt | cgccaatcaa | 1980 |
| aaggcgactt  | ttttgctttt | gactgtacta | tgagcgtaac | gcacaagtca | tggaggagct | 2040 |
| ttagaggtat  | tcatatctta | acgacactga | aaaatcagtc | aattgacaat | gaaatctcca | 2100 |
| agaaaatccg  | tgcgacaggg | ttttacagct | catacggaac | ctctctcccc | gaacctccat | 2160 |
| ccggcagaga  | gcagatagca | tcttccatca | atagaccata | gtatctctcg | tatgagacca | 2220 |
| tagtatcctc  | tcataggaga | ccatagtatc | ctctatagga | gacccatagt | atcctctcgt | 2280 |



|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| aggagacat  | agtatcctct | cgttgagacc | atagtatcct | ctcataggag | accatagtat  | 2340 |
| cctctcgtag | gaacatagat | atcctctcat | aggagacat  | tctttgtatc | tcggggaaag  | 2400 |
| acaatgagca | ggtttatggc | tgccaagtaa | acagagattt | cccaaagttt | cttcagggtat | 2460 |
| atacttgagg | ttcgcaaaga | ctgcatg    |            |            |             | 2487 |

## (2) INFORMATION FOR SEQ ID NO:497

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tacggatcat | gtttccacca | ctgttcatta | tcacctaatg | gtcgatagtc | ataccaatt  | 60  |
| gctcagaagt | ataatttgct | ccctgctgaa | tccttttttc | acggttacat | agattgttcc | 120 |
| ctttgaatca | atccccatat | tggaatata  | tacttgacgt | taggctcatt | actgataaaa | 180 |
| ggaggagcta | tttcttccaa | aagctctgtg | cgtttccgcc | caatacacct | gacatcatta | 240 |
| aagcgggcac | agaataattt | gttgaactgt | tgttttcatt | tccttttcga | ttatagtatt | 300 |
| tnatcatttt | atttcatctg | catctttcga | ctacctactt | cctgccattt | acaatcagag | 360 |
| aatacacaga | gcaaatccct | gaaacacatc | acatatgaca | tatgccgaaa | gataaataat | 420 |
| tatatcaaaa | acgacaaaat | ccaaaagaaa | attctctgtt | accgctcaaa | atcggttttc | 480 |
| ggttttcaaa | catgcctgca | taaaatagca | acacctctca | gatngaggaa | aataaaatcg | 540 |
| nccttgcgga | caacagatcg | cc         |            |            |            | 562 |

## (2) INFORMATION FOR SEQ ID NO:498

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atcggggaag | tcgatcattt | gggaaaatgt | ggtcgtatgc | atgccggtag | atgggcttgg | 60  |
| gatatagccc | ctgtgcgcaa | atcggcata  | ggaatcaggc | attgatcaaa | gagcttttgc | 120 |
| caacccccga | atggccggca | aggagtgcag | cttgccatcg | agtagggatt | tgagatccgg | 180 |
| gaggccttcg | cccgtatcgc | cgacacgtgg | cagcaggggt | aacctatggc | ggtgtagaca | 240 |

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| gccgaagccg  | gtccaattgc | aagcgatctt | cttgcgtata  | gcagtctatt | ttgtgaatac  | 300  |
| aagaataacc  | ggtacgcat  | aggcttctgc | cgtacgcagg  | aaagatcgat | aaagacggtg  | 360  |
| gtagtcaccg  | gatcgttgat | ggtacagacc | agacggcagc  | atccaaattg | gctcccagta  | 420  |
| tatgggactc  | tttcgagagg | tgttggtcgc | cctgatgata  | taattgcgtc | ggggatggat  | 480  |
| tcgtttgatg  | aggccggctg | tcggtcctga | gaagcgggga  | caatctccac | gcgatcgcca  | 540  |
| cggttacggg  | attggtggag | cggatgcctt | tcagacgcag  | attgccttcg | ccatgcagta  | 600  |
| tagctccgta  | ccatccgtgc | aacgcaccag | atactgatac  | ccgtattctt | aattacgact  | 660  |
| ccatccataa  | acggctttgc | ggtgtataaa | acagcgatga  | ggcagaatcg | aaaaactctg  | 720  |
| cttcacgcgt  | gagtgataga | tttttcacgc | ttacacggtc  | atgatttcct | tttccttttc  | 780  |
| ggcaagagtt  | cgtcgatctt | cttgatataa | cgatcgtgaa  | ccttctgcat | ctcgcctctg  | 840  |
| catctttggc  | tacgtcctca | ggagtacat  | cggctcttgac | gctttcttga | tcgcatcgat  | 900  |
| ggcatcgcca  | cgggcattgc | gcacactcac | ctggcgctct  | cggcatctcc | tttggctctgc | 960  |
| ttcaccaact  | ggcgacggcg | tcttctgtca | gaggaggaag  | gccagacgg  | atcagctcac  | 1020 |
| cgttggttctg | ggcgtaatgc | cgagcggaga | gtccatgata  | gccttttcta | tatccttgct  | 1080 |
| agggaaacgt  | cccacggggg | gacaacgatg | gtcttcgcat  | cgggcgtttg | atggatgcta  | 1140 |
| cctgtgtcag  | aggagtggcg | ttgccgtagt | acatgacatg  | ataccatcga | ggagtttggg  | 1200 |
| gctggccttt  | cccggacgcc | atgagcagct | gctgtccaga  | tactcactgg | cttcttcata  | 1260 |
| ttagccgtgc  | tttgctatca | gtcttttatt | tccatatctc  | tatatgtgtt | ggtttggctt  | 1320 |
| gctttccttt  | caagcactcg | tatttgaaac | ataagtaccg  | atttctctct | ctaacacttg  | 1380 |
| a           |            |            |             |            |             | 1381 |

## (2) INFORMATION FOR SEQ ID NO:499

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 751 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...751
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| ggccaacatg | ggatcggata  | tgatgaggac  | tttgtctgtg | atgtccggca | tgctatgtat | 60  |
| tcgatgtgga | tgctgaaatt  | caggcgggtcc | ttatacttct | gtaggcggat | acaaaggcat | 120 |
| tttcacaata | gtcgaaatag  | ttgaggagcc  | atgatggaaa | ggcagtcctg | ctcgaaggat | 180 |
| cgtagcgagc | actacttgct  | ttgggggtacg | gagcactcgg | cctcacccaa | gggcgtagtg | 240 |
| acggtcgcac | ctggttgggtc | atcttcttgc  | tgatctcata | ggccattact | tctccacacg | 300 |
| ttctatatta | cgacgaaagc  | gcagtcgatac | gttctgaata | gtgcatcgcg | catctccatg | 360 |
| acgaatctat | tgagaagaga  | atgctcggca  | ccaagtgtat | tacttccata | attattgttg | 420 |
| tgaggtaggt | tatgcaaate  | tcgaacgaga  | tgttctaaat | accgattcgc | gcaaaaatac | 480 |
| aatatctttg | tgcataaggc  | gttgatctta  | cacaccaa   | aaagaattga | agattattcc | 540 |
| tcagatgcaa | ttcttatata  | attcacgttt  | ttcgttgaga | gtcgtctttt | ttgcctgatt | 600 |
| tgtgcctggg | ccggacgtac  | gctgtcggcg  | caaacggaaa | agtacaaaat | cgccctacg  | 660 |
| ccgactacaa | acgctatcat  | cttgatcca   | tgtagggatg | catgcccagg | atttggttat | 720 |
| ctccaacaac | gggttggtacc | cgaaggagtg  | a          |            |            | 751 |

## (2) INFORMATION FOR SEQ ID NO:500

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1899 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| tcacacgtgc | accactcttt  | ggcaatatct  | atgctgcggg  | ggctatcatc  | ccaatgacaa  | 60   |
| agccaatatg | gaaaagggtg  | ttacaggaga  | ggctggcctt  | gattcacgaa  | tcacaaaaac  | 120  |
| ttcgagttca | atatcaacgg  | atactatcga  | agtggatgga  | tcgcgtgacc  | tcgaagagaa  | 180  |
| tcggaaacga | gtatgtttatc | tcaatggcgt  | tgatgctgtt  | cactgtgggg  | tagaggctga  | 240  |
| ggtcactatc | gtcctattcg  | tcagatcgac  | cttcgcggta  | tgttctctct  | cggtagctgga | 300  |
| cttggcaaaa | caatgtaagt  | tacacttctt  | acgacgaagc  | cggaatgaga  | cagggcagga  | 360  |
| tataacctat | atcaagggtc  | ttcacgtcgg  | agtgcagcac  | agatgacggc  | tgctgtatcg  | 420  |
| gcagacatag | agctgtttcaa | ggtttccatg  | tcataggtaa  | gtacaacttc  | cttggcaaga  | 480  |
| actatgcagg | ttcaaccccg  | caacgcgtaa  | tgacacagcag | tacgaagcgg  | atggcaaaaga | 540  |
| atcgtggaat | catggaagtt  | gcccgatgta  | ggctctgttcg | atctgtctca  | tcctacaatt  | 600  |
| tcaagcttgg | ttcactcagc  | accacattct  | atcttcaaatg | gacaacgtag  | ccgacaagcg  | 660  |
| atatgtgagc | gatgccgacg  | acaatacatc  | ggtaagaaac  | acgatgaggc  | ttcggctctc  | 720  |
| gtatggtacg | gtttcgccgc  | acttgggtcta | ccggtatttcg | tgtaaaacttc | tgatcttaca  | 780  |
| ctgacctact | acataagacg  | gacgaagagg  | gtgtgtcaaa  | atgaaaattt  | tggtcaccct  | 840  |
| ctatatattt | agattctcct  | gaaagccgga  | tttaattata  | aaaggctgtg  | ttgaaattat  | 900  |
| ttttcgattt | cctctcactt  | tttgtcgaag  | cgtttggaat  | ttgtcgaggc  | ctctgcatgg  | 960  |
| gggttgctgc | atttgatttg  | cggttcggga  | gattctttct  | cataggcatc  | gaaatagcag  | 1020 |
| ggtgtagaat | cggcttttgt  | tcctattttt  | gtgactatgt  | tgtgtgtgcc  | gtaaaaactg  | 1080 |
| aaaaagcgag | tacggttttac | ttactaaata  | agattaagat  | gccttgagaa  | ggatcggatc  | 1140 |
| agacgaccaa | atgagaaatg  | aataacagat  | acaataaaaa  | taagaagaat  | aagaaaatga  | 1200 |
| atagaatttg | cgaattattg  | ggtatgaaca  | tccgatcata  | tcgggaggca  | tggtgtggtg  | 1260 |
| cagcggtttg | aaacggcttc  | tgctgtgagc  | aactgcgggtg | gtttgggact  | tattggtgcc  | 1320 |
| ggaccatgca | tccggacaat  | ctggagcatc  | acatccgttc  | gtgtaaagct  | gcacagacaa  | 1380 |
| gcctttcggg | gtgaacgtgc  | ctcttctcta  | tccggagatg  | gcaaaatcat  | ggagattatc  | 1440 |
| atgaggaac  | atgtgcccg   | agtggtaacg  | cagccggtag  | tccaaagggtg | tggaacagcca | 1500 |
| agttgaaagc | tgccggtaga  | aggtgatata  | tgtagtgagc  | agtgccacat  | tcgctcgcaa  | 1560 |
| atcagaggag | ccggtgtaga  | cgccatcggtg | gccgaagggt  | tcgaagccgg  | cggacatatg  | 1620 |
| gacgagagga | gactacgacc  | ctctgtttga  | tacctgaagt  | agtggagctg  | tgaacattcc  | 1680 |
| tgtggttgct | gccggaggga  | ttgcttcggg  | ccgtgagttg  | ccgctgcttt  | ggctttgggt  | 1740 |
| gccgatgccg | tacaagtggg  | gaccgttttg  | ctctgagtga  | ggaaagtctg  | gcgcatagaag | 1800 |
| actttaaggc | acatgcccgc  | cggtcggtgg  | aagggaagata | cnatgctttc  | gctcaaggct  | 1860 |
| tgatcgccta | cgcgactgct  | gaagaacaaa  | ttctatcag   |             |             | 1899 |

(2) INFORMATION FOR SEQ ID NO:501

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...434

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| gccaacctat | caaggaaagc | aacatccaac | atatactctg  | ccgcgagcct | aggcgcgagg | 60  |
| ccttatccgg | agtgatagca | gcaagcaact | cttcgaaggt  | gcacgtagaa | aaatggcatc | 120 |
| attcgatgga | tactcctcca | taatatggga | gtgagtatat  | gttgtttgac | acctatttct | 180 |
| tcgagcagat | caattaagag | agagtctctt | cgatagattt  | tgaaccgtca | tccactgcag | 240 |
| gcaacgatga | caatgtatat | ctatcaggtc | agtcaacccat | ccttgttcaa | agggttgact | 300 |
| tgcttcgntt | ttcgcttaaa | aatagaaaac | atcctattcc  | tttgctcttc | ttcatggggc | 360 |
| caatcttgaa | tttcttcgtc | ttcttggcag | aagacgacgg  | agttttcttg | ccttgtttgc | 420 |
| catactcctt | ggtg       |            |             |            |            | 434 |

## (2) INFORMATION FOR SEQ ID NO:502

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature :
- (B) LOCATION 1...6954

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| aaaagggtcta | ctacgcgcag  | catcatcggg | tgttcgatga  | tttcttctgt | aagttgtcca | 60   |
| ctgtcgggat  | cgtaatcttg  | agcatcacag | gctcggcttc  | ttgtccaact | gtgccagcag | 120  |
| ttctcgcttg  | aggatctctt  | ctgccttgcc | ttttcggggc  | agtggatgtc | tacctccggt | 180  |
| tcgaggatga  | gtactagcca  | tgagaaagaa | tctcttttcc  | ccattggaat | tgctgctcta | 240  |
| cgatgcgcga  | ataccctgct  | cgttggcctg | cttgatcaca  | ctacgcatct | tggtccgaaa | 300  |
| acgtgggtatc | cgacagcttc  | ttcacagagc | ttgccgagtt  | cggaaacggc | ttcatcagct | 360  |
| gtacgccgtt  | ggcttcgtcc  | tgaagccctt | tgccactttc  | aggaagggga | cgatgtgtct | 420  |
| tttctcccaa  | aggaagtctg  | cgtaggcatt | ccttcgatct  | tgccgcgcac | ggtacgttcg | 480  |
| aagagaatca  | accgatgatc  | ttgcccgtag | cgaaagccgg  | agaagtaatc | atccgagtag | 540  |
| catttggtga  | atgagatcga  | acatctcttc | ttcggactga  | tatgcacg   | ttggataccg | 600  |
| tatgccttca  | gagcttttag  | ggtcgagcca | ccactctatc  | caatgctcct | acaaagccgg | 660  |
| gagcctgacg  | catctgctgc  | aattgtcttt | gttcattgct  | tgtctatttt | aataagatta | 720  |
| gcgaaatagc  | ttgtgttttt  | cttgttttcc | tcaaaggtag  | agattatttg | tgagagggga | 780  |
| cggtcgcaca  | tgaataattg  | attcggagga | agggatcttg  | agggctaaag | gtcgaggaaa | 840  |
| atcagccctc  | tcgaatatct  | actcatgatt | gctgcttcgg  | aggtctctct | agcaaggata | 900  |
| aatgcttgaa  | aggctnatac  | tgacaaatgc | gtgatctcac  | tgattaagaa | cgcgcattga | 960  |
| aggatcggat  | acacgatatac | cgtaccgat  | cagtttgcgt  | gccaaaattt | ttgcgcttgt | 1020 |
| ggtcgtgaa   | acatggcgcg  | aaaacttttt | gcttttgccg  | tgaaagtga  | aaaattccgc | 1080 |
| gccacaacga  | aaaaattccg  | gcgcaacttt | tgggaaaaac  | acagacccaa | ttttagcggt | 1140 |
| ttgggttcgt  | gttttcgaat  | gagtgagtta | cgggtatgct  | ctaaaggggt | gatggcgaat | 1200 |
| cattgacacg  | acgtgtcgtg  | tccgtccgtc | cgagcgtgtg  | attcatgaag | gtctataaag | 1260 |
| agggtgacac  | gtaaacggca  | atcgtctgtg | tgccgcgatt  | ttttccgtac | acagccgact | 1320 |
| gcgatagatc  | ccgatctaca  | ggtaaacgtg | caaaccgata  | gtgaagtcga | acgattgact | 1380 |
| cccatctttt  | ccgaaactca  | tcccaaggaa | ccaccgctcc  | gaagagcagt | actcatgctg | 1440 |
| aataagggag  | cgatatagtc  | caatcgattg | cgaatccgat  | accctgggat | tcgattttct | 1500 |
| tagtgatgtc  | ggcttcatac  | gagaggcgat | cagaccgaat  | ccgtagaggt | tccctttcgg | 1560 |
| gtgacattat  | attggagtac  | gaacgaaagt | cggttgctta  | gctttttctc | cagctgcgct | 1620 |
| ccgaataaga  | cagccctttt  | gtccgattcg | tgatggttaga | ggggccaaat | ggaatgaaag | 1680 |
| gtcgtgtacg  | ggtgccttga  | tccgagagcc | gatttccccc  | tttgaccgca | atcgtacagg | 1740 |
| agcagagtcg  | gataaccttc  | tcccgcgttc | tcacgacaga  | atctgacaag | agcataagcc | 1800 |
| cgcctatctg  | atgatggagc  | tgccgaagat | agagggtcgt  | tggtgattga | tcacgtacag | 1860 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gaattggcac  | cgctttttct  | ggttttcttcg | cgagcaatct  | gcacggcctc  | cagtaggaga  | 1920 |
| gactccggga  | taggccggat  | tcggcgatcc  | ttataagtgt  | gcagacgaat  | agccgggtct  | 1980 |
| tcctgactat  | cggtgggag   | cggtgattata | gtctgcgctc  | ttcgttcggg  | agcaaatcga  | 2040 |
| aagcattgtc  | ggagaatccg  | ctccgagtg   | atccggtttc  | acaaatagat  | ccttcaccaa  | 2100 |
| ataggggtacc | gcactgtcag  | ctcccaagtc  | ctcaggcctg  | tcgggcaag   | ctcttgagaga | 2160 |
| taggaggagc  | cacaggtagt  | agcaaatcct  | tgggcgaatg  | atgatataca  | gcgtggaggc  | 2220 |
| ccagacttcg  | ccgtatgctt  | ctccacatc   | ctcccaagcg  | acaggcgaag  | cagggttcgtt | 2280 |
| cgctgcaatt  | cctgtggcag  | ccatgttcga  | tcgggaatgg  | caggacgggtg | gggtgttcgt  | 2340 |
| tgtctacttc  | gaattcctca  | cccaaaaagt  | cggatagcgt  | ttccctcga   | agctgatcgg  | 2400 |
| ccgatgcgca  | gtgccatccg  | atcctctcct  | ttggcttcgg  | gagcatccga  | acgatgctga  | 2460 |
| tcgtgcgccc  | ttcggcatct  | ggaacgatga  | taacgggttg  | aaagctctgc  | gtacctgata  | 2520 |
| gtgcaacggg  | ttccagttcc  | cgtagtagct  | atgccggacc  | atgagatggc  | cggccatgca  | 2580 |
| tcgttgagtt  | gccagtaagg  | ctacccatgc  | agtaggggtt  | ggccgctcgt  | tgggtcttcta | 2640 |
| atccgagcgc  | ataccttgcc  | cctgcatgat  | gagcgatttg  | aatacgaat   | catcgagtcc  | 2700 |
| tttggtcgg   | gatagtctcg  | ccgcatatat  | tcgagtataa  | tctcttgccc  | acgtgctct   | 2760 |
| tctgtctggc  | tttcatgacg  | ggggagtcga  | gctcatgtcc  | tcgggccatg  | caaagctctc  | 2820 |
| caacgttttt  | ctttcgggga  | aatttcaaat  | ccgaattcgc  | tcatgaagcg  | cgggatcctc  | 2880 |
| tctcgcagga  | tcogaatggg  | tcgcgtccgt  | accatactcc  | ccagtagtgg  | ctgtcacccc  | 2940 |
| gaccaaagtg  | gctgggcgtc  | cccagttagc  | cgtgtcgggg  | gatgtctctc  | ataggcgctg  | 3000 |
| gtgggatcca  | atgctgccac  | acgtccggc   | agaagtgcga  | aaacagcttg  | tcgtagtccg  | 3060 |
| tgagaaactt  | ctgatagggtg | gatcgggtgga | gcgtttttgc  | catccccagt  | atttgaggcc  | 3120 |
| ttctcgtatt  | tcattgtgcc  | gcaccagaga  | gccaaagacg  | gatgttcgcg  | caatcgacgg  | 3180 |
| atgtttaate  | ggcctcttct  | ctcaccattcc | gaaggaaattc | cttgtcgcgc  | ggatgggagt  | 3240 |
| gcaagcaaaa  | gcgaatatctt | gccagatgag  | aatcccgttc  | gcaccgccaa  | ctcatagaaa  | 3300 |
| cgctcgtcct  | cgtatatacc  | gcctccccat  | accgcagcat  | attcatattc  | gcttccgaga  | 3360 |
| cagagcgga   | aagctcctgc  | catactcctc  | cgtgcgtgcg  | gacagcatca  | tgggtgccggg | 3420 |
| gatatagttg  | ctcccttcat  | gtatagcggc  | tttccgttga  | tgccgaagaa  | gaagctgcgc  | 3480 |
| cgtgggtatc  | ctcttcacgg  | acgaattcca  | cggttccgga  | tcctatttgg  | ttcggtaggt  | 3540 |
| ctgccatgtg  | gtaccgtctt  | tgtcctgaag  | acgggcacga  | gtgtgtacat  | caggggcagg  | 3600 |
| cctatcccat  | tgggcattcca | ccgatcgggg  | ataatacggg  | gaaagagggtg | cgacaggaag  | 3660 |
| gttgcccata  | gcctgcgtca  | gctcttcgct  | gtgcactttc  | cgctccgttcg | ggctgtacag  | 3720 |
| ctcccaacca  | aacggacaga  | gcggtcggtc  | tgctcgttcc  | aagagagagg  | aaaagacagt  | 3780 |
| ttacctgagc  | atcttttgtc  | agcgtgtagg  | tgacttccgg  | ttcgatgcga  | aggctactgc  | 3840 |
| cccttcgaaa  | cgtatgccga  | caggtcgcga  | acacctgtgg  | ttaccagtcg  | aggccccag   | 3900 |
| ttcccaaccat | agtggtaggg  | gcttttcgag  | tatatacact  | tagcttttcg  | ttgtgggtgat | 3960 |
| cgttgctctga | gggtagtcga  | aaccatcgcg  | ctgtctcaga  | ggcgtaactt  | ccttcatggg  | 4020 |
| gagcggaagc  | ggatcagcag  | ttcgtttccg  | cttttccgca  | gtagaccggg  | tatatccgct  | 4080 |
| tctctgccga  | caaacatatt  | gtggctctcc  | attatctttt  | cccattgagg  | aatacgggtg  | 4140 |
| cataggtgtc  | cagtccttct  | gccataggat  | ggctcgtagg  | cttcggagtt  | gctgttcgct  | 4200 |
| gagggagaag  | agcaccgata  | atcccagtcg  | tgtcttcccg  | gccattgtgc  | ctgttcctcc  | 4260 |
| tgagtctgtga | gttgggatcg  | ggcagcaaac  | catgacggat  | aaggctcgta  | tgacgactcc  | 4320 |
| gggcactgtg  | gccggcagcc  | atgccgtgct  | atcatgccgg  | cgaattccca  | gcccttgtcg  | 4380 |
| agatggagtg  | tgtcggccga  | aatgggtatgt | ccgcttgggg  | ttggaagggt  | atggatatcg  | 4440 |
| ggatcaacca  | taggagaaaag | ttcgggaagg  | gttcttgcta  | atcataatcg  | aaaggagaag  | 4500 |
| aatacagagga | gaattattcg  | tttcccggca  | actcctccgt  | ctcaggacgg  | aacgatgcgg  | 4560 |
| tacattcttt  | ttgggcgaaa  | gtccgaggct  | gcgcactctt  | tcgatagccc  | gacgatgttg  | 4620 |
| ctacgggctt  | cgaccaattg  | accgcgggct  | ttggcagcgt  | ggcaaccgta  | ttttgggctt  | 4680 |
| gttctctcgg  | acgaatgagt  | gtcttgcgaa  | agtgcagaac  | ttatcgtaca  | gcccgttggc  | 4740 |
| ttgctctacg  | attgctgcac  | atttttcact  | tgccgggtcg  | gctgccatag  | atccagagcc  | 4800 |
| atcgcaaaagc | tgcgatcagg  | ttggctcggt  | tcgatgacag  | cacgcgtttg  | tgtaggcctg  | 4860 |
| atcccataag  | gtgggttttt  | ctcgcagagc  | cagcgtataa  | ccggttcggt  | cgggatgaag  | 4920 |
| agcatcacia  | attcgggagc  | tttgtcgcgt  | agtcctgata  | acttttgctt  | gccagttcct  | 4980 |
| ctatatgccg  | gctgatgcgg  | cgatgtgctc  | ccccagcagt  | cgtttgcgct  | cggcttcate  | 5040 |
| ctcagagcaa  | cgaaggaggc  | ataggccgta  | agggatacct  | tgctgtcgat  | gatcactcct  | 5100 |
| gaccgtttcg  | gtagcgaacg  | atcacatcgg  | gacgcatecg  | tctgccgtct  | catcgtaggag | 5160 |
| gagggtagcg  | ccttcatcat  | tggtcagggt  | ctctggatga  | agaactcttc  | tccttcgggtc | 5220 |
| aagccgctgc  | gtcggagcag  | gtttcgagga  | tcatttccgc  | ccagtcgccc  | tgtactttgg  | 5280 |
| ggtcgccttt  | gatgcacggg  | tcaggttggt  | ggcatcatcg  | ctgagtcggc  | tggtctgttc  | 5340 |
| gtgagctttt  | gtagctcttt  | ggcgagagag  | aaacgttcgc  | gcgcttcttc  | ttatagctct  | 5400 |
| tttcgacttt  | ttcttcgaat  | agcttgatgt  | gttcaactac  | ggtttgagta  | tttcaccgat  | 5460 |
| gcgctcttcg  | ttcattccgg  | aaagcttcgt  | gtcttgtctt  | cgaggatctc  | cgatgccgtg  | 5520 |
| gccttgaaga  | gtgcttgatc  | tcttcggata  | tttgtccgga  | gcgtttccat  | tcgcgttcca  | 5580 |
| attcggagtg  | gttgccctgca | agcgtgtctc  | cagtttcggta | cgaatacggg  | tggtcttttc  | 5640 |
| tgctcctctt  | gcagatccgc  | cagcttctca  | gtggcagcct  | ccagtgtgct  | gtcagcctat  | 5700 |
| ctgtctcagt  | gttgtgcctg  | cgatgggaag  | gcctacgacg  | agtcgggcaa  | ctattgcgac  | 5760 |
| gatgatgatt  | agccagtaca  | aaccatttcc  | cctataaatt  | ttactgtttt  | acgaacgaag  | 5820 |
| gtaatacata  | ctatgagacc  | tttcggcaat  | aagcaggcac  | tttgatccat  | tcattttaca  | 5880 |
| tgtgtcggcc  | gattgttttg  | tgtgcttatg  | gtatgatcaa  | tgacacaaac  | gatggcacga  | 5940 |

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| cggggaaaat | catccgacga | agaggtctca | ttcagggagt | catgtcagcg  | aatcgatata  | 6000 |
| ggaaagcccg | gaatgtatct | ttgaccaggt | cgatatgctt | acatgagagg  | atactatggg  | 6060 |
| ctattgatgg | aagatgtatc | tgctctgtgt | cggatggcag | gttcggggag  | agggaggttc  | 6120 |
| cgtgcagctg | taaaaccgat | agatgagatt | gtcgcacggc | atcttccggg  | agattcattg  | 6180 |
| tcaattgact | gtttttcagt | gtctgtatat | agatataaat | agttcaaaaag | taaccgatac  | 6240 |
| aggctatgg  | tcggaggaaa | actgccattt | gaacagcaga | tagactgaga  | gacttgtatc  | 6300 |
| aatcctcaat | cttagcctga | ttgcttcgac | gtcttcgaaa | agctaataaa  | gtagggtttc  | 6360 |
| catgatgaag | cggttgccta | accgactgta | aggagcaaa  | aaagagggct  | gtgacaaaac  | 6420 |
| gaattttgac | acagcccttt | tcttttgga  | tgccaatacc | gacttaataa  | aacaaggcat  | 6480 |
| ccaattcttt | cttgaatacg | tctttggact | gagcaccacg | agcttcttta  | ccacttcgcc  | 6540 |
| gttcttgatg | aacaaaatgg | tggggaatta | cgcacgccat | acttcatggg  | caattccgta  | 6600 |
| tttgcatcca | catccctttt | cctatgatag | cgcgtecttc | atattccgca  | gccagctcgt  | 6660 |
| cgatcgcgga | cctaccatgc | ggcaaggacc | gcaccatgta | gcccagaaat  | ccataccatc  | 6720 |
| ggcttgccct | cagctacca  | gccgtcaaaa | tggtgcatct | gtatttgtag  | tgccataatt  | 6780 |
| ctgttcggtt | tagttgggtg | ttattcttgt | tataatgatt | ggcttattca  | agtgcaaagt  | 6840 |
| taatctcata | agtcttcaat | tattcaccag | ttcgggggac | actttgatca  | gcgattttctg | 6900 |
| ctgtgccagt | cgacatcgaa | agtctccgta | tggtcataca | ctttgataaa  | taac        | 6954 |

## (2) INFORMATION FOR SEQ ID NO:503

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...466

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| ccgaggatgt  | acccaatgca | gcatttcgca  | tccgagggga  | gaaaacgtgg  | gcgtacagtt  | 60  |
| ccatcccgag  | atctaccact | cggaagaagg  | taccaaaccg  | ttggcaactt  | cctcgatata  | 120 |
| tgccggtatga | agcgtgattg | gactccgctt  | ctttcatcga  | agcgactgtg  | caggaacttc  | 180 |
| gcgaacgctt  | aggtgagaca | aggtgatcct  | ggcactctcc  | ggagggtgtg  | acagttcggg  | 240 |
| gggtgggggtg | ttctgaacaa | agctatcggc  | cgcaaccctga | cttgatatatt | cgatcatcacg | 300 |
| gcttgctgcg  | taagggcgaa | ttcgagcgcg  | tacttcagga  | ctagagcact  | tggtgtctcaa | 360 |
| tgtaatcggg  | gtgaatgcat | aagaaaaatt  | ctcgcagccc  | ttagcggcgt  | taccgatccc  | 420 |
| gagcaaaaacg | gaagattatc | gtcgcgggctt | catcgaagtg  | ttcgac      |             | 466 |

## (2) INFORMATION FOR SEQ ID NO:504

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...558

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gcctcggaca | caaagccgat | gaacgtgatt | atggcatagg | cgcccaaate | tgcgtctttt | 60  |
| gggtatcaag | aaaatgcgct | tgatgacaaa | caaccgggca | aacgtatcgg | actggaagct | 120 |
| ttcggcttgg | agatcgtaga | aaatatcccc | tggaaactgc | cccaaatecg | tacaacgagt | 180 |
| tctatctgcg | cacaaaaaag | aacgtatggg | gcacgagctg | cacaacatca | aataagaagc | 240 |
| gattcgcttc | ttaacagggt | cttaaaaaag | ccgtcggacg | tttgtcatac | gttcgacggc | 300 |
| ctttctcttt | aatcggcgaa | aggcgatgtg | catgcggttt | cctctcttta | tccgttatga | 360 |
| aactgttgca | caataacctc | ccacctcttc | attcgatcaa | gacagacaca | agcattgatt | 420 |
| cgacgaagaa | aggaagtatt | tatgcaatct | cttcaaagct | caagtatacc | tctgatggaa | 480 |
| acttggggaa | tttctgtttg | cttggtagcc | atatcttgag | gtttgatctt | tcctgaaaaa | 540 |
| cttagaatca | gctctgcg   |            |            |            |            | 558 |

## (2) INFORMATION FOR SEQ ID NO:505

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...2192

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| gccggcttaa  | tcggccgaaa  | agattaggag  | catgagggta  | ttcgcagcaa | tatctaacta  | 60   |
| tcattttaatc | gtttatctat  | ataatttcat  | tcggatgaag  | gctctcagga | cagcgatatt  | 120  |
| caactcctca  | tagagagctt  | catcgcgaca  | aatgtaagga  | aaaagttcaa | tcccctaaaa  | 180  |
| ggcattagag  | cgggtaaatc  | ctttagcttt  | gtgatcgata  | tagtgtaatg | agcgaagaat  | 240  |
| ataagctgaa  | tcgacagttc  | gaatattgct  | caaaaccact  | gcttttcaag | caaataaatt  | 300  |
| cgcaatcttc  | ctttacacga  | aagccgacgt  | gagatagaaa  | cgaaagatgg | ctatagcatc  | 360  |
| tttggtattcc | acatccggca  | acagggtctca | ttaatgctct  | gcaaaaagat | aaatgccctc  | 420  |
| agaaaacctg  | ccaaaacatc  | accgattttct | aatgcaacag  | tcctgaaaaa | gaaaaagaca  | 480  |
| aagcaacagc  | taaattttca  | aatacaatag  | tcctcgctca  | tcctccaaac | taataaggcc  | 540  |
| ccgtcgaaat  | cttctacgaa  | tttgacgggt  | gcctacgttt  | tatcatctac | aaacagcctt  | 600  |
| tttactata   | cgatttaata  | taaactgctt  | acaatctaca  | gaaagtaggt | tctcaccgga  | 660  |
| aaatatccgt  | ttcctaattct | ttttattttac | aacaatcctt  | tggctataat | ataagatata  | 720  |
| gccacagaaa  | aacattgttc  | cactctctct  | gttatccctc  | tgtgaggaaa | gaaattcgta  | 780  |
| ttttgtcctc  | attatcaaag  | aataacaacc  | tactacgtgc  | aatcgaatat | gctacgtcaa  | 840  |
| aagaaatcag  | agagtcgttc  | aagacttttt  | ttgcctcaaa  | agtcatataa | tcgttccctc  | 900  |
| tgcccccatg  | gtgatcaaa   | gcgacccac   | gtcatgttca  | ccaatgccgg | catgaatcag  | 960  |
| ttcaaggata  | tcatactcgg  | aataccgagg  | ctaaatacac  | tcgtgtagca | gactcgcaga  | 1020 |
| agtgtttgct  | gtaagcggca  | agcacaacga  | cctcgaagag  | gtaggccatg | acacctatat  | 1080 |
| cataccatgt  | tcgagatgct  | cggcaactgg  | tcgttcggcg  | attacttaag | aaagaagcca  | 1140 |
| tcgaatgggc  | ttgggaatac  | ttggtgacgg  | tgttggtctg  | gatccccagc | gtctctatgc  | 1200 |
| taccgtattc  | gaaggcaacc  | ccgaaaaggc  | cttgaccgcg  | acaacgaagc | ggcatcttac  | 1260 |
| tgggcacagt  | ttctcctgaa  | gaacgaatca  | tcaacggcaa  | taagcatgac | aacttctggg  | 1320 |
| aaagggcgat  | accggtcctt  | gcggtccttg  | ctcggaaata  | catatcgacc | tgggtcggac  | 1380 |
| gaagagcgcg  | cccaaataaa  | cggtttgagg  | ctgatcaata  | aagccatccg | cagggtcattg | 1440 |
| agatatggaa  | cctcgtcttc  | atgcaataca  | tcggaaagcc  | gaggtctccc | tgacgcctct  | 1500 |
| gccacacaag  | gtgatcgatc  | gggcatggga  | ttcgagcgctc | tgtgatgggc | cttgcaagggc | 1560 |

|            |             |             |            |            |            |      |
|------------|-------------|-------------|------------|------------|------------|------|
| aagacttcaa | ttacgatacy  | gatgtctttc  | agcctcttat | ccgtactttg | gctacgagac | 1620 |
| gggaatcgga | tacgggtgagg | attctacctc  | ggatatagcc | atgcgctagt | agccgaccac | 1680 |
| atccggacta | tcgccttttg  | catcacggac  | ggccattgcc | ctccaatgcc | aaagccgggt | 1740 |
| atgtcattcg | ccgtatcctg  | cgccctgcgg  | tcgtacggc  | tacaccttcc | tacactgccg | 1800 |
| cgaagcggtt | atgaccgatt  | gctgccgaca  | ctgatcgata | cgatgggcga | tgcttatccc | 1860 |
| gattgcaagc | acagcgcgaa  | ctgatcagcc  | gcgtgatcaa | agaagaggaa | ggagtctcct | 1920 |
| gcgtacactg | gaaacgggta  | tccgcctgct  | ggagaaaaaa | tagccgacaa | taaggctacc | 1980 |
| ggctccaccg | tattggacgg  | tgctcgctgct | tcgaattata | cgatacgttc | ggatttcccc | 2040 |
| tcgacctcac | agccctgacc  | tatcggaaaa  | tgggatgacg | gtggacgaat | caggcttcga | 2100 |
| cacggagtgc | agaagcaaaa  | agagcgtgcc  | cgtaatgccg | ctgccgtaga | agccgggaac | 2160 |
| tgggtagtgc | tacgtgaggg  | tgaatccaaa  | tc         |            |            | 2192 |

## (2) INFORMATION FOR SEQ ID NO:506

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 608 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...608
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| gngcgttcat  | aatcttctgc | gttttagttt | cttattagct | tgatttctgg | tttacgttgg | 60  |
| aatatgagtt  | cggcaacatc | tacggcaggc | gcattgcttc | gaatagggtc | tctccaagct | 120 |
| tttctatggc  | ttcgctcaat | tcttcgaaaa | accatcctct | tttggtagcg | caggcagaga | 180 |
| aagagcgtgc  | tttgcatitt | ctctaacgca | aaagagagtt | tggagtagct | acátgagcgg | 240 |
| tcgattgcga  | accactaaag | ctgacaccat | ccatagagaa | aataactcct | tcgatttctc | 300 |
| agttttgccc  | tttgttttga | attgtacttc | aatacctcgc | tttgtagttc | ggaggtaagc | 360 |
| tcttgccagt  | tcgtgcactt | gggtagtgcg | gctttattgc | atcgaagatg | gcatacctaa | 420 |
| gttgatcatt  | tcctcttagg | catgacgttt | tacagcctct | tttccttcgc | cccatttcag | 480 |
| cagggttaagc | tcggtgagtt | ctttgcagac | ctttgttgag | caatactttt | cattgctggt | 540 |
| gaaattgttt  | tcccttcatt | attcacacga | ttgatacaga | tgtgtaaggt | gggtgcttcc | 600 |
| ctgtcaag    |            |            |            |            |            | 608 |

## (2) INFORMATION FOR SEQ ID NO:507

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 494 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature



(B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| ggccgtaaag  | cgaaaaaaac | ggattccgcc  | gctccgacag | caaccggaga | caggactgga | 60  |
| tggcttacct  | gtaaagaaca | aggagtgtct  | tttcgtcccc | gagaaaacga | agccttatat | 120 |
| ccgaatgggtg | aaaaccggag | gcggggaacc  | cgaaaagacg | accgaacctt | aaccttacta | 180 |
| tctgataccg  | aagggtcccc | gtcctccttt  | ttccatggcg | gatacaaatg | tattgaatta | 240 |
| taaactgaaa  | tccaatcgta | tgaaaaacacg | aaaaacgatg | tgtatcgccc | tgttcttacg | 300 |
| acgctcgcaa  | ccggagcttt | tgcccagggc  | aacggcatgg | ccgaatcaac | gaagccacca | 360 |
| agatggtaac  | ctcctatttc | gacccggcca  | cgaactgatc | tacgccatcg | gagccatagt | 420 |
| cggcctgatc  | gggggagtca | agtctaccag  | aaattttctt | cgggagaccc | cgattccagc | 480 |
| naggaccggn  | gcct       |             |            |            |            | 494 |

(2) INFORMATION FOR SEQ ID NO:508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| agtattggca  | cgaaggcctt  | cagaaaataa | cggtgatcaa  | tccccttata | ccacttcgga | 60  |
| acaaggggtgc | aaagcctttg  | ccgacaatac | ccccgtgcac  | tcgcccattg | tatcacgcac | 120 |
| ctctatgacg  | aactgcgcga  | ccacncctgc | agtcgctcaa  | gcacgtcttc | ctacactatt | 180 |
| tcggcaagac  | cacttatata  | gtatctaccg | caaggaacgc  | tacatcacca | tccaagagca | 240 |
| ggacttatcc  | gtgacagctt  | tgtccggggc | ggattttcat  | ccgatctgat | ccgcacgatg | 300 |
| cgatggtgta  | catgtacgaa  | ctgcagagcg | ccatgggtcaa | gaggactgaa | tcctccgggt | 360 |
| agtacgtaac  | catcgactat  | aggccgatgg | aatttcacag  | ctatgaaact | gcggtttcat | 420 |
| agctgtgaaa  | ctttattttc  | aagtcgagaa | actatagtcc  | catggctgtg | aaactgtaac | 480 |
| cggcctgcac  | gcaagaaaaa  | tttgccgtac | gggaaaaaat  | ttgcttgctg | caggagagtt | 540 |
| atatccctcc  | ttatagaagt  | ttgaaaaatg | gggcgggtta  | ttcgattcca | taattcggat | 600 |
| taataaaata  | catttgccgag | aaaagcgatt | gccatgataa  | caggaagata | aaccgctttg | 660 |
| tcgtgacggg  | aaaaatcgaa  | ccggaaattt | ctgcgaccga  | gaatccgagt | cggcgcgcct | 720 |
| catcaagtcc  | attgcaacgg  | caataactcg | gtgggttatct | cgccacgtcg | aatggggaaa | 780 |
| acggactgat  | ccaattctgc  | tatgacaagg | aagaaatcgg  | caggaactac | tatctttttt | 840 |
| tatcgacatc  | ctccacacat  | cgagcctgcg | cgaatttact  | tactgctcgg | ccgcgagata | 900 |
| tacgaagact  | ctgctgccac  | agagcaaaaa | gtgatcaacc  | tcttcgtccc | gcaccctcaa | 960 |
| gtccgatcag  | tgga        |            |             |            |            | 974 |

(2) INFORMATION FOR SEQ ID NO:509

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

```

agcaaaactat gagtatatac gaatcggctg taaaaaagcc ggtcacaaca tattgatatt 60
cggggcgata gctatttttcg ggctatttctc actgagtcctc ttcccatcga cttgtatccc 120
aagattgaga cgagcaatat catggctcga cctcctatgc cggagccagt gcatcggaca 180
tagagaacaa cgttacaagg tcttgagaga tacgcttaac ggggttagca atctcaagca 240
cattattcga agagtcggga gaatgcttcc gtcattacgc tccaattcaa tgaagtgtgg 300
acatcgaagt ggctaccaat gatgtgcgcg acaagctcga tgcgtctcca acttcctgcc 360
cgatgatgtg aacaaaccga tgatcttcaa gtcgggtactg acgatattcc tatcaccatg 420
ctatccgtgc aggccaaaga ggtacgatgg cctgtgcgaa gatcctcgaa gacaagggtca 480
cgaatgctct gcacgccttt gatgggcgta gtgcggtgag cattatgggt actgtgaagg 540
ggaaatacaa gtgtatttgc gaatccggcc aaactggaag catacaactg accgtagaag 600
ct 602

```

(2) INFORMATION FOR SEQ ID NO:510

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

```

gcataaaagg agcgagtgaag aggggtggca gtaaggagtg aaagtagttt aacccccccc 60
ttgaggagct acttgacga gctcctcaag agaccattca cggcattttt gcgacatatt 120
tgctgcatt gcttgcgat atcaatgtat ttagtatttt acacgtataa acaagagcat 180
aaatatggca accaaaaaac tgaatcggca ccaagctttc tgcaagtata cactcagctt 240
cgcaggatcg catgaaacac tctttcctgc gtcaaatcaa tgccggtttt gattgcgtgg 300
tatttcgcac actgctgaac aagaaatata ccaagacaca gaagcncata ggtaaccctg 360
cctacgatgc gctgttgatg ttcaagaatc tatcttgagg acttggtatg gttttgagtg 420
actacgaagg tttgtggagt gat 443

```

(2) INFORMATION FOR SEQ ID NO:511

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| aggatggcag  | ttcgtatgag | aatatggtga | gcacgcattg  | acagccgctt | cggtgcccgg | 60  |
| agcatcattc  | gccgaaacgg | tcaagaacct | cggaggcatc  | ccgaagagcc | gttcgccatc | 120 |
| ttccccgaag  | ttcgggaaat | gtatgccctc | gcttggcaga  | actggagcag | atcatggcag | 180 |
| agcgtcgcgga | agaagacaac | gttggcgagc | cacccatcct  | gatttggcag | ccaagtccga | 240 |
| tgcgtgtttg  | ccggtcaaac | gccccaaatc | gactggaaag  | ctatagagca | gaaaccaatc | 300 |
| aggctacccg  | ctccgcttct | gccaccgtgt | tgggtactct  | tgcggagaag | tggagaatat | 360 |
| gattgtaacc  | tctgccgacc | tttccaattc | agcaagaccg  | atggcttctt | gaagaaaacc | 420 |
| cacgccatga  | agaaaggaga | ttcagtggag | cattcctgca  | gatgggtgta | tcggagctga | 480 |
| ccatggcctg  | ctctgtatcg | gtatggctct | tcattggaggc | gtcattccgg | cttgccgtac | 540 |
| ttcttcgtat  | tttccgacta | catgaaaccg | gccgttcgta  | tggctgcctg | atggaattgc | 600 |
| ccgtcaagtt  | tatctggacg | cacgatgctt | tccgtgtggc  | gaggatggtc | ctactcacga | 660 |
| accggtggaa  | caggaggcgc | aaattccctg | atggagaagc  | tgacaaatca | cagcggccgt | 720 |
| ngctccatgc  | tggtcttcgt | ncggccgatg | tgcaagagac  | taccgtagct | tggaagatgg | 780 |
| ctatgagaat  | acgcatactc | ctacagctct | gatcctttcg  | cgtcagaata | tcacgatc   | 838 |

(2) INFORMATION FOR SEQ ID NO:512

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...3275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| gaaatcttcc  | aaatggctat | gctcgaaccc | aagctggcta  | ttttggacga | accgatagcg | 60  |
| ggctcgatat  | cgacgctctc | cgcatcgtag | caggcgggta  | aaccgactcc | gctctccgga | 120 |
| gaatgctgct  | attgtgatca | cacactacag | cgtttgctcg  | agtacatcaa | gccggacttc | 180 |
| gtacacgtcc  | tttacagggg | cgcatcgtea | agtcgggagg  | agccgagctg | gctctcacgc | 240 |
| tcgaaaaaaaa | ggctacgact | ggatcaagga | agagatagga  | gaataatcgg | atataaggta | 300 |
| gaagaacaat  | atctgcaact | cttccgagag | aatcgcggaag | caaagacagc | cactccccac | 360 |
| gggtactcaa  | tgagcaacgg | gagaaggcgt | cgtggctttc  | gcctcgaagg | ggttgcctcg | 420 |
| gtatggcact  | gagaactatc | acgtaccgat | ttgtctgaac  | tattcggtta | tgactacgga | 480 |
| gtaaacctga  | tcgtgtcaat | ttccaatca  | gacagaaaga  | agcttttcat | tgtacgttgc | 540 |
| ggatttggac  | acggtctttt | gctacattgt | caatgatgca  | tacgataaga | atggagtcgc | 600 |
| gtatccgaat  | tgccggaagg | agcatttgtc | ggcagtcgag  | cgattttgcc | ctcagccatc | 660 |
| cggagatagc  | agctcgttat | tatgctaagc | cgctgcaccc  | gatcacgatg | gcatcattgc | 720 |
| attcagcacg  | atgttgctca | agatggattc | atcatatatc  | tgccggatgg | tgctgtactg | 780 |
| aagatccgat  | ccagctcgta | caactgctca | gagccgacat  | ggagattctc | gccatcgctg | 840 |
| gttactcatc  | atcttgggaa | aagatgccga | agcctctctg  | ctaattgcca | acacacgctg | 900 |
| gatacgcaat  | ctttcctcgt | aacggaagtc | gggagatatt  | cgctgcggag | aacagtcgat | 960 |

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| tcgccttgta  | cgatcttgaa  | aaagcagcaa | gaataccaaa | cgtatagcat | cggttcatgt  | 1020 |
| acgtcaagcg  | agaatttcgaa | tgtgacgato | aactgcatga | cgattcacia | cggctctgaac | 1080 |
| gcaacaacta  | ctactgccat  | cttgaaggag | aaggggctga | tctgacctgg | gcggaatggc  | 1140 |
| tattgccgaa  | gggaaacagc  | atgtcgataa | ctacagagga | tagagcatct | cgttcccaac  | 1200 |
| tgccaaagca  | atgaactctt  | caaatacatt | tcagccggca | ggcgaggga  | gctttcttcg  | 1260 |
| gacgaatcta  | tgtgcgaaag  | ggcacagaaa | acggcagctt | atcagaacaa | tcgcaacctc  | 1320 |
| ttcggatgat  | acggctcgca  | tgtactccaa | gccgcagttg | gagatctatg | ccatgatgtg  | 1380 |
| aagtgttcgc  | atggatatgac | tacggggcag | ctggacgacg | agctctcttc | tatctgcgtc  | 1440 |
| agcgcggcac  | tcctctggct  | gaagccaaga | tatgcttagc | gtggccttta | ccgatgatgt  | 1500 |
| agtcaagctg  | gttcatatca  | gcagcttctg | gaacgtctgc | gcgacattat | cgaacatcgg  | 1560 |
| ttccgcgggg  | ctgcatgcgg  | tgtggctcct | gcaatatctg | ctactaaaaa | tattttttct  | 1620 |
| cgtccctacaa | aagcttttaca | gctattagga | caagaaaaga | ttggttctta | tccatcagca  | 1680 |
| aggacgtcct  | tgctgatgga  | tttgtttttc | cggagagagt | cgagctacgc | tctacagctc  | 1740 |
| ttcagagttac | gctgtacggg  | atagtcacaa | tcctctacgg | acgtcagttc | gatctaagcg  | 1800 |
| gaaataggaa  | agtaggggtt  | ctgatgattt | caatattgag | ttcagggttt | ttaggcagga  | 1860 |
| tgtgtaagcg  | atgataccgg  | agatcagggt | ggtgacaaaa | ttgttgacac | tcgatgtctc  | 1920 |
| gtgtgctcta  | tctgacagac  | atttttgagc | atatcattga | cgtttcgaac | agggctctct  | 1980 |
| ttctcaataa  | aactttgtca  | tatagatgct | cagggaagtt | ttcatgttct | ttttgatttt  | 2040 |
| ggttatcatg  | tggatgtctc  | gacaaagagc | cggtcacaaa | ggttttggga | aatgtagcct  | 2100 |
| ctatcggaat  | gagtttgcca  | aaaagattct | tgggtgaatg | tcctgtcttc | agaggctctc  | 2160 |
| gtcatcacaa  | ttgcccgggt  | tgatttgata | gttgatgatt | tcacctgtgc | gttgataaca  | 2220 |
| atatgtagct  | tgaatccata  | aaaccaaccc | atgggctttt | gcctttttga | gccccatccc  | 2280 |
| tcatgttctc  | atgcccacga  | gctgtttgat | atgacaaacc | ttcagtgggg | tggaaatcga  | 2340 |
| gaaagagatg  | ccgtacattg  | acccaaacaa | cacatattga | gaaatgctat | cagcttgaaa  | 2400 |
| ccacctgtct  | ttgcagctcc  | acaaagcgat | tataagagac | aagatgtgga | actcggatcg  | 2460 |
| acaagaatgg  | gtaatgtatt  | gaagataaaa | agctttcaat | ctcggtatct | tgacagatga  | 2520 |
| aacaggatca  | ggatgggtcat | gacctcacgt | ccgacatctt | aaactttcta | ttcctgcatt  | 2580 |
| ttttgtctgc  | ctcttcgggg  | tctttttctt | gattgtttca | tcaaaaagct | tggagaaatc  | 2640 |
| atctatatgc  | aaaaaacatc  | aactatattt | gtcttcataa | agtagcgttt | tgtttttctg  | 2700 |
| atcttattga  | ttatcaactg  | ctaagataca | ataaattcgc | tacttttcaa | gcataatgcc  | 2760 |
| catgttcttt  | gggcgtttac  | cactaatcag | aaacaaattc | attggctttt | tcttacgtcg  | 2820 |
| aactgacgtt  | attttttaag  | tcacgtaatc | cattgagcca | tatggttcaa | tggaaaagcg  | 2880 |
| caatttttta  | tccccctcgt  | attcagaaga | aactcgctcg | aatgaaccca | caacaactga  | 2940 |
| aagcatgcaa  | ttttaatgcg  | tcagccctag | ggaatatgta | actcggcacg | cctcggtaac  | 3000 |
| tactgtaaac  | aaccgaggca  | gacaaaatct | aactatcggt | ttaagcgtgc | agcgatgaca  | 3060 |
| taatggcact  | agtactacca  | aataaaaaat | cgagacatcg | ctctactaat | aacttctctg  | 3120 |
| caaactttat  | ggacagattg  | actatcaaac | cctacaaaaa | agacatctct | gaatttgtaa  | 3180 |
| aatatgaaaa  | ttatgattta  | gtcgcataaa | cttacatcga | actcacctta | tgagcctttg  | 3240 |
| aaaaataagg  | agatggaggg  | aaaaggagaa | agcaa      |            |             | 3275 |

## (2) INFORMATION FOR SEQ ID NO:513

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...546

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggagaattgc | tgtttgcaga | ttttatttcg | ttcgaatcct | gacanaagtc | gaatttttgt | 60  |
| gccctctaca | tttcattttc | gcttaagttt | cgaaccgctc | gaaggtgtgg | catgtacaga | 120 |
| aaaagggttg | acagttggag | agaatcggtc | aactgtcaac | cctttttccg | tatgggtgca | 180 |
| ttcgccggag | gaatactgaa | ggtattaagc | atccatgcag | ggtaggcccc | attccgacag | 240 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gcttattcct | tgatagatca | ggttctcccc | ttggatcagc | gcagggctgc | agaagcttat | 300 |
| cggtcagttc | ttcgccatgc | agattacggc | cgatgatagt | gcctcgttgt | cgatcagcag | 360 |
| ggatatgagg | atagaatgga | cgccgtattg | caagctgccg | ggcttgccca | gnctttgtaa | 420 |
| tcggacattt | gcggccatgt | gtaccgagcc | ttgcgatggc | tttcttccat | gctcccgcat | 480 |
| tttcatcgag | gaaaccccta | cgatctcaag | tttccccttg | tagtcggcat | aaaccttgac | 540 |
| agatcg     |            |            |            |            |            | 546 |

## (2) INFORMATION FOR SEQ ID NO:514

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1119

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| ggagatcaag | accgtgaata | ccatcggacg  | agtattcata | tcagccaatt  | caggcgttgg  | 60   |
| cgcagttctc | tnattgtaag | gnccatcgat  | ctctccttcn | tgcgccagag  | gagaatgagt  | 120  |
| ataatacctc | ctatcatacc | acccaaagag  | caaagtgatc | gatgttgcta  | ccacctgcca  | 180  |
| tcggtgcaac | accaagaaca | gctctacaag  | gccgtatata | ataacaaaac  | acttggtctt  | 240  |
| gatggaatgg | ggataaagaa | aaggtagatc  | tcaccattgg | ggaagagcat  | cccagggccca | 300  |
| atagcaaccc | gaatacggct | ccggaggcac  | cgaccgtcgt | tggaaattga  | ggaaagcact  | 360  |
| cttgagcatc | tccgtaccct | ccggaaaagcg | aaaaactcgg | ccggactggt  | cacgatgggc  | 420  |
| atcagatcca | cagcccatac | gtctgctgtg  | ccaatgcagc | cgtaagacca  | cgaataacat  | 480  |
| agaagatgag | aaacgcttcg | ccccccaaaa  | ctgctctatc | agccgtccga  | acatccatag  | 540  |
| gaaaacatat | tgaagaagag | atgcgagagg  | ccatcgtgta | agaacataag  | ghaacgaact  | 600  |
| gtatgggatt | gaaactgtct | gcctgaaaat  | aatgcagccc | atgggtatcgt | tcagatcgat  | 660  |
| attgaatcgt | gcctcaagta | cgtaagcgcg  | aacaggaata | tcgcattgat  | gatgatcagg  | 720  |
| ttctgcgtta | cgggtgagca | aactgataat  | tcctttctct | aaagctattc  | atattatgga  | 780  |
| ttgtcttggt | ttctatttca | ataccaagta  | ttcgtgatgg | gacgattgct  | ctgtgatant  | 840  |
| tcagatcctg | caagagtga  | ctcttcnccg  | atatgacgaa | anataggact  | tgtatgctcc  | 900  |
| tatagggatg | aaactggccg | agatagccca  | gagtgcattg | cgcgagtgcg  | ggtgcaggta  | 960  |
| agcgatgtta | ttttcttcaa | tcgaaattgt  | agttcgcatt | gaatccgaag  | ctccagttcg  | 1020 |
| gtgtaggctg | atattgccgc | gnaagctcac  | cctctgcgtt | acccggtagt  | agtgctcctn  | 1080 |
| ttantgacnt | tgtacntatg | gcagtcggta  | gcaatattc  |             |             | 1119 |

## (2) INFORMATION FOR SEQ ID NO:515

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1290

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

```

ggacggaagt atgcgcagat gaaagagcgc ggcccttaaga tgaaggaatc gacctttata 60
atcccaacgg cacatcgctg aaagatgccg tagtgctatc gacggaggat gtacgggcga 120
ggtcgtttcc gatcgcgac tggtaactacc aatcaccact gcggatacga tatgatccag 180
gtcacagca cgctcggcat aactatctcg aaaatggatt ttgggcgatg agagaagcgg 240
atgaataccg aacaaggata ttcccggtgt attcatcgac aagatcgaag atgtacagac 300
tacgtcaaga aagatctcaa agccatcaaa gatcccaaca gcaggactac ctctctccga 360
agtacctgca aaagttgggt gacaagaagg ccgcaagaac ttttctgcca agaatccggg 420
gctttccgta gagatcaaaag cttctatggg ggcaatctct acctgatgtt taccaaaaag 480
acttatacgg tgttcgactg gtgggagcac ctcccaccag cattggcaaa ttcggtgcca 540
tacggacaac tggatctggc ctcgtcatac tggcgacttc tccatcttcg tatctatgcg 600
gacaagaatg gcaatcccgc accatactct gaagatatgt tccgctcaag ccgaagcggt 660
tcttcaatat ctcccttggg ggagtaaaga gacgactac gccatgataa tgggtttccc 720
cggtaactac caccgtatct caccgcttcc gaagtagacg aatggaaaag catcgacaac 780
gatatcgcat ccgcatgcgt gatattcgtc aggggtgcat gctcagggaa atgtggccga 840
tcctcagatc aaaatcatgt attcagctaa atatgccgct tccagaatgc ttacaaacgt 900
gctatagggt ccaactgggc gatcaagaca ccggcctgcg tcaaaacaaa caggcgatgc 960
aggacaggct gatcgcatgg gagcgaagca gggtactcct cgatatgaag aggccgtaca 1020
cgaaatcgag ctacggtagc caagcgtgcg gatctgcgcc gtcgttattg gatgatagag 1080
aaggcatcat ccgtgggacg gagtttgccc gttctcctat cccaccaag atgagacgaa 1140
agctctgcaa ggcaatgatg cttcgggctcg caaggagcga tcgataagat tcgtacacgc 1200
tacagcaaat ttgcccaaaa ggactcagtg cagagggtga caagaaagtg gccgtagcca 1260
tgctgacgga atactcaagg aaatgcctca

```

## (2) INFORMATION FOR SEQ ID NO:516

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...3212

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

```

aaaaaattgc agattcncag cccagtgccg ttgcccatct atgccatcag aacaaactcg 60
tcaatctcga cgaaatcgcc cacttaaaca aataaattga agcctaactc ccgaccttgg 120
aagtaagcaa agaccaaagt ttatcatcga gggaagagga gcggtgagat cgatgagaac 180
gccgctgaca ggatgatgaa acgaattcga tggggccagca gactgattcc tccatccgga 240
ttactcgccc gaatccgcat ttcaaactcg ccttgatagg acaaccataa gttggagctg 300
gcaacgaatc tgatgggtgc ggccagtatg tagctctatt tccaaagatg gtaattgtcg 360
gacgaagcta ataagcgata agagagagaa gcttcttact gttcggcact ttgcataccg 420
aagcaaagct tttgttcagt cttcgtttcg actgatataa tggacgagcg tatctccatc 480
cttggggagg tttgtttgac tatggcagca tatacctttt gcaccttccc atcgcgaaaa 540
tattattgag tcgcgcctaaa gccttactcg ttttggcaaa aacgaccatc cggccacagg 600
acgatccaaa cgatgggcta caccgaggaa gactttgccg gcttgacata tttctctttg 660
atccactgct tgaccgtttc ggacaggggc tgtaaccagt cttatcgccct tgaacaatct 720
ccccgacagc cttatgacta tgatcagatg attgtcttcg taaacgactt ccataatgac 780
agcctatgaa ccgaacagggt tgattctgat cctatattac atattcatac cgcacaaaac 840

```

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| tggactacct  | gtcccgtcac  | gtacgaagag | aggctactgc | caggaaggta | gctacgttag  | 900  |
| ccacatcttc  | ggcggtacca  | ccacgacgca | gggtatctgt | gcccgcatt  | gcttcttcac  | 960  |
| ttcttcgcta  | agcacggcag  | catatcggtg | atgataaaac | ccggtgcaat | cgcattggca  | 1020 |
| cgacagccag  | tgagcccagc  | tctttggcga | cactcttggc | caaaccgac  | ataccggctt  | 1080 |
| agaagctgag  | tagttggatt  | gtcctgcatt | gcctgataca | cctaccaaga | agccatattg  | 1140 |
| atgatactgc  | cgggtgcgctg | tcccatcatg | atgggatcac | ggcatggatc | atggtgaacg  | 1200 |
| ctgacttcag  | attaacgttg  | atcacgcac  | ccattgttgc | tcggtcatac | gcatacataag | 1260 |
| gccatcgcca  | gtaaaccggc  | attgttcacc | aaaatatcga | tccgaccgaa | gtcagccttg  | 1320 |
| atcgttccac  | cactgtatgt  | ngctgcacg  | aaatccgctg | cattggaagc | gttgccgctg  | 1380 |
| cacgtactcc  | gagccctttg  | agttcttcta | cgaaagcctg | tcgccctcat | cgatattcag  | 1440 |
| atcagtaata  | gccacatcgg  | caccttcctg | gcatacttat | aagctatggc | acggccgata  | 1500 |
| ccgctccgg   | ctcccgttaag | agagctacct | tgttctccaa | taatttcata | ctttgatttt  | 1560 |
| aattagtctg  | gacagatacc  | taccgatcag | atatgtatgt | ccgcgaagtt | tatttatgat  | 1620 |
| cgttaaattc  | ttaaacaactt | tcacttccaa | tctcttcttc | accgctttta | ctgccggaga  | 1680 |
| gagacagata  | ccgtggaaga  | tcagatgctc | cacatctcac | tgattcgctc | gaacgcgac   | 1740 |
| gttccggcat  | gcctaagatg  | tccgtgatat | acggcacttc | cagccccctg | attgagtggg  | 1800 |
| gtaagatctt  | ggcgtaatat  | gggtatcggg | tatagaaaa  | gcattaagcc | gaacaccttc  | 1860 |
| gtcaaaatgg  | aacagatcag  | atgttcttcc | ttgaggtcga | actccttacg | acagctcca   | 1920 |
| ccttccatat  | atcacgaaaa  | aaatcggcac | gaagcgtaac | ttgcgcacga | caatctcttt  | 1980 |
| gattgcttcc  | aaatgcgtat  | agatgaagtc | atcagcttct | tagtcggcgg | catagacacg  | 2040 |
| agagcagcag  | tctccaacag  | ctgtagagtt | cgtccagctc | cttatggaca | acggcaaaat  | 2100 |
| agatatcttt  | ttgcttttga  | agtaagtata | tagcgtgcgt | cgccccctgt | ttgccgatcg  | 2160 |
| gcgatgtcgt  | tcacgttggg  | cttctccaca | ccgatcttgg | caaaggctga | cgtgctacat  | 2220 |
| cgatcatcaa  | gttctcttgt  | tttcgccaca | ctcataaaat | ttttcgattg | ccctatatte  | 2280 |
| tatacggcat  | tctgtttcgg  | aacaatataa | ggtttttggc | gttgattttg | cacgtttgtt  | 2340 |
| tcagtattga  | gcaaaaagtc  | caccgtctta | gcctgtatat | tggtctggac | ggttctatcc  | 2400 |
| atatccaaga  | aaagttcgat  | cgaacaacaa | aaaaaagctg | tctcctttga | aggggacagc  | 2460 |
| tcacgcatac  | ttcttgttgt  | ctcacaagga | ttcgaaacct | acaaacagga | ccagaatctg  | 2520 |
| ttgtgctacc  | attacaccat  | gagacaatgc | gaagccttta | ttgcttcggg | tgccgcaaat  | 2580 |
| gtacaccttt  | ttgtgaacaa  | acaataaaaa | cacatttggg | ttttaattgg | catccatate  | 2640 |
| ttcctcatag  | agttcgattt  | tgaaaagatg | ggttggaaat | ctcgatttta | ggttctaaac  | 2700 |
| cggaacacag  | gtcaagatat  | tttagtcaat | ttttctgtcc | gttttgtact | tttgcgagcg  | 2760 |
| taaagaccga  | aaaaggtcat  | acatcagcat | caagggttcc | atctcaataa | acatcgatga  | 2820 |
| agaatatccg  | caacttctgc  | atattgcaca | tatcgaccac | ggcaagagta | ccttggccga  | 2880 |
| tcggttgctc  | gatataccaa  | caccgtctcc | ggcaaagatc | tgcaagatca | ggtcttggac  | 2940 |
| atatggactt  | ggaacgagag  | agaggtataa | cgatcaagag | ccatgccatc | agatggacta  | 3000 |
| tgagatggat  | ggagaaaagt  | atgtgctcaa | cctgatcgta | ctccggggca | cgtggacttc  | 3060 |
| tctacgaag   | tctctcgctc  | cattgctctt | gcgaaggggc | attgcttate | gtcgatgctg  | 3120 |
| cccaagggat  | acagggccaga | ccatatccaa | tctctatatg | gcgatcgaaa | acgacctgac  | 3180 |
| catcaccccta | ttgtaaacaa  | agtggatttg | cc         |            |             | 3212 |

## (2) INFORMATION FOR SEQ ID NO:517

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2179

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggggtaacct | tcgcgtatct | ctgagtcggt | tgcaggttcg | aatgtccac  | atcttacaga | .60 |
| tagtttctat | ggggactcct | gcttccagag | taatcaataa | gcgaaggaat | gccttcggc  | 120 |
| atggtaggtc | aggtcttctt | ttatgtcgcg | agaaccgcaa | ggcatttcat | caggcgacgt | 180 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| agattgggggt | ggtacacatt  | ggaaagagtg  | tccgacgggt  | atcgctcgttg | tattttctcta | 240  |
| tcaatcaagg  | gcttcgggca  | ggagtttgac  | acaggcttga  | agttcgtttt  | tcttcgacgg  | 300  |
| tattttaagcc | atagacttcc  | ttcatcatcg  | gtgaagagat  | tgttcgtgta  | accgataaccg | 360  |
| catcagcata  | ggaagttccc  | gtatagcagg  | caagaggaag  | agatctcttg  | ccaagatatg  | 420  |
| agagctacga  | tgttcgggaa  | taccaagtca  | cggattttct  | caaaggattc  | ccgacttagg  | 480  |
| gctttcgggtg | cttctcctct  | tgcttgggga  | gactgaaatg  | agcgaaaaaa  | catttatcgc  | 540  |
| atagccttcc  | ttgtaggctt  | tacggcatac  | ttttttgatg  | atggccagta  | gtgtcggctg  | 600  |
| gtctctatgg  | taagcccttt  | gtcgtccacg  | acaaaaactg  | atagtcgtga  | atgaactggt  | 660  |
| cggtcagctg  | accgaaggca  | atgtcctgga  | gtggaaatttc | ttttgaatga  | actccgccaa  | 720  |
| ggttcttcgg  | gtgtaaaata  | ggcgggggat  | gttctctttg  | cccggtctat  | cccgatacgt  | 780  |
| ttacgagttc  | ctcgcagacg  | atgtccgtca  | ttgccagcaa  | ggtcactctgt | gttcgagact  | 840  |
| tccctgaaac  | agattcttga  | ccgcttcggc  | atcaaagtct  | gcttgcgttc  | caccaagggtg | 900  |
| tcgaatgcag  | catgaatgga  | aagcaacaac  | tgtctaattt  | ggcattgacc  | tctactgctt  | 960  |
| cattgtctttt | accgttcaat  | gactctcacg  | gggattccat  | aagtcaggag  | tacaggagag  | 1020 |
| tttgcaacta  | actgcaccat  | cgaacgattg  | acggtaatgc  | gtcccatgat  | cggggccttg  | 1080 |
| ccgacttgctc | gggtctgctc  | tttttcagggt | agagcaaac   | cttgaattct  | ctatcttcat  | 1140 |
| acgctttaac  | tttatgggca  | aaattaccgg  | ttatcaagcg  | ttctctgata  | cgcaaaaatat | 1200 |
| tgataaacag  | ataaaaagaa  | accggttgaga | aaaattcttc  | caataatcat  | tacctcagtt  | 1260 |
| tgttcgggaa  | acaaaggata  | acggtttggt  | aactgaaagg  | tctcaatatc  | ccatactggt  | 1320 |
| ttgctatccc  | tatctgtcgc  | agaacataga  | aaaacaacta  | attcacaacc  | agtaccatat  | 1380 |
| ttccacctat  | gttctcttta  | cgttgcttta  | ggcttgattt  | tccacatggc  | ccggcacaca  | 1440 |
| tttgccacga  | tgtctttgag  | caaaggcggt  | ccatcgaaatc | cgtgtcgaag  | atgctgggac  | 1500 |
| acaccaatat  | caaaacgacc  | agatttacgc  | ccgtatcacc  | aataaaaaaga | tagaacagga  | 1560 |
| catgcttagc  | tatcggataa  | gctggatata  | ttcagatctc  | cgggtgtcaca | agcaaaaaat  | 1620 |
| gacttgaaat  | tgaatacaaa  | ttctataaat  | caatgatatg  | aatacataac  | agcagatgta  | 1680 |
| agcgtcatcc  | ggaataaaaat | tcttgagatt  | cgtggaacag  | agtgatattg  | gattatcatt  | 1740 |
| tggccgaact  | ctacggtgtg  | cagaaaaagt  | gctcaaacag  | gccgtcagga  | gaaatttgca  | 1800 |
| gcgcttcccc  | gaaattttat  | gttcgaactt  | accgaaaacg  | aatggacgga  | actggtcaca  | 1860 |
| attgtgaccg  | gttaccggaa  | accctcaaac  | acagttccgt  | tgctccgatg  | gttttaccga  | 1920 |
| gcagggagta  | gccatgctat  | catcgggtgt  | gcgcagtcgg  | cagcaataga  | agtgaacatt  | 1980 |
| gccatcatgc  | ggactttcgt  | tgccatgcgc  | ggatgattgc  | cggttatgaa  | gaactcaaaa  | 2040 |
| agcgtatcga  | agaccttgag  | taagctgtaa  | tgtgcagttc  | agtgagttgt  | acacggccct  | 2100 |
| gacggagtgt  | tggagcaaaa  | agaaaaagcg  | gaaaagcctc  | gtaatcccgt  | cggcttatca  | 2160 |
| ttccgggggat | cctctagag   |             |             |             |             | 2179 |

## (2) INFORMATION FOR SEQ ID NO:518

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...831

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| tggccccgca | aacggtnaag | ncaagattaa | gatnaaatgt | caaaggccgt  | ctgacgtcag  | 60  |
| gtccaatcgt | tttgctnata | cactcgaaat | gaaggaagcg | atgataatgt  | gccggcttgt  | 120 |
| ggcaatcaat | accatcgaaa | ttgtcaagtt | gaggagattg | aaggttttgtg | gtgtgaaggc  | 180 |
| gttcagtgtg | cagaaatttg | gtcgtcacgg | gtgccaacaa | gtttgaattt  | gagcttgata  | 240 |
| agcctacttg | gatattacgg | ttatttcagc | agtatcgact | ttcagtgggtg | gtaagaaaa   | 300 |
| cttacaattg | agtataaggt | aagcaataca | tcgaccaccc | agctctgaaa  | ccggggagcgg | 360 |
| ttgtaacgct | gttcagcgat | aaggataaca | ataagtcttc | tccggcgggag | atgttgctgt  | 420 |
| tgcaacacag | gagttggctg | cgaataaact | aataccacac | ctcttacgca  | gataatgaag  | 480 |
| gtaaaaggag | gagctcttcc | catacgggca | atttggttct | tacgatactg  | cccaaaagacg | 540 |



352

|            |            |            |            |             |            |            |            |     |
|------------|------------|------------|------------|-------------|------------|------------|------------|-----|
| ttgctactgt | gagatcaa   | at         | cccctatggt | cacgttaa    | ac         | catcttcctc | gaattactgg | 600 |
| atcggaggaa | ctgtaggtaa | gcctaacgaa | tggaaaggcc | gaacaactgg  | accaatgacc |            |            | 660 |
| aagttcccg  | tgccgagag  | gatgttaatt | cgccactgag | gtgaataacc  | cgactgatcc |            |            | 720 |
| gaataatccg | aagtcggtcc | tgccaaggag | aacctgcac  | tggaacgatat | acaccagaat |            |            | 780 |
| ggcaagccgg | tcgcgttatc | ggcaacctga | tcaatgactc | tgacaaagat  | c          |            |            | 831 |

## (2) INFORMATION FOR SEQ ID NO:519

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...692

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| tacaggattg  | tcataattgt | caatgagttc  | cctcatatat | ccctgctctg | tataaggctt | 60  |
| gccatataat  | aaccgacggg | atgccctccg  | aagagcacag | atcagccacg | ggtttatact | 120 |
| ccccgtcttg  | ggaggtattc | ggatcgaagc  | gatggacagg | gagtcgattc | gggctaaagt | 180 |
| attcgggtgca | ttggccactc | ttctttatag  | gcttttacga | actcgtcgcc | gaagaattgc | 240 |
| atgatttgtc  | gtcgtttcct | tttttggtcaa | tcagatctgc | tattccttcg | ttctgaaaag | 300 |
| atcgaaagca  | ttcaaaaaag | aatctccgga  | tgaaccttga | taaccatttc | gcgatagttg | 360 |
| tggaaaaaact | cgtgagtaaa | taggtctaca  | agtcttcttc | ttgcatcgaa | agcgcgagat | 420 |
| tcagggtcaag | gaaaatagca | tatcgcgtag  | actggcatcg | ggaatagtgg | caatcagaaa | 480 |
| gaggtcgttc  | atagcggatt | ggatgaccag  | gctcgttcgg | gtaagtattt | ttttgtcttt | 540 |
| catttgccct  | gtacaatagg | gtgagaaaat  | ccgtatgcag | aagaaaacgt | cggcttcttc | 600 |
| tcgtttacgg  | gcgagccgac | agatattttg  | tctgaggcaa | gaaggcatat | tcgttattgt | 660 |
| agcaggatgt  | tcaagatgct | tgtccgttct  | gc         |            |            | 692 |

## (2) INFORMATION FOR SEQ ID NO:520

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...688

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

|            |             |            |            |            |            |    |
|------------|-------------|------------|------------|------------|------------|----|
| tccttgccga | tggttggttct | ttcggcactt | tctcagatta | ctatcgtttc | aaaagcaagg | 60 |
|------------|-------------|------------|------------|------------|------------|----|

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| ctgattcgct | caaaaaacgag | gcatgacctg | tgtgtctcgc | gaacctcaag  | catatacntg | 120 |
| aaagaaactt | gtggaaatct  | ctgtttgttg | gcagccatac | gcctgctctt  | tgatctttcc | 180 |
| tgaagataca | aagaataact  | catacgagag | gatactatgg | tctcatatag  | aacgttttcg | 240 |
| atttgatgta | cttctttcgt  | gagattgcca | ttacatgctt | gcagcgagga  | atctccgagg | 300 |
| gagattgcct | gtggccgaac  | gcaggccatt | gctgatctct | cgcagaaaaac | acagtctgcg | 360 |
| aattggctga | agatcataca  | caccggatgt | tgcaccctgt | gaagtgtttg  | ctatgtttgt | 420 |
| ctacttgaaa | ctctgccaaag | aattcttaat | caaggagcca | ggcaacaagc  | gaacaactcg | 480 |
| ggcgaatggg | ttatatattta | tactcatcag | agtttgtttt | tgtgataggc  | caagggtaaa | 540 |
| ttatttgccc | agggcactct  | gataacaaac | gaaggagagg | caccgtgtag  | ttcctctcct | 600 |
| ttctattgcc | aaaaactgac  | atttaggaca | cgattgcttt | gacagagtag  | atagtggctt | 660 |
| gagaaganaa | aagaatgggt  | aaaatcgc   |            |             |            | 688 |

## (2) INFORMATION FOR SEQ ID NO:521

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1135

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| gaactccgcc | gcaaaacgat  | tcgactgact  | ttcgctgcac | ctgccgtttg | tcggtgcctt  | 60   |
| atagctgttt | ttcgtcattt  | caggtatgct  | gcctgctttc | caatcagttt | atttgatttc  | 120  |
| ctttgcgtcc | agtgaagca   | gtaatgcgag  | tgaatggttt | agcaggaacc | ggtagatttc  | 180  |
| tttatttctt | tggatgata   | tgaagatatg  | acacacagat | cgtaaaccga | attcggcaat  | 240  |
| ttctctttac | cttgtttcat  | taaaaaacca  | aagatgagta | tgaacatcta | cgtaggaatc  | 300  |
| tgaactatcg | ggttcgcgaa  | gaagacctca  | caggtctggt | gcacagtatg | gcgccgtaac  | 360  |
| gagcgcaaga | gtaatcacag  | acagagaaaac | cgccgctcac | gcggattcgg | cttcgtcgaa  | 420  |
| atggaagacg | agaatgatgc  | agccgtgcca  | tcgaagagct | gttcgatcag | gaattccaag  | 480  |
| gtcgcaagct | atcgctcaaag | aggcattgga  | acgtcccag  | cgtgctcctc | gccgtacttc  | 540  |
| cgacacgaag | atcgctattg  | atccttctcc  | cacttccggc | aagtcgtaca | caacgccgat  | 600  |
| acggctttcc | ctctgagagg  | tcttctctca  | ttattctacg | acacgaatta | caagacaggc  | 660  |
| cgcaggcaca | ccatcatacg  | gtgttcctctg | cggccttctt | gcatctgctt | gtaccatgac  | 720  |
| agcccttgtc | acaaacatcc  | caaccgcaac  | tatatacggc | tctcaccgaa | cattccaccc  | 780  |
| ccccaaactt | ccatccgcca  | cagagcagat  | agcatcttcc | atcaatagac | catgtatcct  | 840  |
| ctcatgtgag | accatagtat  | cctctcatat  | gagaccatag | tacctctcat | aggagacccat | 900  |
| agtatcctct | cgtatgagac  | catagtatcc  | ttcatagtag | accatagtat | cctctcgtat  | 960  |
| gagaccatag | tatcctctcg  | atgagacccat | agtatcctct | cataggagac | catagtatcc  | 1020 |
| tctcgtatgg | accatagtat  | cctctcatgt  | gagaccatag | tattctctca | taggagacat  | 1080 |
| agtatcctct | cgtatgagac  | catagtatcc  | tctcatgtga | gaccatatat | cctct       | 1135 |

## (2) INFORMATION FOR SEQ ID NO:522

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| tacttctttc | ttaatgagac | tgataattcg | ttgttggtt  | gatgtatcct | tttgaacgtg  | 60  |
| atattgaaaa | ggctcttttg | actggcctgt | cttatactga | ttgttaattc | ttctcctcgg  | 120 |
| attcggtgtc | tttgtgatcc | gatgtgtcaa | tatggcactg | gtagcccca  | tcgtaatcac  | 180 |
| atcgccatcg | ttcagttgca | ccattctttt | ttgtccagaa | gacgtcctcc | gacaaaagta  | 240 |
| cctacagact | atcgtcacg  | gcaatcgaat | aaagaaaaga | tccgtctttt | ttnggggtcac | 300 |
| tcgaagtatg | cagtgggtgc | gtcccatgct | tggatcacgg | gtcatactgc | aatgtccaca  | 360 |
| accgagtctt | tgttgcgacg | tcctatcccg | tttcctcctt | tctctg     |             | 406 |

(2) INFORMATION FOR SEQ ID NO:523

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| ttagaaacga | agctgatgcc | ccatcgggct  | gataaaanag  | ttnggcantg | tcagaatcat | 60  |
| gtaggtcaat | nccatcaacc | aaggagaaac  | tttcgtaact  | cnacccctgc | attacgtctt | 120 |
| tcgaaagtag | gcagtcccat | tgacccgtag  | ccatcacgac  | gaaagcaagt | gcagcgataa | 180 |
| acataccgat | cacaatttct | taggggtgga  | aggctccata  | ttacgtttct | tcagaaaacc | 240 |
| gaagagaaga | gcagaagtgg | cgtaagagtt  | actacgaaga  | acgggttgat | tgacggaaca | 300 |
| tttcagctcc | cactattgaa | gtgaaaccaa  | gatcgagttt  | tacctactta | ggtcaatata | 360 |
| atccttagca | aactgagtcg | gcgatactcc  | gtttgggtgga | aagacatcca | gaagaaaata | 420 |
| acgacaccga | aaactgcgca | agagcaataa  | tgcgttggcg  | gatctcatcg | gctgccatct | 480 |
| tgatttcttg | ttttgatctt | tatgagcctc  | agttacggca  | ttagcttttt | gatcagcgga | 540 |
| tattgatgct | tattgatgat | ataaaatcag  | gaaagaaatt  | gccttaaaaa | tacggctgca | 600 |
| aggaaatgca | tagtggaatc | ctgggtgctga | ataccttgat  | atatt      |            | 645 |

(2) INFORMATION FOR SEQ ID NO:524

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggctcttctc | gaacgtataa | ataccggccg | ctaccggcaa | atattgctag | cgggccttgc | 60  |
| ttcacggctt | tggcagacag | ctttcccggg | ggtgcaacgg | atttgctgac | aatgctgtgc | 120 |
| tcgaagagta | tttgaaagct | cattccatca | tgattccctc | atcttgctca | aaggatcgca | 180 |
| cggcatccac | ctcgaaagat | aattcctcta | tgttgaagca | aacccttgct | caaaggcagc | 240 |
| aacaaatctc | tctgtacaac | agatccagca | aatcaaactc | ttggagcttc | cggcattgag | 300 |
| ttagaagaga | ggatacagaa | agaactggag | gccaaccctg | cttggaagaa | ggagcgtacg | 360 |
| atgaggaggt | ggccggcagt | gcggatggaa | ccaagacaat | cttatggggg | acgaca     | 416 |

(2) INFORMATION FOR SEQ ID NO:525

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| agcttgggta | tcttgcaatt | tctgaaatct | gtgcattctat | cacactgtct | ccagcttttc | 60  |
| gaagagcaat | tcgggattgc | ccaanacgtg | tccttcggta  | agagatccgt | actacccaaa | 120 |
| cgatcccagc | cgaaggaca  | gtcggtgaga | gcacgcacat  | gagttttgcc | gaggagaaag | 180 |
| gcaggaacgg | ttcgaagcga | tagccagatt | ggccgttata  | tcagagaca  | gattgaggat | 240 |
| cgtagcacac | ggttcatatc | cgtttttgcc | agcttccaag  | gttccgtatc | ggccgatatt | 300 |
| tattgcctat | acgtgccaga | ttcatcgctt | ctttcagtgc  | ttccggaagt | ggaacgtatc | 360 |
| caactgatgc | tccaaggcct | gcttcacggc | tgaaactcct  | ctatcgtagc | gctgtcgcaa | 420 |
| tcctgcagct | cgcctttggg | cggacagctc | catcgaagta  | tttatgagta | aggaccaatg | 480 |
| cccggttcac | aaattgccga | atatggctac | cagttcattg  | ttgttgcgag | cctgaaagtg | 540 |
| cgccacgtga | agtcgttgct | cttcgtctca | ggagcgttgg  | ccgtgagcca | tagcgcagta | 600 |
| catcctgctt | gcccgggaac | tcttcgaggt | attcatgagc  | cagacggnc  | agttccgact | 660 |
| ggtggaaatc | ttatctcctt | cgaggtgaga | aactcgttgg  | caggcacatt | gtcaggcagg | 720 |
| ataaacgaac | cttcgcacgg | agcatggccg | ggaaaacgat  | ccagtggaat | acgatattat | 780 |
| ccttccgata | aatgaac    |            |             |            |            | 797 |

(2) INFORMATION FOR SEQ ID NO:526

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1398 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1398
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| aggaagagga  | gggagaggaa  | taatccactc | aagccctatt | ccctctatct | cttctcttct | 60   |
| taccgtaac   | ctctctaagc  | ggagtacttt | gacgctgaat | ggcgggtgtg | cataatgcgc | 120  |
| aaattgccgg  | gttgcttgcg  | acattcgctt | cagtcacata | ctttaatcag | cctcagcacc | 180  |
| ttgtacttta  | ggcattttac  | gtacctaaaa | gggggctgtg | ccaagaatga | attttgacat | 240  |
| agcccgtcag  | actctcgggg  | gacaatgcac | ttcgcttgcc | ttttttctta | tccatcaact | 300  |
| tttttcacga  | tggcaaaagc  | tgtggtagaa | acgcctttga | tgcccaatac | tttcagatca | 360  |
| agcaaaaaaca | ccctgatgct  | atcctgctct | tggggtggga | gatttctacg | aaacattttc | 420  |
| ggaggatgcc  | atcggtggctt | cgagatcctg | gggataacgc | tgacacggcg | tgccaacgga | 480  |
| gctgcccagt  | tgctgaattg  | gccggctttc | ctcatcatgc | gttgataacc | tatctgcccc | 540  |
| attggtacga  | gccggcaagc  | gcgtggccat | atgcgaccaa | ctggaagacc | gaaaaagacc | 600  |
| aaaacgctgg  | tcaaacgcgg  | tattaccgaa | ctggctatcc | cggcgatcgc | accaacgaca | 660  |
| atgtactctc  | tcataaggag  | aacaattcct | tgcagccgtc | tctgcggca  | aagaggtcct | 720  |
| cgggtatttct | cttctgacat  | atccaccggc | gaatttatgg | ccggacaagg | caatgccgac | 780  |
| tatgggaaaa  | actcctgacc  | aactaccgcc | cgaaggaaat | cctcgtggaa | cggcggagcg | 840  |
| gtctcgcttc  | aacgacctct  | tccactggag | cggatttatc | ttgatatgga | agactgggct | 900  |
| ttctcctcgg  | agaacaatcg  | actacgcgta | ccaagcactt | tgacctgaaa | agcctcaaag | 960  |
| gtttcgggct  | ggaagagctt  | cgatggcagt | aacggcagcc | ggagccgtac | tgaactatct | 1020 |
| cgatctgacc  | agcaccatca  | gctacaacac | atcacatcgc | tgagccgact | ggatgaaacc | 1080 |
| gggatgtacg  | cttgataag   | ttcacgctcc | gaagccttga | attgcttgcc | cgatgaacga | 1140 |
| gggaggcaag  | agtctgctcg  | acatcatcga | ccatacataa | cgcctatggg | agcaaggcgt | 1200 |
| atacgacagt  | ggatcgattt  | cccaccaagg | accctgcacg | catacaagcc | cgacagcgag | 1260 |
| tggtggagtt  | tttctccgac  | atcctgaaga | gcgagccatc | attgccgaac | atctgacaga | 1320 |
| gatggcgact  | tggaacgttt  | ggtgacgaaa | ggcgccatgg | gacgcatttc | tngcgagaaa | 1380 |
| tggtncacta  | cgtgtcgc    |            |            |            |            | 1398 |

(2) INFORMATION FOR SEQ ID NO:527

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 686 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...686
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| cagggatcag  | gaggaggagg | gctctaacc  | gaatacgatc | cggagaccat  | agacaatcca | 60  |
| caagactaaa  | caacgaaagg | agtgcgtcga | tccgaaagtc | cggcgccactc | tttgtataga | 120 |
| ttcagatttg  | actcataaac | aatcaatagc | ggacttcatt | ctcttaaaat  | aagtatatcc | 180 |
| gcaaaaataaa | taagctatta | caagtaaaat | caactttatc | ttagggttaaa | gctcaaggta | 240 |

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| attgatatac | tctggggttag | gatgataact | athtagttaa  | agaaaaataag | aaaaacttat  | 300 |
| tcacgctaaa | acatggcaaa  | aaaattcaaa | atagaaccta  | ttacaaaagg  | catatgacac  | 360 |
| tacacgaagc | aatggagaaa  | ttactcagag | agctggaaga  | ggtatgacaa  | aagataaaat  | 420 |
| cgcagaaaaa | ttaaataaaa  | aaagtggat  | cagaaaagaag | actgttcaga  | aattagccca  | 480 |
| aatcaaattt | agcgagagca  | agcacatacc | cagagatctt  | ccatcgcaaa  | ggcggaaaaat | 540 |
| ttctctagtt | aatagaaaata | gaacacaaca | atctctatca  | aaagaagttc  | aaaagctcct  | 600 |
| aaaaatacaa | agcagatcca  | cagaaaaaat | ataccatagt  | tgaaaaagag  | ctgctagacc  | 660 |
| aactaaaaat | taaacttgnc  | aaagta     |             |             |             | 686 |

## (2) INFORMATION FOR SEQ ID NO:528

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...4735

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| ggctttggac  | tttgettatt  | cgcttcactc | tgattttgga  | gaccattgct | cggggccaaa | 60   |
| gtgaatcaca  | aactcgttcc  | gctcagttat | gtgctcaaag  | cggtgatcag | gtggaggtac | 120  |
| tttcgagcaa  | aagccagcaa  | ccgaccgaga | gtggttgccg  | tatgtgacta | cggcacgagc | 180  |
| caaatcgaaa  | gtagatcttt  | tctccgacgc | aaaagacggg  | agctgatcaa | tcgtggggaa | 240  |
| gaacgggtgt  | cagtgttata  | cggacatccg | aatccatggt  | ctctgccgag | ctttggatag | 300  |
| gatcgacgcc  | tatttcggtt  | tcctcaatcg | cgaaacattc  | ttcacgccgt | cggtacgggt | 360  |
| acggatatctc | tgcccgaag   | cttcaaaaaa | ctcttcaggg  | agaacatagc | ggtaactttc | 420  |
| tgatgagggc  | tatccgttcg  | gattgaaagc | gggcaaaagc  | aacaaaacct | cctctccatc | 480  |
| cggtaaagccc | cagagaaaag  | ggataagaaa | gcttacaaca  | ccaaaaagac | ttatatcctc | 540  |
| aagaggacga  | attctcccgt  | aactatcaga | ttgccgaatg  | ctgcaaacga | ttccgggcga | 600  |
| cgatgctttc  | ggatttatca  | acgacgataa | tactgtgtcg  | tacacaagcg | atcttgcccc | 660  |
| attgccatgc  | gtttgaaaag  | cagcttgcca | accgcaccc   | ctctaccgaa | tggagcttgc | 720  |
| acagtcgtac  | ctcgtcgaag  | ctaagctcgc | actcaagggc  | attgactcca | ccggtatcct | 780  |
| caccctgtga  | cacaggttat  | ttcgaagat  | ttcaatgtcg  | gcatcaagca | catcagctta | 840  |
| cggccaaaaga | tggcatcttt  | gagggacaaa | tccatctgct  | tggcacagct | ccgacgacct | 900  |
| cctgaagatc  | tgtcatcagc  | ttcgtcagaa | taatacatcc  | agtctgtcgg | acgcataatc | 960  |
| taatggccaa  | gaggtctctc  | cttttgccgt | gccggatttg  | tatgggggtt | actctgcagt | 1020 |
| cgctttacga  | atctctgaca  | ggaaataacg | tgcgaccctg  | gtatattgcg | tttagcgtta | 1080 |
| gctaatacgtc | ccttaaaaag  | acttttaagg | gacgactact  | tatagcgtat | tagcgggagg | 1140 |
| ttcttataga  | aataataatc  | tcacttctta | agcatattga  | gaaaggggtg | atcgaaaatt | 1200 |
| gatttcgggtg | caccccttgg  | tattgtcctt | aggccaaagc  | ctatatgaaa | cgattcttgc | 1260 |
| tgtttttaggc | cttattgcca  | acagtactgt | tcatatggat  | tgaccctgat | tcggattaag | 1320 |
| ctcaaccatt  | ccgggtacgc  | taccgaagat | caggatggac  | acgagaagag | ccagatagca | 1380 |
| taaagctcgg  | ggaaaacagc  | catcaccatg | gtagcacctga | aacgttgtga | ccaccgccga | 1440 |
| tagcctgaat  | accattagcg  | catacctgtg | ttggcggatg  | gcagacatca | gacctactac | 1500 |
| acccagtgcc  | aaaccggcga  | gaaaatagcc | caacctgcaa  | gcagagtaag | agcattggca | 1560 |
| gcaaccaatt  | ggatgatcaag | ccggatgcca | taaagaagcc  | cacgaaacca | tagagtcctg | 1620 |
| tgaactcggg  | agagcactaa  | gaccgatgta | gagaccagct  | gaatcggggt | cttcttctat | 1680 |
| gcgccaacgg  | tagtgttacc  | gcagatcggt | acgccatggc  | acttccgata | ccggtcaatg | 1740 |
| caaccatcaa  | tgcaataacc  | agatagctaa | catttggtcc  | ataatacttt | tgtgttgttt | 1800 |
| agttgttatg  | attttttgaa  | ttgttctttt | gtgatttagg  | agcgtttgaa | cggtgtgtac | 1860 |
| tgttgcccc   | tccttcaaat  | tcgtgtttct | tatagaactc  | tacgaatgtc | aacgaatggg | 1920 |
| gtgaacaagc  | gaactgatca  | tcgtaagacc | gaagtctaga  | catgaccgat | cagcaaaatg | 1980 |
| atcagcatca  | cgatgatccg  | aggtacaatc | taatagaagc  | agtcatatcc | gtagccaacg | 2040 |
| tattgaatac  | gccaccgaga  | tagagcccgt | gagtcggatc  | gcaaacagtc | ggatatacga | 2100 |

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| aagcgtacgc  | ccaaaagtcc  | tgatgctgtg | ttataagccg  | tccacaagcc | gtaccacaaat | 2160 |
| tgataaacgg  | attcttgcca  | ggtgaattgt | agaagaaggc  | taccaacctc | cggcaactgc  | 2220 |
| aatgccgaac  | atgacattga  | tcaccacttc | cggtccttcg  | gtgctatcat | gggtaaagcg  | 2280 |
| aatgccaaata | tactgcccgt  | gatatgactg | cccacgcaaa  | tgtggccagg | ctatacttca  | 2340 |
| ctcctcgtcg  | gatttgatct  | tgataccggc | caaaatcttg  | gcataaatga | tctgtatcag  | 2400 |
| acgataacaa  | cggacaaggt  | catcagattg | tcctgattca  | ggaagtattt | ttgacacttg  | 2460 |
| ccaactgggg  | tacttcagcc  | aatgctatac | cgaagaacga  | ccggtgagca | gaccgattat  | 2520 |
| cgtggtagct  | ccaccagcc   | attggaaga  | gtgagtatcg  | gtttcagttc | cttaccggct  | 2580 |
| ttccctttga  | acagggtgaa  | gcaagcaaaa | taagcaagcc  | gtagcctcca | tctccgaagc  | 2640 |
| aaagccaaaag | aagagcatga  | agaagggtgc | caggaatggc  | gtgggatcca | gctctcgtag  | 2700 |
| ttaggcaaaag | aatacatctt  | cgtaataggt | tcgaagagcc  | gcgcaagaaa | ttgtttcttca | 2760 |
| gcttgatcgg  | caccttgctc  | ccttcttcta | tctcatctgc  | tctacatagt | agccttctcc  | 2820 |
| ggccaatgcc  | tgctccatag  | tcaagcttct | gacaogggtg  | cccagccttc | gagaagcatc  | 2880 |
| agtttgtcat  | cgtttgtcct  | tcggcttgta | ccatggcact  | ggtgaatgcg | aatttgtccg  | 2940 |
| caggaggttg  | tcataggccg  | tgagttcagc | catacgattg  | tcggcaataa | agttttgtcc  | 3000 |
| ttcgcattcg  | cttccaatag  | agcttccagc | tcttccctgtg | gtgacggagc | gtagccagat  | 3060 |
| cgtaatcggg  | tagtttgatt  | cgctcggatc | gggtctggca  | tcctgtttat | gcectatggt  | 3120 |
| gacgaaatga  | acagtgcgcg  | tacggtattg | atagccactg  | ctccgaactt | ttcttccac   | 3180 |
| tcaggttgta  | agccgaagag  | gaagacgaat | agaaattcac  | ttcatagccg | gcttccggag  | 3240 |
| tctttcgatg  | gatgcaaagt  | cgaactgcc  | ccaaacttcc  | atggctccac | ctcccgcttt  | 3300 |
| ttagacagga  | tcgcgccttt  | aagacgggtc | tctcggcgaa  | aagagcctga | gcatcctgca  | 3360 |
| tggcagcttc  | tcgctcagct  | tggacgcaag | tgtcagggtc  | tgttcggcgg | gagcactctc  | 3420 |
| gcttttgatc  | aagcagcat   | gcgcttggtc | tgggcaatct  | ctttacgcaa | attgaggagt  | 3480 |
| cttgcaatc   | cgccacatct  | ttcgtagcct | tggtttcccg  | gatgtgtaca | ccccgatcgt  | 3540 |
| acgcaacttt  | tccaagaaaag | cttcgtactc | acggtgaaga  | tcaggaaaag | gtatttgttc  | 3600 |
| attgcggtaa  | tcatgccatc  | acctccctcc | tttgttacgt  | ttctccatat | tggtctcgcat | 3660 |
| aatcttctga  | gaggattgga  | caaactctct | tcatcctcca  | gatagcgttt | gatcttgctg  | 3720 |
| atgggtcttt  | gtagccgggg  | atttgcactt | tctcaaaaag  | attcactttc | tgttagtctt  | 3780 |
| cttgcgtgca  | tattcgagga  | actccaactt | cagaccgagg  | aatcggcctc | gattccggta  | 3840 |
| tgggccaaagt | tcttcagcag  | gtcaatgcct | tggcaaacca  | tgacggggca | ttgaacaaac  | 3900 |
| tgaagggctt  | gatcgtgtaa  | aaatgtcatc | gagtacggga  | acgactacgc | ctgccacctt  | 3960 |
| ctttgcgaa   | gcttgacacc  | ctccacactg | atcaggctcg  | gtttgaattc | gttccacagc  | 4020 |
| ttaccatgct  | tcggtagcct  | acgatctctt | cttccagttg  | gcgttccatc | gctccacctc  | 4080 |
| gtccttcggt  | cgcttcacct  | ccagacgcaa | tgcgcttcc   | tgcttttgat | cgctcggtaa  | 4140 |
| gtacgctctc  | gcatcttaag  | ctgctttctt | gctgctgaag  | tgaggttttg | ttgtattgaa  | 4200 |
| acttaatagc  | catttagcac  | aaggttatta | tttcttccaa  | taagtgtcca | caagctgctg  | 4260 |
| cttatattca  | cttcggccgg  | tttgaagtgc | ttggagaata  | gctcccacgc | cggctcgagca | 4320 |
| tctctgtcgt  | attcacgttt  | acgtctatgg | ccaagagctg  | agagagtagt | cattggcgaa  | 4380 |
| ttcgagcgca  | cggttgtcgt  | agtccgtaag | tcgaaaccgt  | tctccatctt | ggtttgagca  | 4440 |
| ttggccgcat  | cggagaaaaa  | cgaaccgcgg | cattcatcac  | ctgaggatgg | tcttctcgag  | 4500 |
| tcttcttacg  | ataacgagct  | gcttcaaacg | agagaggctt  | cggaaacggg | ctacgatacc  | 4560 |
| ttacctacgt  | tgctgtcgcg  | acggagatag | agctgacctt  | cggtaataaa | ccggtgttgt  | 4620 |
| ccggcacggc  | gtgagtaatg  | tctcctccgg | aaagatggtc  | acagcgataa | tcgtgataga  | 4680 |
| accaccatcg  | gggaactgta  | cagcttttcg | tagatttttg  | ccaaatccga | atggg       | 4735 |

## (2) INFORMATION FOR SEQ ID NO:529

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...369
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gaaaaaattt | tcgcgccacg | tcttttccaa | ccgtattccg | gctttttctg | aacgacaaaa  | 60  |
| gagaaaaggt | gtctatgtgc | catcggtaac | ttcggacagt | ggcggatgcc | tcacgcagta  | 120 |
| ggccaaaaat | gcctaccttt | ggggcagtg  | aaaaacttaa | tatcaatata | taacaagagg  | 180 |
| atacagcgat | gaaattttta | tcgacacagc | taatttgat  | cagattcgcg | aggcgaacga  | 240 |
| catggtgtct | tggacggcgt | tactaccaat | ccgtctctga | tggcgaaaga | gggttttagtg | 300 |
| ggaaagacaa | ttgcatgagg | cactacttgg | ccatctgtga | gatggtcgat | ggagatgtga  | 360 |
| gtgccgaag  |            |            |            |            |             | 369 |

## (2) INFORMATION FOR SEQ ID NO:530

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1078 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1078

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| tggttttttca | ggaattggat  | cgcttgccgg  | aaggattctc  | ctgtccggag | ggcgcgagaa | 60   |
| accttgggga  | acgaatcacg  | ccgttctgat  | gggacgagtg  | cgattcgca  | accttttgcc | 120  |
| gtcatcaatg  | cggatgattt  | ctatggagca  | atggttttga  | agttctggct | cgtaagctca | 180  |
| tgacttttga  | gggtaacaag  | gcgaatactg  | catggtcggc  | taccgtgtgg | gtaataccct | 240  |
| gagcgaagcg  | gtggcggtttc | gcgtggagta  | tgccaggtag  | atgaaaaaca | tttgttaccg | 300  |
| gtgtggttga  | gcgtaccggc  | atcgagcgca  | cagacgggtac | tattcattcc | gagatgagac | 360  |
| cggaagata   | tgtacgctgg  | cagaggatgc  | accgtttcga  | tgaatatgtg | gggattcact | 420  |
| cctgactact  | tcgactattc  | gaagaactgt  | tcataaactt  | cctgaatgct | catgggcagg | 480  |
| agccgaagag  | gagttcttca  | ttcccttcgt  | tgtgaacgat  | cttattcgca | gcggtcgagt | 540  |
| tcggtggaag  | tgctggatac  | gacagcccga  | tggttccggtg | tcacttatcg | gacgatcgcc | 600  |
| ccggtgtcgt  | agccaaacta  | cgcgaaactaa | cggaagcgga  | gaatacccaa | cgaaattggt | 660  |
| ttaatgccaa  | atatcacaaa  | caatgacaag  | acaatcaagt  | ttctttgcct | tgcgccggca | 720  |
| gtaatcggcg  | cattgtgctg  | accggctgca  | atggcaataa  | gggtcagact | aacgatactg | 780  |
| acagaagcgc  | gaaccgggtac | cggccatcga  | cctcagtgcc  | atggatacat | ccgacgcccg | 840  |
| caggacgact  | tttatcgcta  | ctgcaacggc  | aattggatga  | aaacaatcct | ctcaaacctg | 900  |
| cttatagtcg  | ctacgggtca  | ttcgacatcc  | tcacgacagc  | accctcgagc | gtgtacacct | 960  |
| gattgtggac  | aaccttgca   | aggacagcat  | gaagtcggca  | ctaatagata | tcgnatagct | 1020 |
| acgctctatg  | ncaagctatg  | gatagcatca  | aacggaataa  | agacggagca | gccctttg   | 1078 |

## (2) INFORMATION FOR SEQ ID NO:531

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:



(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...545

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| taggacacta  | atgtttcaaa  | atggcattgt  | gggttgacag | atctatagtg  | gattttcata  | 60  |
| atatgtacca  | aaatcaagat  | cttcagcact  | ctccacaacc | cagggccacc  | ctgaggcacc  | 120 |
| atgtagatgc  | tcaactttctc | aatttttgctt | ttcctgccca | ctctcctaca  | taatggtagt  | 180 |
| cagggtttagc | ttgatctgtc  | cgtcaccgcg  | acgagcactt | cccataggca  | tggaacaatgt | 240 |
| catagcatat  | acgacttcgc  | cgcattgtcc  | ggatcgggcc | cattgccctc  | tttatacaag  | 300 |
| aagcaaaagcc | caatgagagc  | aatgctccga  | ccaaaaacat | ttttttaact  | tcataagcca  | 360 |
| aatgttttaaa | aggattaata  | ttaaattgat  | tcaaaaacgt | cgaaagaaaag | actataaaaac | 420 |
| acaaaacgct  | caagactata  | aaccggataa  | acttaacgat | gaatcctcgt  | tatcacatat  | 480 |
| ccgaacccat  | atctctacaa  | ttctatactc  | ttgcacacta | ttctgctgaa  | cttcacctga  | 540 |
| cagct       |             |             |            |             |             | 545 |

## (2) INFORMATION FOR SEQ ID NO:532

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...302

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| ctgaaaagca  | ggagattaca | tggtgaatgt | aaatcggatg  | gcaactcctt | ttcataaaaag | 60  |
| aaattgtagc  | caccatagaa | tactccgact | tgcatcaggt  | accgatactc | tctgaataac  | 120 |
| ccatctccag  | atagggtttt | ctcgatacat | atcccaccgg  | gctttgaaat | gtaaggcctc  | 180 |
| gtcgttggtc  | tttaagaaac | gaaaggcagg | aaattgacca  | gcaggcgcca | agctcggtag  | 240 |
| ctggttggaag | gataaggtgg | ttggcggtg  | tagcccagata | gggaggcagt | gtctggaaag  | 300 |
| ca          |            |            |             |            |             | 302 |

## (2) INFORMATION FOR SEQ ID NO:533

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...464

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533

```

ccgtaatggt agccaaaaca tcaccagcag caatactacc aatttgagtg tagctttaat 60
ttcatagctc tgggctttcg ttgaaacccat cgcacgtgta cagaacgctc caccgtaacc 120
ttggcctgat tcttaatccc tgcgatacat tggcctcgga tacagcagct tcgatatgca 180
aagcatcaga aggctgaaac aggtcatcat gattgtctca tcagtagtac cattcttttt 240
ggcaactttc cagccgccgt agcaggattt gggccatcgg ctaccgtacc taaacttgag 300
cctgagtaga cagtttcgatt acctctttga atttagcatc aaatctgctg cattaacatt 360
tgccaaaagg gctttttgcct tgccctgcgat gtattgagca ccacatatat tttaaccgtc 420
ttgccgactg cagaattaac ctgatgcctt ttttggtttt caaa 464

```

## (2) INFORMATION FOR SEQ ID NO:534

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...928

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

```

ctttcttctg atttgtggtt cgacttttcc tgatggatcg aacgcttctc ttcgtagggt 60
ccggggccat gcagagaaaa tggtagataa ctaacggact tttagcgact taaaagtgtc 120
tagaaagctg tttttgatgc gtcaacctgc aacaggcctc tgtcatctat ttggagcaaa 180
ttcataccct ttcgattcag tcggaaaagc aaaacgggaa aaaccgaaaa aaagaatcac 240
ttcgacgacg gctttttcat gctctgacaa gtaaaaaaca cttgcatgga gaaatatcct 300
tttgcgacat tttgtttgcc gcagagcagg caaacaggaa taatctcggg gtgccatcct 360
tttgatgttg aaatgcgatt tgcgaagaag cctcgccgca ttctttctct cgcgacagg 420
catggaatcc aaatatattt ggcggaatgt cttgtgaatg aaaaaaatat cggaactttg 480
cggccgttgc atttgtcttt atcacctgaa aattatttga tagggctcgt cgcattctgt 540
aaaatccacc ttatcaaact cagtatgcta tgacggaaaa aactaccgaa aaacgctgaa 600
agatgttgta gtccgattct gcggcgactc cggagatgga tgcagctgac cggaacgata 660
ttctccgacc tttcggcggg gtttggaaca ccatttccac tttcccgac tatccggcag 720
aaattcgtgc tccacaggga cattgggcgg agtatccgga tttcaagtgc acatcggaac 780
ncgactggtg cgtactcccg gcgatttggc tgacgttctc gtagccatga acctgccgtc 840
tcaaagttaa cgggacacac gtaagacggg actncattat tatantcgac tctgactctt 900
tatggcatct gatttgagaa aagcagaa 928

```

## (2) INFORMATION FOR SEQ ID NO:535

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ccctctttaa | aactcgttgg | aatgccctcg | actctagagg  | atccccccgc | tttcccttga | 60  |
| ttgtgacgtg | tactgagaaa | agtcgtatgt | tgttttttgtg | ccgaaagacg | gagaattacc | 120 |
| gagcctaaaa | tctcaaaaac | tcgaacccaa | ggaaaatctt  | tacgcgcgag | atttttttgc | 180 |
| ttttggctcg | agtttttttt | tttctcgaac | catctttttt  | cgatccgcaa | ttgtgc     | 236 |

(2) INFORMATION FOR SEQ ID NO:536

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ccagctattc | tgtgcatcgg  | gccaaccgag | atgatccctt | tttgatctgt | atctgcggag | 60  |
| gtccggcttt | aacgggttagc | catgttcggc | atttccgcat | agccatgcag | caggtaacac | 120 |
| acggggcaat | ctccgccctc  | gctcgccagg | ctatatccgg | aagcactacg | agtacaggga | 180 |
| tctccttatt | catcgagcgc  | ttggcaccga | cagtcttttc | actccggcag | caaatccctg | 240 |
| aacgacgata | ccgatagcag  | tatgatgata | tgtagtattc | tcttc      |            | 285 |

(2) INFORMATION FOR SEQ ID NO:537

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...798

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:537

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| caaaacgcca  | ttgccnatag | taccacctnc | atattcgntt  | gctgtcatgc | tgtccaaaca | 60  |
| ttgnngggcat | cttcatcctt | tcccgttaca | ataaaaatcca | atgcgagaca | tcgaagtcac | 120 |
| aaggcaccaa  | agaccccaaa | gaccctactt | ttggtaagta  | gcaccaccgt | ctttggaacc | 180 |
| gatacagcct  | gacatctcaa | aataaaatag | agagaaatcc  | aacatcacat | agatccatcc | 240 |
| attgttgcca  | cagccatctt | gtaataaaaa | tcctctgaat  | atcctgatag | ggtgacatcg | 300 |
| tctcgatcaa  | tacatcgtct | ccaccaatat | ccatctgggc  | cttgccagag | ggctaaataa | 360 |
| aactatggca  | aaagtcgcca | gcagcagctt | gatgcaattt  | ttaatttcac | aattcttggc | 420 |
| atTTTTatga  | gtgaaacatt | tttgttcata | tcacaaaaat  | acttacctgg | cataaacgag | 480 |
| cgactcacia  | aatcgggctc | ggaacggcta | ctccagcttc  | gtgagcagcg | tactgcctag | 540 |
| agcttgccct  | tcttgctcga | gctctcactc | ttgacgcata  | cgacatcctg | gacatccatt | 600 |
| ccacggcaact | catctgtacc | gtaatcatac | tttccatacg  | atcgaatagc | tgatcttgta | 660 |
| gcattcgaaa  | gtcccgggcg | gagtggaatc | ctctcgatgc  | cctgcacctt | gcgtccgatg | 720 |
| gttcgcagag  | taatcggggc | aacgggaaat | cggccgcttc  | ggccgtaatc | gtcacttctg | 780 |
| catcggcagg  | gactgacc   |            |             |            |            | 798 |

## (2) INFORMATION FOR SEQ ID NO:538

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...826

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| gaattttaatg | tgctatatca | tgggctaggc | ggcaatctgt | ttctcctgct | agcctccgac  | 60  |
| acctgtacca  | tcgtgaagat | gtcgttttca | tcgacagctt | attcaggctt | gcttacgtga  | 120 |
| gtcacttgca  | gaatatccaa | aagtcgacat | gatcggcaaa | gacttgcttc | atcatcgggt  | 180 |
| gaggcacgaa  | tggtgcagtt | cctccggctt | atctcgtctc | ggaatacgca | naaggactcc  | 240 |
| atccaataag  | gtcccaagcc | gaacagtcog | atatagccgg | tcgatggggc | aaggtagcat  | 300 |
| aataataatc  | ggggtagcca | tccaaatcat | aatagcgaga | ataggcatgc | ctttcgtctc  | 360 |
| cagcaaatcg  | gctttgtcct | catagcccat | cggcggaaca | tggccgccac | ctcttcgggtg | 420 |
| cgctcacaat  | gtgctcggaa | agtatgtctg | cgactataag | cgactccatt | cgctccttga  | 480 |
| tccgcacgat  | tctccgggtg | tgatcatatg | agcattcttg | atctgacaat | agtaaccgtg  | 540 |
| gacaatgaat  | gttcgatgaa | aagtttgctc | ccgggcaata | tgtctgcaca | gccttgctta  | 600 |
| atatgaagct  | gagcgttcgg | acgtaagttc | gcataccgat | tcgtccgaaa | aagaagcgaa  | 660 |
| caggacatcg  | gatggctcat | ataatcgaaa | ccaagatctc | gtgtacaatg | attgacttgt  | 720 |
| gcattgaaag  | gacgaagccc | aaatcgtctt | gaaagtactc | tgccactcgc | tctaaagata  | 780 |
| tgctgttgga  | aactcttcgt | agcgatcgag | attgtcacag | tagatg     |             | 826 |

## (2) INFORMATION FOR SEQ ID NO:539

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| agaggatccc  | ctcctctcca  | ctcctgcaaa | tctataaggc | acccgctcgt | tcggccacga | 60  |
| atcgagcggg  | tgtctctttt  | atatcagctc | tccaaacacc | ttttctgttc | tactatttat | 120 |
| atacaaatcg  | aatacgatct  | atatacaatg | gaaaatgatt | tatatataaa | tcgaaaacga | 180 |
| tctgtatata  | aattgaaactg | attaatatat | acatcgccat | cgaaactctt | tcaaagcaga | 240 |
| cctcactccc  | aaaagtccga  | ttcatgaaca | tttttacctt | gaaaacctct | tccttcaatc | 300 |
| gcttattttag | aatgattcca  | aactcttctt | cgttgttgaa | aactttctgg | tctgtatttt | 360 |
| cgtgaaatat  | tttcagatgg  | gatggtgatt | gttccggcat | tatcgaatca | aaaaaacgaa | 420 |
| gtactgcttc  | cggactacat  | aagctaacag | actgcaaatg | tcgaagatca | gactgtaggc | 480 |
| attccgctct  | aatcgggtaa  | aaagctttgc | ttcagtga   | aa         |            | 522 |

(2) INFORMATION FOR SEQ ID NO:540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| ccattgaaag  | gcaatccgag | atTTTTgagt  | gtaaagtcgg | gcaataactcg | ttgtgtgcc  | 60  |
| tatccagcgt  | ataggtagaa | gtttgattat  | ggcccactcg | aataaggggt  | gcgtatactc | 120 |
| tgtcgggtgtt | tttactgaca | cgcttccatc  | tttttccatt | catccttttg  | gttgttgatg | 180 |
| gaaaatctat  | accacatgta | tagtcgcctt  | ccgagagagt | gagaacgtct  | ttagaccaaa | 240 |
| ccaccgatag  | ttgctgctac | cgcccggaac  | ttcagccatt | acccagccca  | aagaattaca | 300 |
| tcgtccgcag  | tagctcctgt | agatagagca  | aaggctacgg | gtgacggatc  | tcacagggc  | 360 |
| tgtcgctatt  | gaactgtact | gtaatcgtac  | tagttcataa | gaattcagat  | ctgcgacaaa | 420 |
| gctgttgggg  | acgatactga | gttgcccttcg | ttattatcta | ccgtgactac  | gacattgttc | 480 |
| gggtctgtcg  | atttacttta | atgctattga  | catatcctcc | ctgtgcatgc  | cgtaccggcc | 540 |
| ccactgttcg  | gtgcctgtgc | gacgataaag  | tagggtgatg | gtgttgatcc  | ttgtgacaac | 600 |
| tgattaggtg  | ccaatgagaa | actctcgga   | tgtctcgta  | tcggtaccaa  | gagatattga | 660 |
| tagatgaaag  | ttttcacctc | tatgactctc  | cgtcagcctt | ggttcaatct  | gtatccgagg | 720 |
| tcaagatttg  | attgccttca | cctgtattat  | atatcgaata | ccctacgttc  | aatccggatt | 780 |
| cactttatac  | tcgggttcta | tgctttcagt  | gccaagatcg | gcaaggcatc  | tgtccggcct | 840 |
| cagcgggagt  | ctag       |             |            |             |            | 854 |

(2) INFORMATION FOR SEQ ID NO:541

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctgtcgggta | tggcttgcca | cggattgttt | gttttgtgcg | acgaggcagg | gcaacgctgc | 60  |
| atgccgagcg | aattgctgca | atcagagcac | taacggcccc | gatgattggt | atttgccttc | 120 |
| cggaggggaa | acgatcaaac | agtggggaac | tgcctgcccc | tatggcgatg | gctgagcgaa | 180 |
| agaggtgctt | cgcgcctctt | ctattattga | atataggagg | cggtagcatt | acggacttgg | 240 |
| gcggctcgtc | gcttcggtct | ataagcgagg | tatccggacg | gtaaatctca | gcacacccta | 300 |
| atgggaatgg | tagatgcttc | ggtcggaggg | aaaacaggca | tagcttcgaa | ggcgtcaaaa | 360 |
| acgagatagg | cactttccat | ctgccgaaa  | cgtcttctgt | gactgtgctt | tcctgtccac | 420 |
| cctaaccgac | cgtgaactgc | ttcgggacat | gccgaattgg | taaagcacgc | tcttctcatg | 480 |
| ggagcggatg | atggaaagaa | gttatttctt | tcgatc     |            |            | 516 |

(2) INFORMATION FOR SEQ ID NO:542

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| ggcgatgcc  | atatcagca  | gcagattcgc  | tacaaaagcc  | gtatcaacat  | ttgaagaaag | 60  |
| aactacggga | ggtaaaggaa | cgttatcatc  | aggatagttg  | cgactggaag  | aaatccgggc | 120 |
| gaacaaacag | gggaatagag | catacggcag  | agagttgtat  | ctgatgaagc  | gacccgaaga | 180 |
| gatcattttt | ctgatcagga | tagcgtccaa  | gacaaaacat  | aacgaaaata  | ggggcagcag | 240 |
| ggatgaccca | cagcagattc | gtgagataag  | ctaccgtgtc  | ggcagtctcc  | ttttatcttc | 300 |
| ggagcagcat | cccagattgg | tacgctttgt  | tgcccggaga  | ttactctacg  | cattgggggc | 360 |
| ggtactctat | ctgctttcct | atgccctgac  | tctgttgccg  | atttggatac  | tcgtacgcgc | 420 |
| aggctctacc | ggatgaatgt | ctttccgggg  | cttttttctg  | agtctcggct  | atattggtct | 480 |
| ttgtacgagc | gattcccttt | ggctcttggt  | ttttgccatt  | ggtgtgatct  | acatgatttt | 540 |
| gcttccttgc | ttctgctctt | caggaaaagga | tcggggagagc | aaggaaaaac  | aagaaataag | 600 |
| attctctaca | aacgaaatat | gcaacctcca  | aaaagtcgtc  | accccgccctg | agacgtcagc | 660 |
| cggacaaggt | tttcgaagtc | agagaaagga  | taccctcttg  | ccttttctcg  | ttcgtatgct | 720 |
| gaaggataat | agccgacgtc | cgtaagcag   | atattgacga  | gacggcaagt  | ttccatcaac | 780 |
| ggtggccgac | tactcgacac | gatgcagagc  | tgaaagccgg  | cgacagggta  | atctgcatcg | 840 |
| gacacagcta | ccggaagagc | tgcgccatcc  | tttggtgccg  | atatttggca  | ggacgactat | 900 |

|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| ttcgtcctga | tcgagaagaa  | agccggagtc  | tcactgtagc  | cagtggcgtc | aataaggaca | 960  |
| ggactgctct | gcgcatcggt  | gcgatcatct  | caagcaatat  | gatccggagg | tgaaaatctt | 1020 |
| tatgctcaaa | gactggacaa  | agattctgcc  | ggaatgggtgc | tctttgccaa | gaataaaggg | 1080 |
| tacaggggtt | tgtgggtggac | aagtgggtcca | aggctcgatt  | ggaacagggt | tcgtgatggc | 1140 |
| gatcgaagga | gagatgcccc  | atgccgaggg  | tacgctgata  | ctcctcggta | tcaaacctcg | 1200 |
| atcaagggca | agcagtctcg  | tatcgggctg  | agactccttc  | cgttcattcg | gtgggaacgg | 1260 |
| ctcgttacaa | gggtttcgtc  | gcgg        |             |            |            | 1284 |

## (2) INFORMATION FOR SEQ ID NO:543

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...696

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tgccacagca  | aagttcgtcg | ttatactgat | agaggggata | ttggcactgt | ggtagccgct | 60  |
| gttgtaaacc  | aaatagccta | tacgatagag | gtactcctta | ccccgctgtc | ttggaagcat | 120 |
| cgtactatgc  | gccttatatc | tggcagaatc | agcaggctat | gggtgggttt | catccggatt | 180 |
| cttggtatct  | tactggcggg | ggccgtcatt | ctgttcaatg | tactgtcagc | aggtatttac | 240 |
| ttcgcggttag | tgtccgaaaa | ctcaccatgg | ctaccgtggc | tttctcctcg | actagggagg | 300 |
| tgaaacgatt  | ttgttcggca | tactgacatc | caatctgaac | ctgacggaga | agatcttttc | 360 |
| actgctcttt  | tcttcggcag | tatcggcttg | tgctattcgt | tttatccttt | atcaaccttc | 420 |
| aaagacgaca  | actgaaatga | cgctatactt | caagcacaat | ccatattcct | qcaaatatcg | 480 |
| gacacgatca  | ggacaggatt | ctctccggcg | aatattcggc | cgacgaaagg | gtaccatctt | 540 |
| ccgcgaattg  | gccgaacaga | tgggaggtca | atcctaacac | agcgatgcag | ctgtcgaacg | 600 |
| cttgcaaatg  | gaaggtatga | tctataacaa | gcgcggatcg | gctactttgt | cagccccaac | 660 |
| gctcgcgaag  | agatccttgc | ctctcgcgca | agaatt     |            |            | 696 |

## (2) INFORMATION FOR SEQ ID NO:544

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...489

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| acgctgattt | tggttgtcgc | tctgctttat | gccaaagagca | aattggtgct | tccggcaatg | 60  |
| tgacgatcac | cgtgaacgac | gaacgcaaga | tggaagtact  | cttggcggtg | ccttggtgaa | 120 |
| tacgcttcaa | aatcagggag | tattccttct | tccgcttgcg  | gcggtggcgg | aagctgcggt | 180 |
| cagtgtcggt | gccgtgagtg | gaaggaggtg | gcgaaatcct  | tccgacggag | aagggatttt | 240 |
| tctctgcaaa | gaacaaaagg | atcattggcg | actttcatgt  | cagacaaaag | taaagaggat | 300 |
| cttagcatcg | ttattcccga | agaggatttc | ggtgtgaaag  | aatggagtgt | gaagttctct | 360 |
| ccaataagaa | tgtctccact | ttcatcaaa  | aattgtggtg  | aagctgcccg | aaggcgagac | 420 |
| tatgaacttc | aagagcggta | gtatgcccag | atcaagatac  | cgaatacaac | atccgctatt | 480 |
| gccgaacta  |            |            |             |            |            | 489 |

## (2) INFORMATION FOR SEQ ID NO:545

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggatctcctc | ggcggataaa | atctttcccg | tagccgaaga | atcggctgcg | attcagtctc | 60  |
| tacttccgac | gtagcgatcg | aggaagagtc | caccggcaga | atacggaccg | gcgaatggag | 120 |
| gtatcctggt | tttgtgcttg | caatgacgca | acgagccgat | cgacagaaaa | aggatcaggg | 180 |
| gtaaaaccgc | aatatgcgta | gtacaggcgt | tctcatcttt | tcaaggtttt | agtgtgttca | 240 |
| atctgtcgat | tatgctgcaa | acacgttcgt | acacggagtc | catcgccgca | tgctattgct | 300 |
| ctcaggagca | tatcgggcaa | aatttcgcaa | ggtctcgatc | agtgcataaa | gtcccttcg  | 360 |
| ataagaagtt | ttcaggcacc | atgaacccgg | ctgaagcaaa | gttcgttccg | ggc        | 413 |

## (2) INFORMATION FOR SEQ ID NO:546

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546

|            |            |             |            |            |            |
|------------|------------|-------------|------------|------------|------------|
| aatacgtatc | tgctcacgat | ggtcagggtat | gtccggccaa | gtggcgtgag | gtcagcagac |
|------------|------------|-------------|------------|------------|------------|

60



|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| actgaaacccg | agcattgatac | tcgttggttaa | gatctaagag | taaaccgagg  | agagaggggtg | 120 |
| tgtcggaatc  | gcaaaaatgag | gcgatcaaac  | acaccctctt | tctttaaggc  | acgaaagagt  | 180 |
| tctccatgct  | gtttctcgaa  | tacagtgaga  | taatcggaac | tcttgattaa  | ggtccttttt  | 240 |
| aatcatatcc  | taacgactat  | gcttgataaa  | gatactcttg | cccaagtggg  | ttctactttg  | 300 |
| cccaactgaa  | aaagtcctat  | acattacgac  | tcaatgctca | tactctcatc  | cttcctacaa  | 360 |
| cgaggcgaag  | gaaatgctcg  | atgggcttgc  | atcgtttcgg | atcatgttcg  | tgcggaatac  | 420 |
| aatgcggcag  | atgatttttcg | ttcgatctgc  | tcgtagacgg | agcggatagc  | gggatcggct  | 480 |
| tccgtgggtat | ccgggtggcc  | atgaatttag  | ctcactgctt | cttgctattc  | tcaacaatgc  | 540 |
| ggtatcggaa  | ggaatatccc  | cgatgaagga  | gtacaggata | gaatccgcgt  | atcaatgggc  | 600 |
| cgatagagct  | gaaaacctat  | gtatccctct  | cttgtaaat  | tgtcccgatg  | tggtgcagac  | 660 |
| cctcaatatg  | attgccattc  | tcaatcgact  | atcaatcaca | ccatgggtcga | tggttctttc  | 720 |
| ttcccggacg  | aagtgaagtcg | ttgggcatcg  | cttcctgtcc | gacggttatg  | gccggagatg  | 780 |
| aagtatccat  | gtggggccgt  | ggcgatatgg  | ctgccttgct | gaacaagata  | gaaccaaata  | 840 |
| tggtctctgtc | cctgccgagt  | cggcagataa  | gacgctgcgg | ccttcgacct  | ccttgctcg   | 898 |

## (2) INFORMATION FOR SEQ ID NO:547

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...672

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cgtattgggc | gatctggctt | tgatcggaaa | atatattcgc | ggacgcattt | bgccacctgt | 60  |
| ccggggcaca | gcatcaacaa | caagatggcg | cgccctgatc | caaagaaatc | aaacagaacg | 120 |
| aagcacaggc | ccctgtctac | aatccgacaa | agagccgatc | atggacatca | atcggatcaa | 180 |
| agagcttcta | ccccacgcta | tccgttccta | ttggtcgata | agatcatcga | agtagggccg | 240 |
| gactaatagt | cggagtaaag | agcgtttccg | gcaacgaacc | atttttcccc | ggtccttccc | 300 |
| tggtgagcct | gtgatgccgg | gagtcctgca | agtagaggca | atgcgcaggt | gggagggctc | 360 |
| ttggtactca | ataccctgac | cgagccttcg | agtactccac | atacttcctt | atgatcgaca | 420 |
| aagtgaaatt | ccgccgtaaa | gggtacccgg | cgacactttg | gtgttcaagc | tcagaatgat | 480 |
| ttccgagata | gcagaggagt | cgctaatatg | cgcggcttag | ctttcgtagg | agagcagttg | 540 |
| cctgtgaagc | tgaatttatg | gcacagataa | tccagaataa | agaatgattc | agagacaaaa | 600 |
| atcagtcctg | tgccatgggt | ggatccgcac | gccgaagtag | gaagtaggtg | ttgagatagg | 660 |
| tcccattgcc | gt         |            |            |            |            | 672 |

## (2) INFORMATION FOR SEQ ID NO:548

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...362

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548

```

catatatata cagagtcccg ttcacgcgcg tgcgtattat cagcgatatg ccggcgaagg 60
tcgggataac tttgcggagt atatggactt ctggcgcagg cttctccggc taccttttct 120
attctcgaaa gagtattcga tgcaatgaga aataagacaa tcccgatatg gagatggaaa 180
aaattccocag ttttcattag atcatattcg cctcaaacga ggcataatg tctcccgcaa 240
ggacttatag ggggagaggt ggttacgact ttcgatattc gaatgaaaga gcccatcgcg 300
aaccggtgct tggggcaccc gaacttgcac acgatcgagc atttggtctg aaacttatct 362
gc

```

## (2) INFORMATION FOR SEQ ID NO:549

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...393

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

```

agcagaacgg cggcaggaga gccgagccgc cttttcgccg gctctctcgt gcactgggag 60
ccggggggcg catggaagct gaatgtctcc gtcgcgcagg tcattctttt ggcgggttgg 120
agggatttcg ctccggctat acgcgcagga ctaccgcacc tacctgcttc cttcgggctt 180
catgagcgag aggcgaattc gggggcaaac ttttcggctc actatggcga cgtgctgcac 240
ctgtttatct tcatctgaaa gccggatatt cgcgcagtcg ctccaacgaa ttgccactt 300
cgactcacgg cggaacataa tatcatcccg ttacgagcgc tatggcaccg atcttaacgc 360
tttttttcgc ccgatatgcg tctgagcaag ttt

```

## (2) INFORMATION FOR SEQ ID NO:550

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature

(B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggatctcttg | ataaattggc | aattccaatt | tatcaagaga | tcccctcttt | tttgcgtag  | 60  |
| agatacttca | tcacagatgg | atttgcttat | ttgctcactc | tataattcaa | cccaacctgt | 120 |
| ttttcattgg | gtttgtcgct | caaaaaggaa | tagatcccct | cgtaaaatag | ttggcgtaga | 180 |
| ctgaatgaaa | aacataagag | accattgcac | aataaccctt | ccatctcctc | atatngatca | 240 |
| aaacaacaca | tgcatcgatt | cgg        |            |            |            | 263 |

(2) INFORMATION FOR SEQ ID NO:551

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| tagaggttcc | ccggccaact | catcggcttg | tgcgtaggacg | acgctaacga | tccgaccaga  | 60  |
| ccgaagctcg | tatggagcgt | tgatcgctg  | ccatgggctg  | taattaatgt | tctctaagag  | 120 |
| ccggagatcg | agatcagagg | gaaactgtta | gcgcgaaata  | aaagcgtatt | tgtcatcaaa  | 180 |
| gcttactcct | cttctcgctt | tcggctctct | cgttaccact  | cttttctctt | tccccttctt  | 240 |
| tccgtattta | ttcgactcct | gacgatggac | acgcaaacac  | tcaatagcga | tctggcgtag  | 300 |
| tcatgcacca | tatatacgag | tttgaaaaag | gtgtgcgaag  | catgtactcg | ctacactggc  | 360 |
| taacgacgac | atcccatatg | cggaagaacg | gcgcgaagcc  | ggcagatccc | ctatattcgcc | 420 |
| cagcctactc | cgaatacgga | ggtaccaatc | tctttttcgg  | ctgcaaggag | tgtatgggag  | 480 |
| gctatccgtc | tttcgtgagt | ggacgcttct | ctgaacaagc  | ctgacttccg | gaggaagaat  | 540 |
| catcatcggg | gctatgctcg | gatacgatat | ttgcagacag  | tgcgaacgta | ttggtagcc   | 599 |

(2) INFORMATION FOR SEQ ID NO:552

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552



|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| tccccagct  | tccaatgtac | gaggttccag | cccttcgggc | agaacgatcg  | ttgtttgttc | 60  |
| tcttgagcac | gtctgataac | gtcttgaatg | agatccatga | taataacctta | tagttattat | 120 |
| agttattgta | atgatgatct | tgaaaagaag | gcgagcagaa | ataacgcctt  | gtttgcagtc | 180 |
| gcaaagatag | ttaaaacacg | ggcaataaga | gagatacatt | caaaataactt | tggaatgga  | 240 |
| agtatgcttt | ggcagggctg | tacttccatt | ctccccattg | cattaatatc  | ctttttgctg | 300 |
| ttctatctag | tacgtgacga | aagaggatga | cgcaaccctt | ctacgacttc  | agatagactt | 360 |
| cggctgcacc | gattctcagc | tccatcctga | taggacaggt | attctattgg  | catcattcgt | 420 |
| gagccatag  | gtaatagcct | tttgggattc | ttgaatgttt | cggattcgtt  | tatgagcatg | 480 |
| gatacccgat | agtatgatag | ttgataccct | ttttcgtttt | ttgtacttca  | gaactttcga | 540 |
| ttgaaagaaa | cagtcgatcc | cctttttccc | tgcaaatatt | cttaccggat  | gcgctctttt | 600 |
| gtactctttg | accagtcttg | tcgagcgaag | atagagttgg | ctcctatcat  | atccagagat | 660 |
| at         |            |            |            |             |            | 664 |

## (2) INFORMATION FOR SEQ ID NO:553

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1446

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| ccgtcactga  | tgatgctgat  | ctgctctatc | tgctccagcag | gttgtttgca  | gattgtcttc  | 60   |
| ccgtacttcc  | ttacgagcac  | atggttgcca | ctgataccat  | gaaagctcct  | ggctcggtaa  | 120  |
| ctaccaaate  | gaatatctct  | cccctctttg | caattgtctt  | ttttgctgct  | gacgcaggat  | 180  |
| ttcgctctct  | ttcttttcgg  | gaaattgtct | gcacttgaga  | ccactgtctg  | cgcgatagcc  | 240  |
| tctcgagagt  | ctgtttgccc  | gtttccgaag | agagaaaagcc | cagccgtaga  | agatgtcctt  | 300  |
| ggcgcttttc  | cgagcctcgg  | aggtcggtaa | tgatgcgatg  | tgatggcata  | gacagtggcg  | 360  |
| gcaacttcgt  | caatagcctc  | tatgtccacc | tttcgagcag  | tttgcggtag  | tactgtccca  | 420  |
| tgccatggat  | tgtctccgag  | aagctgagaa | gttttcgggtg | tcgcgatgga  | gcgcgagtgt  | 480  |
| gatcttgctg  | tgagtccctc  | tttcttgctc | cggctcatgc  | tccttgaacc  | atctgcacaa  | 540  |
| acgtaatacc  | gaggaaaactg | aaagagcttt | ttatgctcga  | taccacaagt  | ccctattcag  | 600  |
| cttcagccct  | ttgcggtatt  | tcaaagtgtc | gctcaggctt  | ggagagcatt  | tagcggatct  | 660  |
| actttctccg  | gcaagaagag  | tagcagtcgt | cggcatagcg  | gataaattcg  | gttggttatat | 720  |
| gcccggcgat  | gtagcatccg  | tgtcttccaa | gtagaggttg  | gaaagcagag  | gggccagagg  | 780  |
| gcttcctgtg  | ggatgccgga  | ggatgcacga | gcattattgt  | gcttcgggtc  | cacactccgg  | 840  |
| acttcatcca  | gaggctcaac  | atacgggtaa | ggaagggatc  | ttggttggtc  | tttggacttt  | 900  |
| ctgcaataga  | gaggggacag  | ggatagaatc | gagaagttgt  | caatatcgca  | gcgcaccact  | 960  |
| gtatggttct  | catccagaga  | tccagcagat | gctgcactct  | acgaacggca  | gccacagctc  | 1020 |
| ccttccccctg | cgatagccat  | agctctgtgc | aatggataaa  | gactcgggtga | tcggataggt  | 1080 |
| atgccggcaa  | ggcttctctg  | caagtggaga | tccactgccg  | aagggattgt  | agctgtcgggt | 1140 |
| aagagccatc  | ccccttggggt | atgttcacag | agtgatgggc  | tgcggtatat  | agctgcaaat  | 1200 |
| acgtagggct  | tccaacaaat  | cttgtgctcc | gcttctgcca  | tggaaggtc   | acgatccgca  | 1260 |
| gccagcgaag  | agagcacttg  | cgatacaagg | tatcgttgcc  | cgagtgtctc  | ctatctgacc  | 1320 |
| attcccacga  | ttgtatgatt  | gcctatatgc | acccaatgcg  | ccattgagag  | caaaggctgc  | 1380 |
| ttacggatcg  | tagggaacac  | gatagaagag | ctgacccaat  | agccgacatg  | tcgtactgct  | 1440 |
| gtttcc      |             |            |             |             |             | 1446 |

## (2) INFORMATION FOR SEQ ID NO:554

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554

```

cggccgaagc ttttcgatcg gtatcagtcg gatgtccttg cacacgtcca tcggatcgcg 60
tacgggctcc gtcccgagca gatagagtat ttcagctagg tagcaccttc gctttcgatg 120
aagctactac tccatagcgt aaagctgctt tcgtaggaag ttccgccattg tgacggcgag 180
cgtagtcggc cagcattcct ctgccatctt cttccctttt tcccatgcag ctgctgatgg 240
tgtggctcgg cattgataga gaagaggttt cttccggtag gaagcgtctc cggatggcga 300
tatagtcgcc acccggcgaa ggtgccgtat aaccggcgga gaggcgttca tcatagaggt 360
cagctccagc tgtgggctgt ttttgagtgc ctatagtaga aaggatatctg ggcaatagca 420
tgcttgagtt cgctgatgct cctgccatgg ctttgtcttt ggaggtaagc tctcgtagctg 480
gctgattcgt atggccgggt gcttggcttt cgacttatca ggcattcatag cttttgcctt 540
tccgaatgtg ccgcttgcat agaatccttg ccgtgagaag gcgttgcggc tctgctccat 600
cactcttcat cttggcggcc

```

(2) INFORMATION FOR SEQ ID NO:555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555

```

ggcgaagctc ccgacgttcg ccgcaagttc gtcgcggcag gcgtggcact atccttgctg 60
tgagcgggtt tcacgtgggt atcgtatttg ctgccctcgt tttctcatgc gtattctgcc 120
gataccgcag cgatggcgtc gggcagatgg ctgcttccgc ttgcaggggg atggatatac 180
gcattcggtt gcggttgggt gctcctgtag tccgagccat gctgatggct accttatata 240
tagtcgtaaa tgctcgggca gaccgtacgg atggattgaa tgtttgggct gcggagcgtc 300
cattacactc gtggatcgat cccctctctt ttttatgacg tgggatttgg tggc 354

```

(2) INFORMATION FOR SEQ ID NO:556

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| ccgacaaaac  | tcacggaaat  | gttcttctgc | gtaaaataag  | aggttacgga | cgg tactccc | 60  |
| gaacttcgtc  | ataaatccgg  | ttgatcagct | ccattcgtct  | ttgtcgttca | tcgacagggc  | 120 |
| attgtttttg  | agaagcgttt  | tcagctcttg | agcgactcac  | cgctcatttc | aagcagtttg  | 180 |
| gcatagcccg  | atgccaaagcc | gaaagtctct | ccggactgta  | gttcggatct | ttgagcatgg  | 240 |
| agcgaacccc  | gtgacgtaaa  | tatccgtgat | atcgccctacc | atcaggatga | tctctttacc  | 300 |
| ttgtaggcat  | ccccgatcag  | gttattgacc | cgtcttgagc  | gcgcgtaagt | atTTTTTccc  | 360 |
| ctgatgatag  | actttctcca  | cttccttgaa | gtgttcaggg  | tgTTTTTTac | cgtcttgga   | 420 |
| gccgttgcca  | tctccttgac  | ctgttgccga | tggtgccggc  | aaaatttggt | cggatcggtc  | 480 |
| acgaccctact | ggcattgtac  | gctgccacag | cagaccggca  | gtac       |             | 524 |

(2) INFORMATION FOR SEQ ID NO:557

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...3287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| ttcatttcga | gtggtataag | caaacgattg  | acctgacgtc | agaccgggct  | tgacatttat  | 60  |
| cttaatcttg | tcttcaccgt | tcgcgagtca  | aagtgactct | tccgttccgg  | caggtgaggc  | 120 |
| attgactcct | cccggatgcg | tattgtcgga  | gcataagaac | ccgtcacata  | cttaaagccc  | 180 |
| aacggcagcg | tgatttcaaa | tatgccttgg  | gggtagtttc | tccacctacg  | accgtttgca  | 240 |
| ccactttact | cttttgggag | ctttacagtc  | cgattgtgat | gttgtgggtcg | taacagctgc  | 300 |
| gtagaagcag | aagtcgtgta | gggctctata  | gtcccattha | ttcaattgga  | ggcgtactta  | 360 |
| tggcaagacc | cgatcccttg | gcattctgat  | taaagcatta | cggccgtcag  | ctcttacacg  | 420 |
| gaagttcttg | ccagatacga | agaacactcg  | gtctttatgt | agaacttcac  | caaaaatttta | 480 |
| cgttgattgt | gttggattcc | ccctctttca  | ggcccttgag | atagcctatg  | gtagtcaatc  | 540 |
| aggatgctgc | aacagattga | cgggaattatt | gaccacattg | agtgcagcca  | attaccggaa  | 600 |
| ccggcaggat | attccacctg | tacctgattc  | ggtgtcacac | caatccctct  | tcgggggaaga | 660 |
| tgctgaaagt | aggactataa | acgttccatt  | atctgtcgat | tgaatgctgt  | aaatatattc  | 720 |
| caatgtacta | cacaagtagc | agcagctgta  | ggatctggaa | cagctatctc  | agtaagctcc  | 780 |
| atggagctgg | cagtggtctg | agcttgagat  | cgatcacctg | cgaactgcaa  | acaactcatc  | 840 |
| caaaactaag | ggatatgcac | tacagttcca  | gccccccatc | gcttcaaagc  | gataggagag  | 900 |

|             |             |             |             |              |             |      |
|-------------|-------------|-------------|-------------|--------------|-------------|------|
| caaccagaat  | aggtaaagt   | aatggatat   | taagcgaga   | acctactgga   | acaccagctt  | 960  |
| ccgacaaaacg | atacatcttg  | caccagaata  | agttgtaaac  | gccatttcag   | tacctgccgc  | 1020 |
| atcagttact  | tttcgatggt  | cagccccgat  | gttgtaggca  | atgccaaacca  | aacataggag  | 1080 |
| ccgttgcaact | cgatgggttg  | ctgatacgca  | gcttccactc  | tcccggtttac  | ccacaagctc  | 1140 |
| tacctcacct  | gactgattga  | cgagcgcaat  | agaagggttg  | tagtataaaag  | gataggcctg  | 1200 |
| ttgtaaacat  | tgagggcgga  | aacacgtaga  | ttccgttgct  | gccagccgat   | tgatcggcta  | 1260 |
| ctatgtcaag  | gctataggta  | ctgttggtcg  | cgttgctgca  | taatagtaat   | agtcaatgta  | 1320 |
| atcacatagt  | atgaaatttt  | atcataatta  | gttgctacag  | cagacgacgc   | acagtgggag  | 1380 |
| atacattttac | tttaagagct  | gctccatagg  | catttttttac | ttaatatattga | agtgcgcctt  | 1440 |
| ttcgttgtct  | gcaagttgat  | acttatagat  | ttatatccac  | cctgtgaagt   | cacatctgta  | 1500 |
| tgattttattt | cctcgaaagc  | atggttgtac  | ctaacgaaact | atggttacgg   | tgattgctat  | 1560 |
| actccaccta  | ttcagcgtgt  | aggacttcgg  | tactttcaga  | tagatatattc  | taatcttaca  | 1620 |
| ccaggacgat  | attcattggc  | atattcaaact | gcaccagagc  | cgaaacacgg   | gcgtagtggg  | 1680 |
| tagcaacgcg  | tcccagatct  | gttggagtag  | attgtaaatg  | acatgtggat   | cggtaccggt  | 1740 |
| tacaacaaaa  | gtacccatga  | tgtaatctcg  | ggcacaagta  | tgagacaagt   | taacggattg  | 1800 |
| gcttcatccc  | atacgggtgac | acattggcgg  | tagagttgta  | gaagaaccac   | tccctaccga  | 1860 |
| ctgcgtatct  | actctatgag  | cattctggga  | tgttaccgca  | taacgggtaa   | cacatccact  | 1920 |
| ttgtctctat  | caagcaatcc  | accagcagga  | aggattgaag  | aaaatcccag   | tcgatcacct  | 1980 |
| gotctgcatt  | attattttcg  | cgtattgaag  | gaatgtcgta  | tatccatcta   | ccgatacaat  | 2040 |
| ctgaaccccc  | tcacggaaat  | cttaatatcg  | gccgaaagag  | gagtaagcgt   | ttctactcga  | 2100 |
| tcgacaccgt  | agccaaaaca  | aaacgggcgc  | ccaaagacga  | agcagtacca   | tgctggtaga  | 2160 |
| agtcgctgta  | atgttgactt  | cggtccatata | tagggcttta  | gccaatcgta   | agccgatata  | 2220 |
| ttgctacgag  | attgacgggt  | ccgcacgta   | taatcgctta  | gcccacgaa    | ttgtcggcac  | 2280 |
| gttctatctt  | aggcaccgaa  | gttccgcacc  | tctaccgcag  | ggaggatcgc   | agcccaaac   | 2340 |
| ataacgcttt  | gcgtgttaca  | cataatagga  | cctaccgggc  | aaagacaatc   | aggggaagtga | 2400 |
| agtagttgaa  | tacctctcta  | atcttatact  | ccacaaccat  | ttcgtgatta   | ttgtacagtc  | 2460 |
| gtatttcaca  | ccatggaggg  | ttacaaaacc  | tctttcttgc  | tgggcgaaac   | gatagtcatt  | 2520 |
| gtgtttcctg  | atgtcgtgat  | atttgcatag  | ggagggtta   | cggtggagt    | aaaactaagg  | 2580 |
| acccgtctat  | cggtatgattt | ttatattggt  | ccattctata  | tccgatttgg   | gaggcatagt  | 2640 |
| catacctgcg  | ggaatactat  | ttctaccaca  | taccgcgtat  | tgggattggc   | gtacctatat  | 2700 |
| tattatatga  | gctgaggatg  | gaatagtagg  | aagtcattat  | cttcggtcga   | aaggcgtatc  | 2760 |
| cttctctatt  | acagtaggca  | tgtgagaggc  | atctgtaccg  | actcacgaga   | caaatacaaa  | 2820 |
| tgagtactag  | aaagattgaa  | cccggtgttg  | gatctatcca  | tgagggttcta  | tcacaagatg  | 2880 |
| tctgatatag  | tttttaagaa  | tcaagccctt  | atcggacaaa  | tcatttggag   | cgttgttgca  | 2940 |
| gccgtaaaact | gatcacactt  | tagccgcacc  | gttacagtaa  | tcgtaataga   | gctccgacag  | 3000 |
| gaagatcatc  | ataaaaatccg | tcaccgtcaa  | catcatccaa  | ccaacccccg   | gtccgtcagg  | 3060 |
| atcttctgta  | aactgtccat  | caaaacgagg  | tcgagctctg  | agccatcggt   | tttgaaattc  | 3120 |
| gttaccggct  | taccgttact  | ttgacatcaa  | taaattcgtg  | taaaacaaac   | cctcttggtc  | 3180 |
| tataaagtcg  | tttctaccaa  | tagtattgat  | attgaatgct  | gcccccatag   | agccccagca  | 3240 |
| ccggaatttg  | agaacttaat  | agtcaactca  | aacggttggc  | aaaagaa      |             | 3287 |

## (2) INFORMATION FOR SEQ ID NO:558

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...562

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gggcaataac | taccgttctt | gcctcgtgac | agcagaggct | gcattgaagc | ttatccatac | 60  |
| accaagcatc | gcgaagagct | ggtcttcctg | atgcttcagc | tatgtacgaa | gaggcctctt | 120 |
| tcagcgtcag | tgaaaagttg | caaacgctta | ccgtgatgta | gcggaccagt | actttgccta | 180 |



|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| catcaacgaa | tttcccacgg  | gaaatacctc | aagcaagcca | aaaagatcta | cgacagcgtc  | 240 |
| agcaacatat | ctcacaaagac | gcttgacgaa | tgctcataca | cacccgggga | gtctccatcg  | 300 |
| cagcaacata | aaggagacgg  | cagagggtgg | atcaacaacg | gaacgatcgg | aagaaaaagg  | 360 |
| ccctgacaca | agttccgact  | aataacaaaa | acatcaaaaa | gatatatgga | gcttaagaaa  | 420 |
| atgaatgtcc | ccatggacac  | cttacacgtg | acatggtgcg | tctgagcgaa | gacacggaga  | 480 |
| acgtgtacga | gacagtgatg  | atcatagcca | agcgtgccaa | tcaaatcggg | cagcaaaaata | 540 |
| aacaggatct | tggaagaaa   | ct         |            |            |             | 562 |

## (2) INFORMATION FOR SEQ ID NO:559

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...926

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| tggcgcgaga | atgaaaaaaa | tctcgcgcca  | caaagaaaaa | aaagtcgagg | tattttgcag  | 60  |
| aaaagcgggt | ccgctttttc | tcctttttcac | gctcgtgatt | tcacccctcg | ctccggctgc  | 120 |
| acacccctct | ctcctgcaga | atgaatactt  | tcaaataccc | ccccccgcaa | aaaaacaatc  | 180 |
| aggacacaga | gtgggggtat | atgccactct  | atgtcccgat | tgcgttagga | gggaaatggt  | 240 |
| gcttaggatt | cgccaccggt | atcgtctgtg  | tgtggaagta | ttttgaacga | gaagaactgt  | 300 |
| gacgtctcga | gccgaagcag | atattattcga | tttgaacatc | agtcacacct | gcgatcggtc  | 360 |
| gggattgccg | tcaggatata | gtcgtaaaaa  | ggttttcggc | ctcgttgcca | aagataagcc  | 420 |
| cctgaccacc | ggagggataa | agttgttcgt  | cttgattcgg | aaagtagtag | gaagcaaagc  | 480 |
| cggattgaaa | cggccgggat | attcatgacg  | atgttcagtg | ctttatcctg | qgtcttatga  | 540 |
| cctgacaaga | gactgcgttc | gaagtggctg  | tgtattctgt | gaatgcattc | ctgcaccctt  | 600 |
| ttgtgtgcgg | actgcaaatg | gattggtaac  | ggnagggttc | ctcactacca | cacgcaccag  | 660 |
| acgtttgagg | tcaggattat | cttgtgtccc  | acaatgatgt | ctgacgtaca | tgagcctgaa  | 720 |
| ccgggtgttg | cagccatgac | aacgaaatcg  | taccgttggt | gttagtagca | ccgggttactg | 780 |
| catcccgcta | tatgtgacgg | tgatcagatt  | gttctgctgt | gttacgttgc | caaattcgga  | 840 |
| taataagccg | ctttgattgt | gcccgttgtc  | tgcccatcgg | taaggccaag | taagtatgat  | 900 |
| ccacttcgat | cttacctttc | cgggga      |            |            |             | 926 |

## (2) INFORMATION FOR SEQ ID NO:560

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2787

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tgaacttaca  | gttcttaccg  | ggcactgtcc  | tgcaacatgg  | caacattaca  | cctgccaaa   | 60   |
| aaaaatcctt  | caaagccgtt  | tgccactgcc  | cgagggtagc  | tgtacggcca  | agcgaatatc  | 120  |
| cgtaggttcc  | tccgctgaga  | gaaagcttaa  | tctccctgtc  | cgatcgtaga  | ggcatagccg  | 180  |
| ctgggaaaact | tttgtggata  | gaattcggtc  | tatataggaa  | ttgtttccga  | ccaaaggccg  | 240  |
| gcgcaagcca  | ccgctgcgag  | agtagaaatc  | gtacagccat  | gtttcggcag  | gaataggaaa  | 300  |
| ctacagatat  | cgccacggtc  | atatatggct  | gaaagagctt  | ccgcatcatc  | gtgcgcataa  | 360  |
| tgccttttggc | acgatgatcg  | gggtgtgtgc  | atctccggaa  | atataaccgg  | ctgagaaaaga | 420  |
| agtgcacaaa  | attcgcagtt  | gtaaggaagc  | atttgcagat  | gtgctacagc  | ctctcctgtc  | 480  |
| tcgctataat  | tagcaaggta  | taatcctcac  | ggaaaacttt  | gtggaaataa  | agctcaatga  | 540  |
| aggctcaggg  | tctttgaagc  | agatgcgcca  | tagccgcaca  | gatgcttccg  | cttggattcg  | 600  |
| gtcatgatcg  | cgctcgagta  | tggctgtttg  | tttgggcaaa  | gaatggcagg  | gcgataagat  | 660  |
| agttttggcct | ggcgcagtc   | cggcagccca  | aatcctcctc  | gcgattgatg  | tagcggaaatg | 720  |
| tgtccgggat  | cgaacggcaa  | attctctatt  | aatcatcgca  | aacgcgcctt  | ccaccatagc  | 780  |
| atcgcccttt  | cgatatgtac  | cccaaaagtg  | tcgggtattga | taggggagcc  | taacagaaa   | 840  |
| ccactaccgg  | gccaccgact  | cgtagtactc  | ccccgaaaag  | cccagctcct  | gacgatgccg  | 900  |
| aaaagcacgc  | tctaccatct  | ctacctccag  | cctcttccgt  | cctgatcacc  | tcggctatcc  | 960  |
| agccatagat  | gagccagcat  | aagcattcct  | cggcatcgct  | atccttaaca  | ggatcgtagt  | 1020 |
| tatagttaga  | tagagagaga  | caaattttatt | gatatgattg  | cgcttggcct  | gcaacttttg  | 1080 |
| cctgacaaaag | tcgctaaact  | ttcacgttctg | tatatgtagt  | cgcaatagct  | tcctcctcga  | 1140 |
| taaagtaata  | ctcagccgag  | caatgttctc  | ctataactcg  | tgaatatcgg  | gagtcacacc  | 1200 |
| cataaatatc  | aagggataat  | cttcggcact  | acttctgctt  | tcagtcgatg  | ggcagcggcc  | 1260 |
| actacttgct  | caggtcagct  | cccacaggaa  | agagatagac  | cggatgacta  | cggcttttcg  | 1320 |
| gttgaaacgg  | atgatcagac  | agccctccac  | aatagcccaa  | gacgtgccat  | agcgaactc   | 1380 |
| cagcaataga  | gattgaaaaa  | agccaggtcg  | caaattcctg  | caactgaaga  | aaggtgatag  | 1440 |
| ttgttatagc  | tgatctgtca  | gcaggttcta  | cggtttgaat  | ttaattattca | ttcgcattgg  | 1500 |
| ttttgtcacc  | ccctgttcaa  | tagaaggag   | acgttfaattt | atcggtgaaa  | cacctttaac  | 1560 |
| accgaaaagt  | ttcatctctt  | tccctatttc  | aattcggcaa  | atgtgtcacc  | tgccggagaat | 1620 |
| ctcctgtctc  | gaaccctcgt  | ttgaaccaat  | acatcctctg  | agaggagtgc  | catgtgcgaa  | 1680 |
| agcatcaggt  | accacatagc  | cctgcgattg  | tttccaacag  | gaagatgggc  | tataccacag  | 1740 |
| ggcagatggt  | ggtactccgt  | agagataacg  | ggctatcccg  | tacggctcct  | cgagctacgc  | 1800 |
| tgtagagctc  | agcaggtacg  | ctctacagcg  | tagcgagccg  | agccgtagag  | ttccgctccg  | 1860 |
| gggcccgtaga | ggtggccgag  | ctgagccgta  | gagcttggcg  | cggtagagccc | tcagcgtagc  | 1920 |
| tcgaagagcc  | ctagagcgca  | gctcggtagc  | ctctacggcg  | agcccagatc  | gctgtagggc  | 1980 |
| gtagctcgac  | ccccttccgg  | agtatatctg  | aacggctata  | aaacaatgct  | tatttggttg  | 2040 |
| gagtaaaaaga | gtcgcgccgt  | cctttttatg  | gaagccgggc  | gaccgattaa  | agcgatcggt  | 2100 |
| tggtagacat  | accgatcgaa  | aataatcatc  | tcgttacttt  | acagcgagtt  | tctctagtag  | 2160 |
| gacttgccgt  | caacgacaac  | catgactgca  | tagtggccgc  | cctgaccgtg  | taaacaaccg  | 2220 |
| tgttgcgacc  | cgctgccaga  | cgacgaccgt  | tcattcgtag  | atcatagctt  | cgccttggca  | 2280 |
| agttaccgtg  | atcgtctttc  | ctaaactgtc  | agcgtgtaag  | gcttctgagc  | cgttacgtct  | 2340 |
| gccaacgaag  | tgtattcaac  | gtagcagttt  | cgatagctga  | ttctccgttc  | gggtaaacaa  | 2400 |
| ctttacaccg  | tacgtgtaaa  | aaccggtagc  | caagtccgga  | tctcggtaag  | agtctccgtt  | 2460 |
| acgcctgatg  | ctatctgtgt  | attattacga  | tagatcgtaa  | ggtgtaagac  | ggagcgttcc  | 2520 |
| ctgaagtgat  | tacaacatca  | tcaaggttat  | ccagaagaag  | tccgtacagc  | cgaagtgacg  | 2580 |
| gaaggcaaca  | tacttagacc  | cgcaggcaac  | tgtaccgtct  | tttgatacca  | ggtgccctga  | 2640 |
| gcacgatacc  | acgaatggct  | tcaggtgccg  | taacaactgt  | ccttgccgctc | agcactcttc  | 2700 |
| caacaaagcg  | ttggcggaagt | tggaagcgctc | gttacccgta  | gaagtgcgta  | cacggcatag  | 2760 |
| tgctctgatg  | cataattggc  | atcttgtg    |             |             |             | 2787 |

## (2) INFORMATION FOR SEQ ID NO:561

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...525

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| tgaaacgggc  | tgctacgatg  | gctatcgcg  | atttggcg   | agagactgtc | ccgacgaagt | 60  |
| actgcgagcc  | tatggcaata  | ctcagttgca | cttcgggagg | actactttat | tccaagccg  | 120 |
| gtggatcctc  | gtctgatcgt  | tcgcgtacta | ctgccgtagc | acgtgcggca | gtcgagagcg | 180 |
| gagtggtctga | gcattccattg | cggattgggc | tgcttatgag | gccgaattgt | tgggacgggt | 240 |
| gggacgatga  | gccaccttac  | gcgtcgtcct | catgaatctg | ccaagctcaa | tcctatcgcg | 300 |
| tgatctatgc  | agcctgcgag  | aatccttcgg | tgctgaaagc | tgcttatcgg | cacgtgcaca | 360 |
| tggaatagcc  | cgaccgatca  | tggtggggga | tggaagcaaa | ttcgggattt | tgccgcagag | 420 |
| ttggatttat  | ctttggagg   | ttcgaaatcg | ttaattaccc | gcttccgatg | aaagaaaagg | 480 |
| cttcgcgcgtc | ttcattatgc  | ccgtgtcttt | gccgaacaga | actgg      |            | 525 |

## (2) INFORMATION FOR SEQ ID NO:562

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cgacagaaaa | acacacgtat | gccagcagg  | acaaaagcca | gtccgaccac | agaagagaag | 60  |
| ccaaaaaaat | tgtagtcatt | tattgctata | tttgcgata  | caaaggtaag | attttcttac | 120 |
| ccacagagaa | gcacaattaa | taactcaagt | aataacaatg | aacattacag | atctcaaacc | 180 |
| cacaaaagt  | tggaagtgtt | ccacgaaatc | actcaagtgc | cacgtccttc | caagaaagaa | 240 |
| gagaaatcct | ggcttacctt | gtgaaatttg | cagaagatcg | caacctcaaa | tatctacaga | 300 |
| cgaggtaggc | aatctcgtaa | tagagaaacc | cggcaacacc | cggtacgaaa | cacctcgaaa | 360 |
| cggtcatcct | tcagagccat | atgggatatg | ggatgccgaa | gaagaatgcg | ccgataangg | 420 |
| ttcatgactt | tcgaggaacc | gccttatcc  | cg         |            |            | 453 |

## (2) INFORMATION FOR SEQ ID NO:563

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...502

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563

```

gccggccggt gagaaaagga ctgtcgcggc ttttcgtttc gccccgatcg cctgcttctc 60
gttgctgcgg gagctttctc catacagctg acacgagacg actgacagct acttcacgct 120
acaagctgtc ttcattccgac acttttcggt catcggggaat ccggagccac gcgagggcaa 180
actgcgaatg caggtaaact gacaggaggc tcctcccat cttatatcct gtacatccga 240
cacgagggga atacgagccg gtcgctcgcg gcgatatgct caagcttagg aaatctatgc 300
ccgatcggtc gaagaatggg agcagaaagc tccggcaatg ggggggtatat ggcgggcaaa 360
ggactgtccg gcagtctgca tgccaagacc gggatgtaga aatcttgctg acagccaaag 420
ggcggttctc cctcaggcaa aaggttttgg atctgtcgga tcgcttggct gccacattgt 480
acgaactctc ccttcgctac tg 502

```

## (2) INFORMATION FOR SEQ ID NO:564

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...349

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564

```

ggatggagtg gagcgtaagc tgacggccga ggatctgatg atatgcatc gaacggcgat 60
cccattgtgt tggcgggctg tttcggtggt cttcactcgg tgtaacggaa aagacaacag 120
atatattcct cgagagtgcc aatttcaccc gacgatggta cgccgtacgg ctgcccatt 180
gggtctcaat acggacgttc tttccgcttt gagcgcggtt tggatccgga gcgcacggat 240
tgggcttgcg tcgtgctgct tcgcttatat tagagattgc aggaggccat ctcgtgggat 300
gacagatggt tattccaatc ctctgaaacc gcacctaatc agttgtctt 349

```

## (2) INFORMATION FOR SEQ ID NO:565

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1062

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:565

```

ccttggaacgg tcccctcaat atttgtctca gaaatggatt ccttctcggt tttctctgtc 60
agtgtcaaga caaagataga catacgaaac cataatgcga taatatctat gctaatacat 120
tcaatgataa tcatatccat gcattagaaa gccgaaaaat cacttttccg gtatcaaaca 180
ggatattgag atgaaaggct tttgagcaaa gggcttcttt tcggtggagg aagttttgtt 240
ttcaaaaagg aaagatcaat agtgatatat ataccgatgt cttactgctt ccatacccca 300
tataaatgga aattctattt atccttattt tcatgaacac ataaaaaaga catggaaaaa 360
ggattcaacg cctacgtagg tggaatgtat ccgtattgaa taatatatat ctgcgagggtg 420
agttttccat gtcgatgaat gaatgaactt aagatggctt atcctacgag tataaacgag 480
gaaacagccg ttttaagagta ttcaggcctt acattagtct gatgaaaaac aaggggggtat 540
ccggtttaac ataggctctt atttttcctt ctatagacaa aaaacatccc ggaactattg 600
agagagaaat ctctttttta tattgagcca catgcttaat cgaattagta atgagtaacc 660
agcatcgggtt aatgctgtct gtctctaagc tgtttctcct tcaaccatcg attacttttc 720
tcagcagatt ttggcaaagg atacaataac ctccaattac cctcaaaaatt atcgaaccct 780
tttgaaaaag gtttaaggga aacttatcct atgcctattt cagcttggtt aacggccttc 840
gatgtatggc aatttaagtt atatcaagga tagagatacg caattaccgt cacaacctca 900
aagggactat tgatcagtaa tttttatcaa gtggaggatg gagcaataca ttaagaacaa 960
acgcctattt gagtaaggga tcggcacctt ttcattggac ataaaatatc aggtaaatat 1020
acgctcagca acacaacctg atgcgtgtag ataaagaaga cg 1062

```

## (2) INFORMATION FOR SEQ ID NO:566

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 649 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...649

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:566

```

gaagaccgtt gcctgtcgtc gactctacag gatccccaac aagctgacac gcttcccagt 60
cgaggattga ccggtgcacc gtacttaagc accagggccg gccagactga atcaaagagg 120
tgaaatgttc gaagctgtcg cgataatctc tgccgtgccg tatatatcca tatgatcggg 180
atcggcagat gtgatatagc cataaaagggt ttcagatggt ggaatgaacg atcgaattcg 240
tctgtctgac gactactaaa tcacttttgt ccgatagcaa cagattcgat tgatattgtt 300
ggaaattcct ccagaaaacg cattgcagtc cacatggctc tgttgagcaa atgtgccagc 360
aaagtagagg tcgtagtctt gccatgtgtt ccgcgacaca gagtgcacgt tccatcagag 420
ttatctcgcc gagaacttct gtcgcttcac cagcgataa ccattggatc tgaagtaggt 480
caattccgag ggtcggccgg cacagcaggg gtgtaaacga tcaacgaatc ggtgggagaa 540
aaaagctttc gggatcatat tcaggtcac actgaaatga acctcaatcc tcttgatcaa 600
ttgatcggta atgggactcg gagtcagatc ataccaaca cattaaatc 649

```

## (2) INFORMATION FOR SEQ ID NO:567

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:567

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| cgtgccgggtc | tgctgactac  | agaccatggc | cccatagaga | ctcccatctc  | atgccggtag | 60  |
| gcacgggtcgg | gagcgtgaag  | gccgtacaca | tgcacgagtg | gaagaggata  | ttcgggctca | 120 |
| gattatactc  | ggcaataactt | atcaccttat | ctccgtcccg | gattggatgt  | gctcaagcgt | 180 |
| gccggaggct  | tgcacagttc  | aatagctggg | agcggccttt | gctcacggat  | agcggagggt | 240 |
| ttcagtgttc  | tctttggcgg  | agaatcggaa | gatcacagag | gaggggtcga  | ctttcgttcc | 300 |
| catatagacg  | gctccaagca  | ccttttttca | cccgaagg   | tcaggacatc  | cagcgcgtta | 360 |
| tcggagcggga | catcatcatg  | gctttcgatg | aagttgcccc | ggtgatgccg  | accgcgaata | 420 |
| tgcacgccgt  | tcgatgctcc  | taccggaagg | tggttgagc  | gttgccctgtg | tagaatgcgc | 480 |
| gagacggagc  | actctatgga  | tatgaacagc | agctattccc | catcgtgcag  | ggatgcatca | 540 |
| tcccgatctg  | cgccgcgggt  | cgccggagat | ggtagctgcc | gtcgatgcgc  | cggaaatgcc | 600 |
| atcgagggat  | tggccgtggg  | agaaccgacg | gaaaagagta | cgagatgac   | gaactgacca | 660 |
| acgagatcct  | tcccaaagat  | cgccgggcta | cctcatgggg | gtaggtactc  | cgatcaatat | 720 |
| attggaagcg  | atagacgtgg  | tgtggacatg | ttcgactgca | tcatgcctac  | gcgcaacggc | 780 |
| cgtatgggca  | gctctttacc  | tgcacggacc | atcaatatcc | ga          |            | 822 |

(2) INFORMATION FOR SEQ ID NO:568

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2778 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2778
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:568

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| aaagggttcgc | ccgtgaagaa | ctccgccctc  | acatccaccg | gtctggttct | ttcatggaac  | 60  |
| gctactccaa  | cagtacgcgc | gaagtagctc  | aagacggcgt | cgcggtgcac | ttatgctgtc  | 120 |
| cgtatccatc  | aagcatcccg | attccgatcc  | ttcatcgatg | ccaaaatgac | cgaaggcaag  | 180 |
| gtgacgggag  | ccaacgatcg | gtgaagatcg  | acgatgaatt | catgcgtgcc | gttgtcgaag  | 240 |
| gcaaacctat  | aaacaacagt | accccatcga  | tgccaaagaa | ccgaagtggg | agaagagatc  | 300 |
| gatgcgcgta  | ccctctgggg | caaaatcatc  | cacaacgctt | ggagtcggcc | gaacccgggtg | 360 |
| tactcttctg  | ggatacgatc | atccgcgaat  | cgtacccgat | tgctatgccg | atctgggctt  | 420 |
| ccgtacagtc  | tcaccaaacc | ctgtgggtgag | atccctctct | gcccctacga | tagctgccga  | 480 |
| ctgctcgcta  | caacctctat | tcctacgtaa  | agaacccatt | cacgagcgaa | gcctccttca  | 540 |
| cttcgagctt  | ttccgtaacc | acgtcgtttt  | ggcacagcgc | atcatggaga | catcatcgac  | 600 |
| ctcgaaggcg  | aaaagatcga | acagatccta  | agcaagaagc | cagcgatccc | gaaagcgaag  | 660 |
| aagtcaagac  | ctcggagcgt | aacctcggca  | caagatccgt | cgcaagaccc | ttgccggctg  | 720 |
| tcgtacaggc  | gtaggatcac | cgccgaaggc  | gatatgcttg | cagcgatggg | attccgctac  | 780 |

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| ggttggacga  | agctacccaa | ttcgccgaag  | aggtacagaa  | gaccctcgca  | ctcgcgcccta | 840  |
| tagcagctct  | gtgaccatgg | ccaaggagcg  | cggcgcccttc | gactgttcga  | tgccaaacgc  | 900  |
| gaagagaaca  | atccctttat | agcccgata   | ccgaagccga  | cccatggctg  | tacgaagaga  | 960  |
| tgaagcagta  | cggacgacgc | atatcgctg   | ccttaccata  | gtccctaccg  | gttccaccag  | 1020 |
| tctgatgacc  | agacttcctc | cggtatcgag  | cgggtattca  | tgccgggtcta | caagcgcca   | 1080 |
| gaaaggtgaa  | tccgagcgac | aagaacgtac  | agatcgacta  | tgtggacaag  | tgggcgacag  | 1140 |
| cttcgaagag  | ttcgttgtct | accaccacaa  | cttcgtactt  | ggatgcgcac  | caacgggttac | 1200 |
| gaccccgacc  | gcaaatacac | gaacgagaga  | tcgacgacct  | cgtggcccg   | tcgccctact  | 1260 |
| acaaggccac  | ggccacgatg | tggactgggt  | agccaaagtg  | aagatgcagg  | gacgcatcca  | 1320 |
| gcatgggtag  | accactccat | cagcgtaacc  | atcaacctcc  | cctccgatgt  | cacgaagagc  | 1380 |
| tgggtcaatac | cctgtatgtg | gaagcatgga  | agagcggtcg  | caaggctgta  | ctgtctatcg  | 1440 |
| cgacgggttcg | cgcagtggcg | tccttatcac  | gacaagccga  | agaagaaaga  | caagaaagag  | 1500 |
| gagcggcgag  | ctctccaaac | acagtacaga  | gcatgcttat  | ctcccgtccg  | cgcgagctgg  | 1560 |
| aggcagagtc  | gttcgctttc | aaaacaatcg  | tgaaaagtgg  | atcgctttcg  | taggcctaag  | 1620 |
| gatggacgtc  | cttacgaaat | cttcacgggt  | atagccgatg  | acgacgaggt  | atcatgggtac | 1680 |
| cgaagagcgt  | taccacggc  | aagataatca  | agaacgggac  | gaaaacggcg  | aacgacacta  | 1740 |
| cgacttccag  | ttctgcaaca | agaaggtttc  | aaggtaacca  | tcgaaggctt  | ggatagcaag  | 1800 |
| ttcaatccc   | aatctggaac | tatgccaagc  | tcattctcggg | cgtcttgcc   | tacggtatgc  | 1860 |
| cttcgagcag  | gtggtacatc | tcgtacaggg  | catgtcgctg  | aacgatgaat  | catcaatata  | 1920 |
| tggaagaacg  | gcgtggagcg | cgccctgaaa  | cgttacctcc  | caatggcacc  | accctgtcgg  | 1980 |
| gacaggtatg  | tccgagttgc | ggtcaggagc  | attggtttat  | caaggaaggc  | tgccctgctat | 2040 |
| gcaccagttg  | cggagcttca | aatgcggata  | aagcacaaaa  | cgggcagggt  | atcggttcta  | 2100 |
| taacatatac  | ctctgctgcc | actctacatt  | tcctttactg  | ttcaagaggg  | catgtcgggc  | 2160 |
| tatgattcgg  | catgccctct | tcctttgtacc | cttttttcca  | tattatttgc  | atgccacaca  | 2220 |
| cttaattttc  | tatagatttg | caactaatcc  | acaacattac  | aagtatgatt  | acaacattag  | 2280 |
| gcgagtatgc  | attaaaagca | gctttaaaaat | cggcttgaat  | atccacagtt  | ttcatcgttc  | 2340 |
| tgaagtcatg  | gacagatccg | atccgctttc  | gaatatgccg  | taaatgattg  | gtcgaaacac  | 2400 |
| gtgtgggaat  | aaccacacga | atcaacctaa  | aacaagcatt  | agaggcctat  | cccaaatcc   | 2460 |
| gacttcattc  | aagccggagg | atcaagaaat  | acgagattta  | ttgcctgttt  | tgagaaacga  | 2520 |
| cttgctgaat  | ccaaacacca | agcagcctca  | actacttgac  | ccaattggag  | aatagagagg  | 2580 |
| aacataccca  | aatcatgcaa | ccatcaaaga  | aaaaggcctt  | gatccacggg  | atattgaacg  | 2640 |
| atactttaa   | aactgccaat | caaagaaggt  | caagcaaaag  | cggaacaggc  | catcgagatt  | 2700 |
| tataccaaag  | tcgtgaaata | gaactccctt  | tgcgcgagat  | attgaaatca  | tagtccgaaa  | 2760 |
| tctgttcgaa  | cactcggc   |             |             |             |             | 2778 |

## (2) INFORMATION FOR SEQ ID NO:569

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1205 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1205

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| gctttaaata  | ttgcagccga  | tggaagtttt | accatcaaga  | aagaatttag | ttggatggct | 60  |
| ttgaaattaa  | agatacagat  | gttcttgctt | tcgtacacat  | ccaatgtcca | atgcggaaaa | 120 |
| ccattctatt  | atcaatgccg  | ggcaagaagc | cttgataaag  | cagagcctac | agctacagaa | 180 |
| caaattgttg  | ctacccctct  | gtcaaagcat | atgttcagaa  | tggcaaaatt | gttgtagagg | 240 |
| aagagattcc  | aagatggaag  | tattcaatgc | aactgggtcaa | cttgtcaaaa | atgatccctt | 300 |
| gtccccgggtg | tctatgttgt  | ccgtataacg | gcaaacgggtg | taagtatttc | cttaaagtct | 360 |
| tggttccttg  | atztatagag  | ctaagattta | aagaaaactg  | cgccttctta | atgttttata | 420 |
| agaaggcgca  | gttttcgttt  | tctcattcca | ttctccgggt  | ggtcgtcgaa | ggggactgcc | 480 |
| tgtcatcttt  | aaacaggagaa | tatcagctcc | cctcacacaa  | cacgatgtcc | acaaatccag | 540 |

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| ttcatagcct | atttgagacc  | tttgaaaaaa | gagaagggtt | cttatatcat  | aaaggcacta | 600  |
| aaaatcagtc | gattgacaat  | gaaatctcca | agaaaatccg | tgcgacagtc  | tcacttatat | 660  |
| agatgcggtc | aatgggtctga | tatatcaggc | tggtgtggat | ggaggatagt  | acacatagtt | 720  |
| ttgcacctga | aacaacgttc  | atactaaact | aaaaacaaaa | gcattatgac  | tcctatcctg | 780  |
| aacacgtttt | ccccgagttc  | aaactcaatg | cctatcacaa | tggcgaattc  | aaataatcac | 840  |
| caacgaagac | ttgaaaggca  | agtgggtctt | ggtcgttttc | taccgggtga  | ctttaccttt | 900  |
| gtatgcccga | cggaattgga  | agacctggcc | ataaatatga | agaattcaag  | caacttggag | 960  |
| tagaggttta | ctcttgca    | gcgataccca | cttcgtacac | aaggcttggg  | ccgacgcttc | 1020 |
| tcctgctata | agaagggtaca | gtatcccatg | ttggccgatc | ccttcgggtgc | actcactccg | 1080 |
| atctggtatc | ctgatcgatg  | atgttcatat | ggcttaccgt | ggctcttcgt  | gattaacccc | 1140 |
| gaaggcatta | tcaaaatcgt  | agagctgaac | gacacacgta | tgccgtgatg  | cagaagagat | 1200 |
| cctcc      |             |            |            |             |            | 1205 |

## (2) INFORMATION FOR SEQ ID NO:570

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...465

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:570

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gcaggatgca | aaaaggaacg | tcagtgcggc | gaaaaaaatg | agctttctgt | tgatcatctgt | 60  |
| ttttgtctta | tgatggactt | aacctcgcaa | agatagcctt | ttctatatat | aatgtagttg  | 120 |
| ccgtgtacag | attccagtta | taaatgcaca | ctaagtcaga | tctagtaaga | agcgttcgaa  | 180 |
| ggggtgggct | atattcgggc | tgaggcattc | aaaacagcgt | tctatatggg | gctgtgtcaa  | 240 |
| aatccaaaat | ggattttcca | acaaaaagac | acaaatgcc  | ccttaatcat | atcggaanaa  | 300 |
| cgctatcaag | taggatgatt | ttgtcctttt | ggtagcgggt | tcttatataa | attatacaaa  | 360 |
| tgatagtatc | ctttactcta | aacggaattt | tgcacactct | catctatctt | ctgtgatcag  | 420 |
| aagataggca | aggaatcggc | tgatcggtcg | gtaatggtga | gggga      |             | 465 |

## (2) INFORMATION FOR SEQ ID NO:571

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...563



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

```

ggcagtggca ctttctccat atttgtcgaa cgcgccttgc gggagacctt cattacaaga 60
aatcgcttcg ttacatccat cgctctctcc ttcccggtag gaatggaaag acatgattcg 120
taaggaactg gcagaaaaca gacctgttat tatgccggtg cagacggatc gatgggacat 180
gctttcgttt gcgatgatac gaaccagacg gaacgttcca cttcaactgg ggatgggggtg 240
gcatggtaac ggtaattttt atctcaatct actcaatccg ggttcgcttg gcacggcgca 300
ggcgatggag gctactctac tgaccaagag gttgtcatag gcaagagccc ggccagcaat 360
gaagtccccg gtatcggtac cggatccgac cacacgcttc tatggattgg caacacaata 420
tgtctgatga aagcactttg actgagtgtg aaaatcaaga acctactcca catatgcagg 480
gggatgtgaa attggcttat cgctgacgc ttcccaatgg aacggaaacg actaaccac 540
cgtcaccgtc cctatcgttg gga

```

## (2) INFORMATION FOR SEQ ID NO:572

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature:
- (B) LOCATION 1...843

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:572

```

gccatgcttc gtgccacgac acaggaggag cttttcgctc ttatggacgg gtggagaaga 60
tgataggatc ggctgattca gcggcggtat agtcgcttga caaagctccc cctgccgatt 120
gcttcaatcc acaggtctcc gcatgcaatc cgtcaactcg gcatcatggt tgccgggtgaa 180
catctcgttg tggcatcgca tagcaaccag agcagatgat cgaaggcggt cagctgttcg 240
tccgaagggc ggaaacgagt gtctcggcac aaaggcgtag gttgggaaag agatgaccag 300
tacctttctt ccctcagggg taatggagac acgcatactt ctggatcctc ctcatccggt 360
ctctgctcga tcagattagc tttcagcaga cgcgcgatgac ttctgcgccg gatgtttttt 420
ccatggcatt gaggttggtc actctgtctt ggtcatgctc tcaccgttca tcaggctgac 480
cagataggta attcgtcttc ggtctgtaat ggagattccg tcagagcttt cttgatataa 540
aacgggaata acgatggagg aggctgaccc ctgcgctat gttcttagtc ctgctgctcg 600
ttcccgggtg acagagacaa cttcttcttc ctgtttctct ttttgccaca gcgccaactt 660
aaaaagtcgg caaagtcttt tatttcggtt cgtgcgagcc tccgtcgtgc aaactttcaa 720
atgcatcgag gtagtaataa gatcgaaaag cagttttttg tacttcataa attactccga 780
ttgataaatc gtccgttcga tgtaatcctt ttgaagcata aatgtacatt tttcactgaa 840
aag

```

## (2) INFORMATION FOR SEQ ID NO:573

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...3043

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:573

```

gcacncaagg natatgacgg cccaatgggtg atccgttacc cgctggtgcaa ggggtgcttga 60
ccgactggcg caacactccg cgactgggtc aaatagcgga ggacgctgtc tgacggaggg 120
cgaagctata gccttcctct ccataggccc ataggcaata tggtagagaa agtgggtggaa 180
cggttggtcg agaaagtgtg tctgcagccc actacgatat ggtattcctc aaaccgcttg 240
acgaganatg ctccatggca tgcgaaagaa gtttgatacg atcatctccg tcgagatggg 300
tgcatccaag gcggtttcgg atcgggccgc atggagttta tggagaccat gactaccacc 360
cacgcatccg acgggtggga gtccccgac gcttatcggg cagggatctg tgcccgaaca 420
gtatgcagac tgtggcatgg agcagactct ttgttgactg tgaccgaaga acttctgctg 480
catccgtagg aaaaggaacg aaggatgctg cacggatctt acaaacctta atgtagcaaa 540
tgaatattgt tatagccggt gccggcgagg tgggcacaca cttggcgaaa tgctttcgca 600
agaggaacag aacatcgctc tgatcgacc caatcccaac gattggaact ggccgccatg 660
cgttccgagc tgctccctca ggtgggaatc cgctttctcc ttcagacttg ctgcaggcca 720
atgtgaagta tgccgtcttt tcacacagct gatgcgggag gaggcggaac acattttggc 780
ctgtcccttg cctcacgttt gggagcagga aaaacgctgg cacgcatcaa caaacgcaat 840
tcctcaaaac cgacatggca cagtacttcc gcgatatggg agccatacca tgattttacc 900
cgagctgctg gctgcacggg agatagtatc gccatcaaaa acccggtggc acgtcaatac 960
gtggagttgt tcgatggggc ttggttctgg tgggtgtgaa ggtgcgtgag ggtgcgcaca 1020
ttgtaggcaa taccttcatg agctgaccg gacgggaaat aagatatctc acatcgctct 1080
atcaagcgtg accttgagac gatcatcccg aaggggggta cacaggtctg catggagaca 1140
tcgtattctt cgccacggct caaaaccact tggatgagtt cgcaagctcg caggcaaaga 1200
caatecgncc gtccacaaag tgggtgcatg ggaggtagtc gcatagctat ccgttccata 1260
gagatgatcc cgagaacata caagtggcga tcatcgagaa ggacaaggag aaaagcatgc 1320
ggacagtgcc atcgctccga ccaacgtaca ggtgtacaac ggtgacggac gactcggac 1380
atcctcatag aagccgggtt ggatcagacc gatgtattca tgctctgacg gaaaattcgg 1440
agacgaatgt cctcgccctg ttgggagcca gcgtttcggg gtattcaaga ccatcgccaa 1500
ggaagagaaat atagactact ttcatgtggt gaccgccttg atataggcac gctcatcaac 1560
aaaaaaacttt ggccgcgggc tccatctacc gcatattcct cggcgaagat acgagtagg 1620
gaagtgcctg acgctggcca atgccgatgt ggccgaacte gtggctatcg cggagcacc 1680
gtcaccaaaa gaccggtgaa agatctgaac attccgagg gattacctc ggccgcatgg 1740
tgcgcaacgg tgtcccgaac atgaccatgg cgatacgggt atcgaaacct acgaccatgt 1800
agtgtatttc tgttgaatac accactgaat atcctgaaag acttcttcgg ctaacctctc 1860
tttcggacgg cacggcgata tgttgacgca catcaatttc aaattcgttc taaggtggta 1920
ggctctctat gcctgtccga gattctcttt ctgttgattt tctgggtata tccgtctact 1980
acaaggggag cgatctgttg ccctttgtta cactatagga gtgatggccg cggtaggctc 2040
ctgtttctac ctgctggggc ccgtgctcgt atgaacaacg caagtccggc cgaagggatg 2100
cctactgcac ctgacgtgg cgatcctat cgcttgctgg catgcttcct tttgtctcgg 2160
cggatatact ccctccgtga cggatgcttt cttcgagacc atgtcggctt cacgaccaca 2220
ggagccacga tattccccga ggtggagtct ttgcccagg cattcttttc tggcgtagca 2280
ttatgcagtg gcaggcggtg tcgtatcggt gtctttacgg tagggctgct cctatgctc 2340
ggtgcaggaa gtccggtttc caaatataca atgcggaaac tacgggcatc atccacgatc 2400
gtttctgccc cgtatccgtc aggtgccacg ccggtctgct ggtgtctata tctcggaact 2460
gctgtactga tactgctttt gtgggtgggc ccgatggggg gttcgatgcc atttgccacg 2520
ctttcacttg tatttccacg ggaggctatc cacgcgcaac ggcatatcg cggagtttca 2580
gtcctcatal atcgaaattgt cacctcgttt ttcatgttct acggcagtct cagcatcacg 2640
cttcagactt tctgctggta ggaaaaccgg gaaaactgat tctgtgatgag gaaatcgac 2700
ctttgtcgte ctgaccctct gtgccgtttt gatcactacg ctatgctttt gtatcggggg 2760
gaatatccga gcttgaggga aaatttccgt catctctctt tcaaacctat tcgatcatca 2820
gtaccaccgg ctataccacg gcgattactt ctctgtgggg cctttcttct ggagtatagc 2880
tatcgtgatg agattgtctg cggctgtgcc ggatcgacga cgggaggaat caaaatcagt 2940
gcctcgctgt cctgatgaaa aacttgctga acgaatttaa gaagcgtacc accccaattt 3000
gatggtacct gtacgaatca atgggattat catcacagac aat 3043

```

## (2) INFORMATION FOR SEQ ID NO:574

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2375 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| gtataaatta | aatncagggtt | gaaagtttcgg | ggcgtgcccc | tcgttttcgat | tcttgctatt  | 60   |
| cacaattgaa | aaagtaaaaa  | aatgacatat  | aatgaattca | actggaattt  | ggagccggtt  | 120  |
| accgcagagg | aacgttccct  | cgggacatat  | tctgtcggga | gctaaggctc  | gcgcccgtag  | 180  |
| tggggtgcct | attggccgca  | ggggaatagc  | ttcgttagag | gaagctaagc  | gtttctttcg  | 240  |
| cccaaattgg | aggatctcca  | cgatcctttc  | ctgatgaagg | atatggacaa  | ggcttagctc  | 300  |
| gcctgaacag | ggcagtaggg  | cgaaaggaaa  | aaatcatgat | ttaggtgact  | atgatgtaga  | 360  |
| cggtaccacg | gcagtggcac  | tcgtctataa  | gttttgccgc | ccacgggctg  | ctccgaaacc  | 420  |
| caattggatt | actacattcc  | gatcggtagc  | atgagggtta | tggtatctct  | tatcgaggaa  | 480  |
| ttgatttggc | cactctctcg  | gaacgaaact  | gataatcgta | ctcgactgtg  | gtatcaaagc  | 540  |
| gtcgaaaagg | tggcatacgc  | caagtcgctt  | gacattgatt | ttattatcgc  | gaccatcaca  | 600  |
| atccggatga | aacgctacct  | gatgccgttg  | cggtgctgat | gccaaaagag  | ctgacaatac  | 660  |
| gtatccttac | gaacatctct  | ccggcttggg  | gtcgggttca | agtttatgca  | agcctatgct  | 720  |
| cggagcaaca | atttgccgaa  | tccaagctcc  | ttcctttgct | cgacctcgtg  | gctgtcagta  | 780  |
| tagctcggat | attgtcccta  | tcattgggaga | gaaccgcata | ctcgccctatt | acgactgcgc  | 840  |
| caacttaata | aacgcccttg  | tctcggcttg  | caggctataa | taatgtatgc  | ggtctgaaga  | 900  |
| agcgaaggat | agatatgaac  | gacatcgtct  | taagatcggg | cctcggatca  | atgcttcagg  | 960  |
| tcgtatgatg | aatgggggta  | ggctgttgaa  | ctactactct | ctcaggatgc  | tgtggaagct  | 1020 |
| caaagccgac | ggccaatata  | gacgaataca  | acgaccaacg | ccgtgagctc  | gacaaggagt  | 1080 |
| gacggaacag | gccatcgata  | ttttgggcga  | gctatccgat | gtggacagaa  | gatcctcgtt  | 1140 |
| atctaccggc | cggaaatggc  | caagggcgtt  | atcggctagt | ggccagcagg  | atgaccgaac  | 1200 |
| gctattcgcg | ccgacgatc   | gtgatactaa  | gagcggtagt | ttcatttcag  | gctcggctcg  | 1260 |
| atccgtagga | gggtcgatgt  | gtacaaagcc  | atcgaacatt | gcaaggactt  | gctgggtcaat | 1320 |
| ttcgagggca | tccttttgcc  | tccggctctga | cgatcaaaga | agagaatctg  | gaaccttccg  | 1380 |
| aaagatgatt | acggactatg  | ccgaagaggc  | tgtatcgccg | gactattggt  | gccacaaata  | 1440 |
| gatgtagatg | ccgaaatatc  | catcgaagag  | tcaattacaa | acttctcgac  | aacctcaagc  | 1500 |
| ggatggggcc | attcgcccg   | aaaactccaa  | gccggtcttt | atatcccgac  | aactgtatga  | 1560 |
| tgccggtgta | gcagggctgt  | aggaaaagct  | tccgaacacc | tgaagataga  | tgtgagatgg  | 1620 |
| gatcgggcga | acgccatccg  | gtgagtggga  | ttgcgtttta | tcaggcggtc  | attgcatga   | 1680 |
| gatcaaaaac | ggctcatttc  | gtctttgcta  | cacgaagaag | agaacgaatt  | caacggcaac  | 1740 |
| aatcatttgc | aactattggt  | gcgcatatta  | agcccgaaga | agaatctgct  | attaacggaa  | 1800 |
| aaacaagatg | aaaaaacgct  | cacgatgaat  | ctgggaggca | aggtcttcca  | catcgacgag  | 1860 |
| gagcctataa | cctgctggag  | gagtatctgc  | acaatttagc | ctcacatttc  | gtcgggagaa  | 1920 |
| ccatacggat | tgtaaagacga | tcgaggaatt  | cgaagcctac | tgtccgacat  | gatggtggtg  | 1980 |
| cgtttgcata | gcgaacacgc  | cgtaataaga  | tcggcctgat | tcgtgaagtc  | atagaaaaga  | 2040 |
| tcaatacggg | agagcacttt  | cttccaatga  | agacagtacg | actgccggat  | attctgcagg  | 2100 |
| ggccggtaca | gtcagaagga  | gagagaaact  | tcaggctatc | gatacatgtc  | cggggagctc  | 2160 |
| cgaagcgga  | gttttatcgc  | gacatggatc  | atgccgtttt | gtgtgcgtgt  | gtagcggtat  | 2220 |
| tgctgcatat | acgagatgga  | atgtgaatgc  | tatcgtgtga | tagtcgtgtt  | gatgacgatt  | 2280 |
| ttggcttctc | cgctcttttg  | gatatcatta  | tcggttattt | ggccgtttgg  | atgatagctc  | 2340 |
| caccggctat | aatgcttctc  | agaaattgga  | gatgt      |             |             | 2375 |

(2) INFORMATION FOR SEQ ID NO:575

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tacatacggc  | gctgacntc  | gacgtaggc  | tcgaaat    | cgaggncgat | gtgcgaaaag | 60  |
| cctccacgtc  | accatcctct | gcacgccata | aagccgctct | tgtgaagtgc | cacggtcggc | 120 |
| tcggaaatga  | acctccttgc | catagcgtgc | accaatagat | ctgtcagttc | actgagcatt | 180 |
| tcctgccgaa  | aggaggcata | cgtttttgca | tcgggtttat | attttgaggt | ttcaccgttt | 240 |
| gagcttcgtg  | tttacttggg | caaagtccgt | gtatccctcc | accggaagca | aagcagcgac | 300 |
| catgccaacg  | ccagcgatag | ctgttttctc | ttcttcatat | tatactattg | aatttagaat | 360 |
| gaatctctcc  | aaatgtaacg | acaatcgagg | agtaggat   | aaattttgaa | taaaaagcag | 420 |
| ctatagagtc  | acgcagtagc | gttggtgaaa | taaaaagaga | cgtacctccg | gaggggagat | 480 |
| acgtctctgc  | ttttcgtttt | tgtatctgct | ctgtatgagc | aggggagtga | aatcagggat | 540 |
| agcaaacgcc  | ctgagctacc | atagccttgg | caaccttcac | gaagccggga | tattggcacc | 600 |
| cttcacatag  | tcgatgtagt | tgccgtcttt | accgtattaa | cgcactgctc | gtggatgtct | 660 |
| tgcattgatct | ggcgagcca  | cttgctactt | cttcattcgt | ccaaacgagg | tgcatagcgt | 720 |
| tctgcgtcat  | ttcgaacctg | agcaagaac  | accacctgca | ttaacagcct | taccgggagc | 780 |
| gaaggcatct  | tggtttgctt | acatagtatt | cgctggcttt | cggccgacaa | ccctgttaga | 840 |

(2) INFORMATION FOR SEQ ID NO:576

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 978 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| taaaagatta | ggtacttttc | aagaaaacca | tcaagtactt | tcacaaaaaa  | ttaggtactt  | 60  |
| tttattggat | tatcaggtac | ttttgaaaat | agatttatat | atttgtagat  | gtattttaaga | 120 |
| aaacgccttt | cagaggattt | ctccgacttg | ggaaggttta | tcaagtggag  | actaaaacgt  | 180 |
| atgtaataat | ggcaagaaac | cattgcaatt | tgtggtcgta | gagcgaaaaac | tgaatgtggg  | 240 |
| taaaacgcag | gtaaagtaat | gcagatagca | agaccgacgg | ggagacatcg  | tgtaactttc  | 300 |
| gctccttttg | cgaacgtgta | tccaagtcca | ccacattcaa | cgcgaagaag  | tcgaggctgt  | 360 |
| attgaactat | gctacagaga | ttgccaaaga | catgtatcga | acggcgacat  | cgtggagt    | 420 |
| ggagaccttg | gcacactaat | gcttctttca | aaagtaaggc | ggtagaacag  | ggggtaaagt  | 480 |
| tcaatgctaa | gttcacatcg | aaaagcctgt | tgtcttggtc | caaccttcca  | aaaagtactt  | 540 |
| actctcaccg | atgtaagcta | tgaacagaca | actgccaggc | caaagaaaga  | acaaaacctg  | 600 |
| ctccaaagcc | tgataccgga | agtgggggga | atagcgggag | ggcatataag  | aattagataa  | 660 |
| gcccacactt | aacctttcag | aagtttttaa | accagaatag | agagtttgct  | ttgccttgga  | 720 |
| gcaaactctt | tcttttagac | ttttctgaat | cttgattagc | cccttttggt  | catcatcttt  | 780 |
| gaggggcttt | tgatggtgtc | ggtctcaacg | tcttttagtg | catcggcaaa  | aacagt      | 840 |

```

gggaaagagc catctcgtct tgtttgccga cacagaaatg ctccaaatat tccaaccgaa 900
atgatacagg tctaaagaga tatgaaagcc ttttgtctat cactatacaa actccgtttg 960
aatcatcagc atagtaag 978

```

## (2) INFORMATION FOR SEQ ID NO:577

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 464 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...464

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577

```

tattctttgc tccctgagaga gggctgggtt ctatcctaag tcgctacaat tcactatcga 60
ggagaactca cccgaggagc aacaagtggc actagaccag agctactcgg caaggtcttt 120
gagaatctcc tcggagcata caaccccaga ctcaggagac tgctcgcaac cagagtggct 180
cgttctatac tccctcggagg ttgtcaacta tatgggtggat gagagcctga tttcttattt 240
aggagtagcg atctgggtgcg ctctctgttt agaccagatt tcgtactgca ggagacaaca 300
aagtgcaatg cgaagctatt gcaagcaaac tcaaagcagt caaatactag accctgcttg 360
tggctcggga gcattcccaa tgggattgct cataggatga ttgagctact tgagcgcata 420
tctccccaag agaaaagcta tatctcaagc tctttgtgat cgag 464

```

## (2) INFORMATION FOR SEQ ID NO:578

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1007 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1007

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:578

```

agcggagatc cgcgtcctct tcgatcctgt cggctcgatca ggagctttct caagcggatt 60
cgggttttct ccaacgcgca atcttcaccg ctggaactag tataagcggc acggttacga 120
ccctcagtg tgccataaccg catgccttgt cttggcgata gggccgctac aggtgagcaa 180
tgctcgcttg cttttcctat ttccatgcct gaagatgagg ggggtggtacg gttggtgggt 240
aacaaacgga tgagtccgac ctgcaagtgg ctgtcgtatc gctacettca tttgatcgct 300
ggacgatcgg gcattccggc tgcaagctcg tgagcccaga gagtgaatct ttcgcttgcc 360
gtacctcgca atatgcctcc ggggatgaag gagagcctct cgttttggag gtaacctctc 420

```

|             |             |            |             |             |            |      |
|-------------|-------------|------------|-------------|-------------|------------|------|
| ccgaaacagg  | aaaaaaagcc  | gtgattccgt | catgggtctcc | ttgccgctgg  | tggacaattt | 480  |
| ccctgccctc  | ctgcagccca  | aacaggcggt | atggaactca  | gcacctattt  | ggacatgggc | 540  |
| agttggatgg  | agagacgaca  | aaggctgcga | tagagattcg  | caacgctcgtg | ccggccctct | 600  |
| ccgattgcat  | agcgtcacca  | cacgcaatcc | ggctttgctg  | ccgtaccgga  | ccggacggag | 660  |
| ataaagcccg  | gcggaagcac  | actattcgga | tcgctgtgga  | tccgcagggtg | atgaaggctg | 720  |
| aggggtggca  | gagtaagctg  | ccgatatttc | cattatttgc  | aacgatccgc  | aggctccgct | 780  |
| acgtgtatca  | agggtcaaagc | cgaactgtag | cttttccccg  | tagagctgct  | gccagcggta | 840  |
| ctgcaagcga  | gattgcccgc  | agatctgata | aacagaacat  | tactatggac  | gaactacttc | 900  |
| atcatcccg   | aaatgatgat  | tgctataagg | gctgaaagtg  | aacaaaggcg  | tttccaatat | 960  |
| gccccatcatc | aatccctacc  | gaataggaca | agacgcaaga  | agcttga     |            | 1007 |

## (2) INFORMATION FOR SEQ ID NO:579

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2523

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:579

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| gcaaaatcga  | aaggaacttg  | acgttcgcga  | tagtcgagag | cagctctgaa  | aagtgcgaca  | 60   |
| ggacggaatc  | aggaagatgg  | agacgataga  | tacctgcagc | cgcgaaatgtg | caaggaatga  | 120  |
| cgaaagggat  | tccaaggcga  | ctcctcctgt  | ccactgctcg | gatcttcttc  | ggtatggact  | 180  |
| accgagcaac  | tatccgaccg  | gcataaagaa  | cgatgccgat | atggctatat  | tcttgtgccg  | 240  |
| aagagccttt  | ttcctgaaaa  | gaccggaata  | ccacgaagtg | cctaagcgac  | agataggtcg  | 300  |
| ccatcgcgca  | attccgttcc  | ttcggggaag  | gcaggtacaa | aaacctttct  | tjccctgccct | 360  |
| gcgagcatgc  | actcagacag  | agcagaaaaag | aaggagaga  | atgcaccggg  | taacgaatgc  | 420  |
| attaagacgc  | aaaactgtaa  | accgaaggga  | tgcttatttc | ccgatcgctt  | catcgacaag  | 480  |
| ccatttgttg  | cgatattcac  | cacatgaacc  | gtggttgat  | catcttcgaa  | atccagatag  | 540  |
| tgacccaagc  | ttccttctcc  | acaatactat  | ccttgataaa | ggtaaactgt  | agtttggttt  | 600  |
| ggcctctccg  | cccaaagcac  | catacagatc  | gacaagctat | tggtgcgttc  | cgtgcaatac  | 660  |
| ttcttagcct  | cttcataatt  | ctgtttgcca  | tgttctccga | gaagttcttt  | acagcatctt  | 720  |
| tcggggccgga | cgatgacagc  | cggccatcaa  | ggcagcggca | aacaatgccg  | ctccgatttt  | 780  |
| ccatttttca  | tattagaatt  | tttacttttt  | aagtatcagt | tgcttagcaa  | agaagcgaat  | 840  |
| atccctatct  | cctcattcgt  | gcaggtgaca  | ataatcgctc | gaaaaggccg  | aaaggagaga  | 900  |
| caaggccagt  | aaaatgtgga  | gccggaatca  | gagaaacatg | gttccaaaaa  | atctgaaaaa  | 960  |
| tcgaacccaaa | acaaaaactt  | tacgttcggg  | aatttttttc | ttttggcgcg  | agttccaaaa  | 1020 |
| aattcccagc  | catgttttta  | gggatgtggt  | ttgattggtt | ttcggcgcac  | gaaaagaaaa  | 1080 |
| atggtcagct  | tcccccttcc  | tcttcgctct  | ttttcatttc | ccccaaagta  | aacagggggc  | 1140 |
| gcagagtttt  | cggatcggac  | ggattcgatc  | gggaacaaat | ccggccgatt  | ctgtttaacc  | 1200 |
| atatgagacg  | aaaacctgtc  | gaatgtgcca  | atatgcaatc | atgaatgtac  | cctttgaaca  | 1260 |
| gaatcatcaa  | cttaaaacag  | tcaattatga  | agacaaaaag | actttttcta  | ctggcgatca  | 1320 |
| ttgactatgc  | agcattcatg  | catcaatggg  | gcttgacctc | caaaaacgag  | taaaagggaat | 1380 |
| gagcaattcg  | cctctgaaga  | gcgtttggca  | gagcctttca | cgcccttcgg  | catcaggcag  | 1440 |
| cattgatatt  | cagatcgaat  | actccccata  | aggcaccctt | ccgaatagaa  | gccgagtcga  | 1500 |
| acatcatacc  | actaatcaaa  | caacgggtaaa | gaaaggtgtc | ctgaacatcg  | aattcgaaaa  | 1560 |
| aaaacgttca  | tatcgccata  | tgctgcagtg  | cgagttatcg | tcagtgtgcc  | ggaaaataaat | 1620 |
| cagtcacact  | gggcggtagt  | ggcaatttga  | ttttcggttc | cggtttaacc  | agcccaccct  | 1680 |
| gaaagtaacc  | attaacggta  | gcggcagtat  | aaactcatcg | atacaaaaagc | ggaacaaactg | 1740 |
| gacatcgtag  | tcaatggtag  | cggtagcttc  | gcggcagcat | ttttgctcat  | aaggatatac  | 1800 |
| gcataaacct  | gaaggatccg  | gcaatatcac  | tctttccata | gacgaaacca  | agacgattca  | 1860 |
| agtaatatga  | aagggaagtgg | aggtattaag  | ctgacaggaa | aagcttcgaa  | ccgatactga  | 1920 |
| gaagttcggg  | aagcgggatg  | ttcgactgcc  | aaagcctgac | actgaccatg  | ccgacataaa  | 1980 |

|            |             |            |             |            |             |      |
|------------|-------------|------------|-------------|------------|-------------|------|
| aatgagcggg | agcggaggcg  | gccgcctcat | gtaacgaaga  | aaatcagcgt | caatctatca  | 2040 |
| ggatccgccc | gtttcaccgc  | catggaaagg | ctaaaaatagg | ttcttataaa | ataggacgct  | 2100 |
| cttcttcttc | agtatgcaac  | cgtaagcggg | tccacatctt  | aagccaataa | atacttcctt  | 2160 |
| tttcgtaaac | gaagaaaaaga | cagaagaacc | gagaagagtc  | gagttcagct | tttgcttccc  | 2220 |
| gactcttctt | tttttagctct | caatgcgatt | gaacgaggag  | tgatttccct | ctttcgaacg  | 2280 |
| taatgttttt | gcgcccattc  | gagtagagag | ttcgagaaaa  | aacggtttga | gatgtaacat  | 2340 |
| ttcggggggc | tgccgtctta  | ctgatagaac | gactaacaag  | aaaccaatca | atcatgtgga  | 2400 |
| caaaagactc | cttttcctcg  | tgctcgcggc | agcaagtatc  | agttttgcat | tgcccaaata  | 2460 |
| atctcatgga | aacgcacaa   | gggtaacggg | aaagttcagc  | agaagagcgg | cgtatagggtc | 2520 |
| aat        |             |            |             |            |             | 2523 |

## (2) INFORMATION FOR SEQ ID NO:580

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...513

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| gttacgtaga | cttgggatta | aaatgtgcct  | gcccctgcag | atggatcgat | cgaatatctg | 60  |
| gcacgaggcc | ctcatgagaa | ttatgtggat  | cgtaggcaag | tgctttcttc | ggactgtatt | 120 |
| ccgaccgtgt | gagccgtatg | gtcgaacct   | tgtacgcccc | cagagtacgg | gcaatagaac | 180 |
| cggccttaga | gctctgccct | gacggatgat  | tccggcaggg | gtatcagggt | ggaagcttcg | 240 |
| ggacagtcga | tttctccatt | cttccctatg  | aggacgaaca | tcttgcgcg  | aetctcatca | 300 |
| atgggaatta | cccatgcctg | cgcatcatat  | cttgcgcttc | gacatatgca | gpgcggactg | 360 |
| ggcaatggaa | gttgcgggcc | cggtactgct  | ccacatacct | ttgcccctca | tcgggcactt | 420 |
| attccttcga | acttcgtttt | ctcctctctg  | aatgtgtccg | cagctacttc | gaatgcgaag | 480 |
| agaacgggac | ttaattctct | ttcgggtgaag | ccc        |            |            | 513 |

## (2) INFORMATION FOR SEQ ID NO:581

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...808

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:581

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| agacaggatg  | cattcatgcc  | tgagatctct  | tgagcagtcg | gattcgtgac | gctgcccacg | 60  |
| agagcaaaat  | cgttagaaat  | gctctaaaaa  | caatactttc | atcatgatag | ccattatttg | 120 |
| attcgttaatt | tttccgtatc  | tataatttct  | gatcaacatt | tagcgttacc | aggtagaaac | 180 |
| cgggatcaaa  | gttggagtat  | tgaactgtat  | gctgtaataa | ccttcggata | gatgtttggg | 240 |
| caaccggtta  | tatcagccga  | ggctccattt  | attccatata | tttttattac | agaaaggaag | 300 |
| ggttatcggg  | atagtagatt  | attgtttacaa | cagctttcgc | cggttgggcg | aaatagagat | 360 |
| tatcttggat  | ttatcaaggc  | ttgatttgtt  | gcttctaata | gaggcaggag | agtacctgtt | 420 |
| gattcgggaa  | gagttgacaa  | caataatttt  | ttacattttg | atggctttcg | agcgattttc | 480 |
| tttgttcaca  | gaaagtatgt  | tcaaattctat | accagtcctc | ctgagtgagt | ctaactgcaa | 540 |
| ttccaataaa  | tgtcaccaag  | gtcaatgact  | gcaaaaacac | tgtcctgaag | gagatttcac | 600 |
| tattcaagcg  | attttctgtac | caatcgatgg  | cagactgtag | ttttcacaca | caatatcgca | 660 |
| tcgcgcagac  | aggaaatcag  | ctgtcgggaa  | caagttctgg | gaagagatga | tggttggatt | 720 |
| ggatctgaaa  | taatcttcaa  | gccttcgtaa  | tcgntgcctg | acattttctc | tatcctgaac | 780 |
| aattcttcaa  | agcagctatt  | gcaaaaagt   |            |            |            | 808 |

## (2) INFORMATION FOR SEQ ID NO:582

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggacttacga | gaagtttctg | tccgaggggc | ggcatgggga | aatggactac | tggagcgcaa | 60  |
| cagggagctt | cgctattcgc | cggcagagct | gttgccggta | ctcgtagcgn | tatctccgtg | 120 |
| gcactgaact | attaccccaa | gatcaaaaaa | cggcctcggc | tccacaaata | gcttactatg | 180 |
| cttatggaaa | agactacaca | aggctgtcaa | acgcctcttg | gacaagctac | tggattatat | 240 |
| tcgtcggagg | tctgcccctc | cgtctcggga | cggctcttca | gcgactctgc | tcctttgccg | 300 |
| aacgctattg | ggcttgccgt | gcaggatatc | gctgggtagg | gcgagcggca | tgctcatttt | 360 |
| gccccgaggg | ggaactttct | ttttcttggg | aggctattgg | tgatatacga | tctgcctccc | 420 |
| gatgctccga | tgccatcgcg | cgtggagctt | gccggaactg | tatcgagagt | tgtcccacgg | 480 |
| gagctatttc | gaagaaggca | tggactctcg | tctctgtgtg | agctatctga | cgatagagct | 540 |
| gagggggaga | tccctccgga | actggtcggg | aaagctgggc | aaccgtttta | cggatgcgac | 600 |
| aagttgccag | cttctgctgn | ccttggaacc | gatatgccat | nca        |            | 643 |

## (2) INFORMATION FOR SEQ ID NO:583

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:



## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...495

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aaaagagact | aaaaattttc  | aaacgcaatc | gccctgacca | tctgtccgaa | tgggatccat | 60  |
| ggtattatat | cgtcttcctc  | ctcattggta | ttgttggcgc | tactgtgtac | cgacgcggta | 120 |
| gccggatgga | ttattggagc  | cggaggagta | tcggctcgta | tggacgcaat | gtgaatcaga | 180 |
| cgccacagcg | tggcaccaaa  | gtgcatacac | gggtagcgaa | gcgatgggtg | gaggagcaca | 240 |
| agtgcgttgc | cggctcatgtc | gttgaatgtc | tcaaaggggc | actcattaaa | gggggtaa   | 300 |
| ttccactagt | ggaaaaagaa  | gtttccactg | gtggaaagtt | tatttccacg | ggaggaaa   | 360 |
| tatctttcca | ctggtggaaa  | accggcggtg | acaaatagtc | gcctgacaca | caataagaag | 420 |
| aataaaca   | agcgctgct   | tttgtgcaaa | gggccatta  | attcgaactt | gttaataacc | 480 |
| gaacgtagca | tcggt       |            |            |            |            | 495 |

## (2) INFORMATION FOR SEQ ID NO:584

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1393

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| cgttttctat | accggggata  | atggcacaca | agccacgacg | tttggcctcc | gtacctcctc  | 60   |
| cggattagtc | gcctgcatca  | ggctctcggg | atgcgagaca | cttgggagcg | aatagcttcc  | 120  |
| agcttacctg | tggcatagtc  | cgtggccgct | tcagagaagc | atcgtctcgc | tcaccttgcg  | 180  |
| gcagatatgc | taccatacac  | acgcatcgac | aagccccctc | cgcattctcg | gagcatcgac  | 240  |
| cagtgaattc | ctcttttcgt  | aaaatcaaat | tccggacaga | agtgcattgg | cgtgccacat  | 300  |
| gcgaatccag | cacaattacg  | gagcgggtga | ccgctttggc | ttggcaaaga | gagaagcctc  | 360  |
| ggcgacaaa  | tgctcgaaca  | attgctgctg | acggtgtcac | cggcataggc | catttgctcc  | 420  |
| ggatgccatt | gtaccgacag  | gtaggtttct | ccggataggc | ttccatagcc | tcgataacgc  | 480  |
| catcggaaga | agggctgtca  | cgcggaaggg | tttcggcact | ctgctgactg | cctgatgatc  | 540  |
| aggctattga | caccagcag   | ctcgccatcg | cttaggcca  | gtattcgtcc | aagacggaat  | 600  |
| cgcctgttaa | acggacttgg  | tgtgccgcaa | acgatatggg | attttcggat | taagccctac  | 660  |
| cggattttcc | gactgggcat  | atatatctga | tacattcctc | cgcgaaagc  | tgtcgcaagg  | 720  |
| agttgatgcc | cccggaaata  | ccgaggatcg | gcacattgcg | gcgagtggct | tctgccacca  | 780  |
| atagagttcg | ccccgatctc  | gctcgggatt | gacttcgccc | agtgtgggaa | tgggtcttct  | 840  |
| cccaaatagg | acgggagtaa  | atcgtcccca | ccggaaagaa | tcgcccacgc | atgaacgtgg  | 900  |
| cataatgacg | tatgacctct  | atatccgtag | taaagggata | agtaagggta | aacctcccgc  | 960  |
| acgtattaca | gactcgggat  | ggctctggca | atacacgagc | ccgaggattt | ataattcgct  | 1020 |
| gtcaaaccat | aacaggctga  | gagggagact | ctcctccctc | aaaagcttgc | ggcgacctc   | 1080 |
| aagctcttca | tagagctgtc  | ggagcgccgc | aggataatac | tgatagtctt | aggactaagc  | 1140 |
| atctattctt | gcataagtag  | catttttctc | tataaatccc | tgcgcggacc | tacctcgtct  | 1200 |
| cccatgagca | tggagaatat  | ggcattgcct | cagcagcatt | ctcgatcgtc | accttacgaa  | 1260 |
| gcgtcctttt | ctccgatcca  | tcgtcgtctt | ccaaagctgc | tcctcgttca | tcttaccaag  | 1320 |
| gccttgtagc | cttgtagcatg | cacacggggt | tcattaccat | cggcataacg | gtgacaaaacg | 1380 |
| cttgacgctt | gtt         |            |            |            |             | 1393 |

## (2) INFORMATION FOR SEQ ID NO:585

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585

```

gctctttttg gcaccggcta cggctctgac gaatttggat ttctgagccg agcttccggt 60
gcgggcttct tttttttcga gcgaaagaag taatcgcttg tgcttcagcc ttgaaaacgg 120
gcaggatgca ggcgacagcc atgcacgagt aaagattctt ttgttcagtc ttgattatag 180
ggtttgattt atgattattt ttcttctgtc gtagcaccac agaggcaagc cggctcggct 240
cccgttatgc caagagatcg gccggtgcta tccgaagctg taagcctcgc acaccgcgct 300
gacatatata taagggaata ccatgcaagt atgatggata tagatggata agcctttttc 360
atcccgatgg gcgaacagcc ggcacggata taccocgtga gcggaagaag ctcgctctgn 420
ctgatcattt tccacgcttt ttt 443

```

## (2) INFORMATION FOR SEQ ID NO:586

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586

```

ccttgatttc gcagagacga tcggccgcag gttcgtgtcg ttagacgccga tcgcagcggt 60
ttctccgccg gtctattcgt agctgtgctt cgttgcggtc agatcggccg ggtagcccag 120
tacatcggtc agataatgga caaagtgtgg cgcacccact cctccggcgt cagagccaca 180
tagcgacgcc gaatgcgtcg aaaatgaaca tggactcacc ttcttgggtga atacgatgtt 240
cgtaagggga aggttttagtt gaatcaccct atctttgctt cgctcccgaa tcttgaattt 300
ttggaacgag tgttacaaat ataggtctgt ttctatgaaa acgagcaaga gatagttgag 360
aactggttac cgcgatatac gcagaggcag ctatcgattt cgaaccgtac atcctgctga 420
cgaacttttc gcactatctg ctgtcttcgc cgagcactac ggggtacctt tcgtcggaga 480
acatacctcc tgccgaatgc ttccggccgaa ggcgtcacc ccatcaactt cggcatggga 540
gtgccaatgc ggctaccatc atggacttgc tctgggctat acaccccagg ctgtgatctt 600
tctcggcaaa tcgggaggcc tgaactgga aaatgcttgg gcgattacct cctgcccata 660
gctgccatac gcggcgaggg tacgtcaacg actatctgcc cgaggagggt ccctctctgc 720

```

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| cctcattttc | cgtacgag    | ccatttcgctc | agccattcag  | aacaaaggca  | aggactactg  | 780  |
| gacagtacgg | tctatactac  | gaaccggcgg  | gtctgggagt  | acgatgagaa  | gttaaggact  | 840  |
| atctgcgcag | tacgcatgca  | agcggcgtgg  | atatggagac  | ggtacgctca  | tgacggtagg  | 900  |
| atttgccaat | aagattccca  | tgggagcgtt  | gttctgattt  | ccgacagacc  | tatgttccca  | 960  |
| gaaggtgtca | agacggaaga  | agcgatcagc  | tcgtaacgga  | caactttgcc  | gaagagcatc  | 1020 |
| tgatgcttgt | atcgatgctc  | tcgaaatcat  | tcgggagaac  | aaatcttcca  | tcaagcattt  | 1080 |
| cgcttcaact | ggtaatactc  | ccccctcatc  | tctatggcct  | cctattcgat  | attgtcgatt  | 1140 |
| ctgtacgtaa | gtgccaatte  | tcgccacttc  | tatctgtggc  | cggccgaaaag | aacccttcta  | 1200 |
| tatagacgag | ttggccactc  | tgctgagacg  | cacgtgggtgc | cggtagatga  | atgggacttt  | 1260 |
| caacagggtt | atccctacgg  | cgacaaaacc  | tccgtagccg  | atatagcgaa  | cgaagcgcgc  | 1320 |
| cgttcccgat | gatgggcccgg | aggcagttga  | tcgtcgttcg  | ggaggcgag   | ttgtggacaa  | 1380 |
| tatcgacttg | ctcgaagcac  | attatggcac  | tttccccgat  | atacgattct  | ggtcattgcc  | 1440 |
| tataagaaga | aacccgataa  | gcgaaaggct  | tctatacgaa  | ggctgaaaag  | ttcgggaaaag | 1500 |
| tattcgtgtc | cgagaccatc  | ccgactataa  | gatgccggac  | ttcatcctgt  | cggctgctgc  | 1560 |
| cggcaagaac | tgagcgtatc  | gcccgaagtg  | gcataatatgc | tggccgatta  | cctcggcatg  | 1620 |
| atctggagaa | gttgatgaat  | gagctggaca  | agctcattct  | cataaccaag  | atagtagggg  | 1680 |
| agtggtcacg | tccgagatcg  | tgagcagca   | tatcgagtaa  | gcaaatcctt  | caataatttc  | 1740 |
| gaactccttc | gtgccatagt  | caatgcgaaa  | cgggcaaaac  | ctttcgcatac |             | 1790 |

## (2) INFORMATION FOR SEQ ID NO:587

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 970 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...970
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587

|            |             |            |             |             |            |     |
|------------|-------------|------------|-------------|-------------|------------|-----|
| agaaaggctg | gcgtctgctg  | ctatcttcca | aaagccatac  | gctccttaag  | aagaggactt | 60  |
| cttcacaaaa | gatgagcgca  | tcgggatacg | caaagatttg  | aaggagcaac  | gaacgatgat | 120 |
| gctttcttct | gtcagagata  | ctatcgctca | aaaatttcaa  | agaggtagag  | ggcgaaaaga | 180 |
| ccaaggtgtg | caagcaccac  | ccgtacgaga | gcacgacttc  | tgctttgcgg  | tgcttttggg | 240 |
| gaccccaggg | atataaaaaca | cgaagagttg | aataagagaa  | tcgtctacct  | cggtgagaac | 300 |
| gacaaccttt | tcttatggat  | cttatggagg | taagtgaaga  | gacttcaaac  | tcaacattga | 360 |
| gagttctact | cttacgagcg  | atgagaagca | ctcaccgtgg  | tacttctatc  | cgatgctatg | 420 |
| attgaacctc | agctccttga  | ggggtaaaa  | ttgcaagcac  | ggaggtgaaa  | gactttgcct | 480 |
| gtttgctcac | catgtaggaa  | cacgcagggt | ctacaacaag  | aagaagaaaa  | gagaggaacg | 540 |
| aacatcgaag | aagttgaaac  | ggctctaagt | caccaacatg  | aactataccc  | agaggttccg | 600 |
| tgttttactt | cgatactaaa  | gagcaagcaa | atcaatttgt  | gaggacctcg  | agaaggtccc | 660 |
| caacttccat | accatcggct  | acaatctgct | atcatcatcg  | aaccaacaaa  | aacaaaaaaa | 720 |
| taacaacaat | cagaaatgaa  | aacagcagct | tatatgatcc  | attgccttac  | caatatgcat | 780 |
| gtggtaaggg | agatgccacc  | tacgaagtgg | tggaacaaatg | tgtacagcga  | gattaaccac | 840 |
| agggatgccc | tcgatctact  | cctccagcct | caaggagcctt | tggaacagttc | ttttcgaaac | 900 |
| aaggctttgc | cgagcttaac  | tattgttttt | ggaagatcag  | agcagggtta  | gaaaaatatg | 960 |
| gcatgagaag |             |            |             |             |            | 970 |

## (2) INFORMATION FOR SEQ ID NO:588

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 946 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...946
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggacgattgg | aatacaatat | ttatagaagt | gcctatcagc | acatttgctc | ggtcaagacg | 60  |
| gtcaatgacc | tcttgcgacc | tgagcaccaa | ccctgtcaag | ctaaaataat | caaccataa  | 120 |
| taaacaattc | cccaaaaatc | ttttaaaaac | aatgacaaac | gatatcttgc | agcgtcttgc | 180 |
| gtctttgcgc | aaagtctgag | tcatgagcat | atcgatgctt | atatcatccc | gagttcggat | 240 |
| gcccactaag | cgaatacaca | ccggaacact | ggaaaggctc | ccgttggatt | tccgtttcac | 300 |
| cggatcggcc | ggcacagtag | tggtcacagc | aaataaggcc | ggatatggac | ggacggacgc | 360 |
| tacttctccc | aagcaggcca | acagctcgaa | ggacttctat | cgacctctac | aaagaaggca | 420 |
| tccccggaac | tccctccatc | gacagtttct | tgccgcccag | ctgaaagccg | ggcaaacagt | 480 |
| gggtatagat | gacgttgctt | tccggcaggt | gctgcctctg | caaccgaatc | ggctttggaa | 540 |
| tatacggcat | caaactaagg | actgacaagg | atcttttcga | tgaagcatgc | gagatcgtcc | 600 |
| agaaatccct | cgtggagagc | ttttcgttca | gcccgtagt  | atgcaggaga | aagcgtgaaa | 660 |
| gacaagatcg | cacgtgtcaa | taaagactgg | cgacacaagg | tgccaatgcc | actattatca | 720 |
| ccatgttgga | cgaatggctt | ggatattcaa | tcttcgtggt | agagatgtgg | agtgcaaccc | 780 |
| cgtagagttg | cttttggtta | tgtatcggct | cgagaatctg | tctcttttgc | tttcctgaga | 840 |
| agattactaa | ggaggttcgc | tcagctatgg | aagaaggcgg | ggcaagaata | tgccctacga | 900 |
| agccatatat | gaatatatcc | cagcactacc | tccgaataaa | gctgct     |            | 946 |

(2) INFORMATION FOR SEQ ID NO:589

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...4250
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gagatgcaga | tgttacctca | cacatgggcg | catctacggt | atgcaagggtg | ctgggagatt | 60  |
| tccagcaagg | tatgttcgaa | gcagcttgca | gaatgtgagc | cgtgggtacaa | cctggccaaa | 120 |
| gcaatacgtg | gggagccttg | agcctcgcca | cgtctatgaa | ttcatgggag  | gcctcacgct | 180 |
| ctctgtccgc | caagtgcggg | caaagatccg | gaagcatact | tcaacgacct  | gcgcaatcgc | 240 |
| cacaaacgcg | cgtgcaagag | ctgaaacaag | ccatcggcgt | cgaagccaga  | accagatcct | 300 |
| caatcctact | tatatccaag | agcagctcaa | agagggacag | aatctgccaa  | cggcattgcc | 360 |
| gaaactatcc | gcaataccta | cggctggaat | gtatgaagcc | ttcggccatc  | gacaaggaat | 420 |
| tgtgggatga | catctacgct | attatgtgaa | ggatgagaag | aatctcggcg  | tccacgaatt | 480 |
| tttcgcgcaa | acaaccctgc | cgctttgcag | gaattcacgg | ccgtaatgat  | ggagaccgcc | 540 |
| gcaaagggat | gtggaaagct | acccccgaac | agctaaaggc | tattgccgat  | tgcatgccaa | 600 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atccgtggct  | gaattcggag  | ccggctgtag  | cggattcttt  | gcgacaatgc  | caagctgcgc  | 660  |
| agcttcatcg  | gcgaacgcct  | cgatgcagtg  | acaagaaaagt | ttacgaagaa  | aaggtagccg  | 720  |
| atgctcgcga  | agtatgatca  | aggatgccaa  | aaagggacgg  | cgactcaaga  | aagagacccg  | 780  |
| ctcggtgagg  | atacctccag  | ccctgtcacc  | tcttacctgc  | tgcttcgagg  | agtgccttgc  | 840  |
| tggtgataat  | cctgatactc  | ttcctcattg  | ccaagcgcag  | aaagggaaaag | aatgagagaa  | 900  |
| gtcctgctga  | ctatagcctt  | attggctacg  | ccaagtatct  | gttcgaggag  | ggagtacata  | 960  |
| attccctcct  | cgtccggtgc  | tgcattgcggc | ggcttacgcg  | gctttcatcg  | cactcgtaca  | 1020 |
| cggactgacc  | agcacgtcag  | ccggatggaa  | gtcagagacc  | tctgtacttc  | gcccgaagcc  | 1080 |
| tgcgcaatgt  | ctctctggcc  | gtcatgggtg  | atctgctgta  | cgctgtaata  | tatgtacgca  | 1140 |
| ccggccctcc  | tccttccgct  | tgtaccgcac  | ctgggtcgcc  | atctgcccc   | gtcctgttgc  | 1200 |
| ttccccaccc  | tcttctatct  | gcgtcgagtc  | tgttctacgt  | cctgcccgggt | tattcattcg  | 1260 |
| ttggagtttc  | catctgatgg  | ccctcatagt  | ggcagccctg  | agtataacgg  | ctccctatct  | 1320 |
| gtgagagcac  | tcggactcaa  | gcgagaagcc  | ttgcgagaac  | cacttggtct  | acttcgctct  | 1380 |
| gcacctttgt  | cttcgtcatt  | gcagccggag  | tattgcaccc  | cactccgcgg  | tgcaaacagc  | 1440 |
| cggcatcact  | accgactggg  | ggcaggcgct  | tatctcttcc  | tgatcgtctt  | ggcaggtgcc  | 1500 |
| tcgatcggct  | atcttgccct  | cgcttggtgg  | ctataatcag  | aagaaaaaac  | aactgaaaaa  | 1560 |
| aataatcacg  | aatcggaccg  | gatcctcatc  | ccacgccgaa  | ccactcacta  | acaatacttc  | 1620 |
| ccaatgaact  | tcctgtccaa  | cgctcatgtt  | tgggtctcca  | acggccgttg  | gtaccggtag  | 1680 |
| tcgcccggact | catctatctc  | ttcatcaaat  | cccttctctc  | ctcggcacc   | tcttcggcac  | 1740 |
| gtggcagagc  | taccgccgcc  | ggcagagacc  | ttcgctgca   | tcacgaaaa   | caaagccggc  | 1800 |
| ctcgacaccg  | aagcctcaga  | gccgaagcgg  | ccaaacgccc  | ccacgctccg  | ttcgaaaaatg | 1860 |
| tgtggccgaa  | gtcctcgatg  | cagattccgc  | ccgtcgcaat  | ctgctcatcg  | gcggtacgaa  | 1920 |
| ctctctcgtg  | aacagcgtct  | gagttcggcc  | aaggtactta  | caagttcggc  | ccgatactcg  | 1980 |
| gtctgatggg  | tacgtctatc  | ccgatgggcc  | ggccttctgc  | ggactctcca  | cgggcgacat  | 2040 |
| cggacagatg  | gcctacaaat  | gcaagttagc  | tttgccacca  | cggctatcgg  | tatgtttgcc  | 2100 |
| tcggctgagg  | gtatatagcc  | ctgcacatcg  | tgcgcaacta  | caatcggaac  | gacctctttg  | 2160 |
| gctcgattac  | atcaacgaaa  | aactctctcg  | atcgccatgt  | ccagagacgc  | ttccacgaag  | 2220 |
| aagacacgga  | tccttccctca | cttgtatcca  | acctttcgac  | gtagccatgg  | tctttgccgt  | 2280 |
| ggcactgatg  | gttgccctcg  | tcacaaatcc  | aacatgaccg  | aagtcttcag  | caaggaagac  | 2340 |
| tacacaatcg  | tcagaatccc  | ggcaaggaca  | acatggaaat  | cttgatcaag  | aaaggcgaca  | 2400 |
| agtggagaag  | tacactccgt  | ccgacgaatc  | ctccgatgga  | gccggcagca  | aggcaagcgc  | 2460 |
| gtaggtgtag  | cttaccagct  | cgaagcgggc  | gaaatcatca  | cgtgccggaa  | gactaagacg  | 2520 |
| gagaaaccgg  | ctattatcat  | ccgcccctcag | cccaaaagct  | cttttttcta  | tttccctccg  | 2580 |
| ccctgcgaaa  | gctctttcgc  | agggccgatt  | ttttatatcc  | gctccccttc  | cctctctctc  | 2640 |
| tgcattgtct  | cacagtaata  | gcttttgcct  | ggctctttgc  | attgtatgag  | actttgcaca  | 2700 |
| acaagcaggc  | acatttcttc  | attcttctgt  | ttgtctggca  | gtcaacacct  | gcttgctatt  | 2760 |
| tgatctttcc  | cggagatata  | aagaatgaac  | ccaacgagag  | gatattatgg  | tctctcatga  | 2820 |
| gaggatacta  | tgggtctcata | tggaggatac  | tatgggtctcg | catgagaaga  | tattatggtc  | 2880 |
| tcacatgaga  | gatactatgg  | tctcacataa  | gaggatacta  | tgggtctcata | cgagaggata  | 2940 |
| tatgggtctca | tacgagagga  | tactatggtc  | tcatatgaga  | ggatactatg  | tctcatatga  | 3000 |
| gaggatacta  | tgggtctcata | tgagaggata  | ctatgggtcca | catgagagga  | tattatggtc  | 3060 |
| tcatacgaga  | ggatactatg  | gtctattatg  | gaagatgcta  | tctgctctgt  | gtcggatggc  | 3120 |
| agattcgggg  | agtggggggt  | ccgtgtgagc  | tgtgaaaccg  | atagatgtgt  | ataggaacag  | 3180 |
| tttttgacaa  | gagggcaatc  | gaaccttttt  | ccatttcttt  | ttctgattcg  | gttaagtcaa  | 3240 |
| tgctccaaca  | agagtttgat  | cgtttaagttc | ttatgagagt  | cagaccatat  | gcttatatcg  | 3300 |
| aactcatgta  | atgaaagata  | atgtctataa  | aacaaatcca  | tcagcaaggc  | cggaccttgc  | 3360 |
| tgatggatta  | gaaaaaactg  | tgttgtctca  | agacctgtaa  | tgcttttaca  | ggacaagaca  | 3420 |
| atgccccgac  | atttgcggaa  | tgggggcttc  | acgatctcag  | ccttgagttg  | acgaccgcga  | 3480 |
| ccatgatgcc  | aagctctgtg  | ccgaccttgt  | tgaactccgt  | agccacatgc  | ccataccgat  | 3540 |
| acctttctta  | aggcaaggag  | acatcgttcc  | ggaagtacct  | ctccgatgat  | ttgcccttcg  | 3600 |
| gcattggcaa  | tttcatagtg  | ctggcgggaa  | tacccttgtc  | tttcagttcg  | aaggcaacga  | 3660 |
| gcttgcgctt  | gagactccgg  | ctttctgtct  | ttccatgatc  | ttacggctcg  | gcatacccat  | 3720 |
| tttgctcggg  | tgaacttggg  | gatccagccc  | agcccagcct  | ctatgggaga  | agtgtgtcgc  | 3780 |
| atatatcatt  | gcatagaga   | cagaaaccca  | tctccagacg  | aacgtgtcgc  | gagcaccgag  | 3840 |
| tcggccgggt  | ttgatacctt  | cgggcttgcc  | gcttcgaaga  | ggcatccca   | tatcttctga  | 3900 |
| gcgtattggg  | gatagaaata  | agttcgaagc  | cacctgtctc  | ggtataaacc  | gtagccgaaa  | 3960 |
| taattacgtg  | gggcatccgg  | cgaagagccc  | tactttgaac  | gtatagtaag  | tgatctcgtc  | 4020 |
| aggtcgatgt  | ccgtgaggcg  | ttgcatcact  | tccgttgctt  | tcgggcctgt  | acggcaagtt  | 4080 |
| gggcgatgtt  | gtccgaggca  | ttttccaata  | tggctccatc  | gtattctgct  | gccggcacca  | 4140 |
| ggcccagtc   | ttggcgatat  | tggcacgttg  | ggtaccatca  | tatatttttc  | ctcttcgtag  | 4200 |
| cgatagagca  | ggaatcgtcc  | actataccac  | cgtcgttatt  | ggggaagcag  |             | 4250 |

## (2) INFORMATION FOR SEQ ID NO:590

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 525 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...525
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590

|            |            |            |              |            |            |     |
|------------|------------|------------|--------------|------------|------------|-----|
| cggctcgcag | atgcttagcg | ccaaggcggg | aaagagccgc   | agcggaacct | tatacagcag | 60  |
| ggaatagaaa | tgagcattat | tggccggatt | gtccatcagg   | caaaatccag | ctcatgcccg | 120 |
| gtacggatca | tccaacggga | atcggagctt | tgagagggaa   | cgtcttctct | cccaacaaat | 180 |
| tcagtgtcca | tctcctaacc | gaaggggtga | caaataagggtg | tcgcgcgtta | tgcttcgcgc | 240 |
| accacgacca | tataggcaga | atgaatgcgg | taggcggact   | gtcccggtgg | caacctctac | 300 |
| tcgaagaatc | agttgcaaac | gctgtattgc | taccgtggga   | agatcctgcc | cccatgccaa | 360 |
| caatccggtg | agtagcagaa | gcggaacaa  | aatgcgtatc   | gtctattcgt | tttcatcgtc | 420 |
| gtcgaattgc | aatcgctgga | tccaagagt  | tcgtctctta   | tatcttcate | ggaagcaatg | 480 |
| gcttcgggtg | aacctcggcg | aagctctcgt | ccggatcggt   | tgttt      |            | 525 |

(2) INFORMATION FOR SEQ ID NO:591

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5545 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...5545
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttccgaaatg | caacgaggat | atagtcggca | tcttcggtct | gatactcttg | gtaagcgaac | 60  |
| ttcattggct | tcgatctctg | catacttctt | ttggaagcgg | agggtgttct | gtcccataac | 120 |
| ggccgaatca | agctcgagag | aggtaatata | ttcggttgac | gacctccttt | tcgaccgaga | 180 |
| ggtgcccacg | ggcatttttg | cggatttcat | cttcggtacg | acgctttttg | aacggaggca | 240 |
| atatcccttt | tccatcatct | gaccgatgat | accgtcggaa | aggatgagtg | cagggtgcgg | 300 |
| tacttgaatg | ccagctccag | tcccagacca | acgaagtcaa | ccactcttgt | acggagttgg | 360 |
| gtgccaatgt | gatcagacga | tagtcaccat | gtcaccaccc | ttgacagatt | ggaaatagtc | 420 |
| ggcctgtccg | ggttggtatg | tccaagccg  | ggacccccac | gcataacatt | tacaatcaag | 480 |
| cagggcaatt | ggcaccggca | caatagctca | ctccttcttg | cttaagactc | ataccggggt | 540 |
| ggaggaagag | gtcatcacca | ttttgccaca | gctggcaccg | ccataaacat | gttaatggca | 600 |
| gcgacttcgc | tctctgcctg | caagacaacc | ataccggcgt | atcccatgga | tgctcctcca | 660 |
| tgagcgtttc | cataacttca | gactgcgagt | gataggatag | ccgaagtagc | catccacacc | 720 |
| gttacgtatt | gccgatgcgc | aagggtttca | ttgcccttca | tcagccttat | ttcttctgtc | 780 |
| atatttttct | ctgtttttgt | tacaatttca | ctttgtaaac | cgtgatacat | gcaccgggca | 840 |
| taccgttgca | caactgggtg | agccgatata | gctttcggga | tcttcatata | agagtaatga | 900 |
| tagcctttgt | cattgacttc | attcgggtgt | actccagcac | ttttgtcggg | caagccacta | 960 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| cacatagatt  | gcaacctttg  | aacgctgggt  | attaacgacc  | acagctcctc  | tgattttttgc | 1020 |
| cattatagta  | tcttttttaat | aaggacttcg  | aatacctaaa  | agttagtaat  | cttgacgctc  | 1080 |
| aaagataggt  | attcttttccc | tcttgatacc  | tataaagacg  | gttttttgat  | cgtttacgtc  | 1140 |
| ttttttgtcg  | ggaaaatggt  | cttttagcatg | ttttggctcg  | tgctgttggtg | atgaagtcaa  | 1200 |
| tccgagataa  | gactcttttca | agtcgagtcg  | cctatatcac  | ccctatcaat  | cagggcaata  | 1260 |
| cggtagcgtc  | ccccgacgat  | gcgctaactc  | gcttttcatt  | tcgttcatgc  | tcgcgagttc  | 1320 |
| gttattattt  | ctaattgcaa  | ttcgatgtcg  | ccggcttttt  | gagcttgtgc  | gattcttttt  | 1380 |
| gcaaagcacg  | gatttgtacc  | tgaataaaaa  | catttttgat  | gtgagaagtt  | cgcgttccac  | 1440 |
| tcgcatctga  | aggtcttctt  | ccgcattgct  | tcatccctt   | tcccatagtg  | aatacggctc  | 1500 |
| aatgcatagc  | ggttggtcat  | agctcgactg  | cgatatgact  | gatctgtgca  | ttgggggtgat | 1560 |
| ctctgaaaaa  | ttggctgcga  | caaaaaccact | gtcgaacgat  | tgttcggcag  | cctcatcaga  | 1620 |
| atctgcctaa  | acacatcagt  | accaatatcc  | actccatccg  | cattcagttc  | gatttgatgt  | 1680 |
| aattatgcaa  | ggcaacctcc  | gatggagtct  | gctttccgct  | ccttcttcat  | gcctgtatat  | 1740 |
| gaggagtttt  | ctttcgcgtg  | agcgatgac   | agacggagta  | actcctcttc  | gtattttggcc | 1800 |
| ggatagtaag  | gtttctccacc | tccgctgaac  | gattatcggt  | aggagtttcg  | gcactatggg  | 1860 |
| ttccgcacct  | acgagattgt  | cggaatcggt  | ttttcttttca | gagccattcg  | cggctgttgg  | 1920 |
| gtggcggggt  | gcgggggagga | gtacgtactc  | ctacggaacc  | catcttttgg  | acttcgcgag  | 1980 |
| ccagcagtcg  | ctcatccata  | ctaagcggtg  | gcctgtctct  | tggacataga  | cacggcggtg  | 2040 |
| gatgtcatcg  | gggcatcagg  | gatactgccg  | ataatatcgg  | taattagctg  | tgctcttctg  | 2100 |
| atggggtagc  | ctccatatcg  | ctcagataga  | gctgtgtctt  | gaagcgaata  | aaatcctttc  | 2160 |
| atgctgctcg  | atatattctt  | cgaactctgc  | tacggataga  | ttgcggcaaa  | actgtccgga  | 2220 |
| tcttctccat  | cgggcaggag  | ggccactttc  | acgtcatgcc  | ttgctccagt  | agcaggttga  | 2280 |
| tacctcgag   | agctgccttg  | attcagccgc  | atcaccatcg  | tatagaactg  | tgatgttcga  | 2340 |
| agtaaagcgg  | tgatttggtt  | gatctgctgc  | tgtgtcagag  | ctgttccgga  | ggaagccacc  | 2400 |
| aattttcgat  | accggattga  | tgcatcgaaa  | tgacatctgt  | ataaccctca  | caagggaagca | 2460 |
| cttatctcgg  | cgagcaatct  | ctttcttggc  | caagaatagc  | cgtacagctc  | tttgctcttc  | 2520 |
| gagtagatga  | tgctttcggg  | agaattgaat  | acttggcggc  | cttgtctttc  | tttcctaaga  | 2580 |
| ttcttctctc  | gaaggctcga  | tcttgccgct  | tacggctctgt | acggggaaaa  | tgactcgccc  | 2640 |
| gcggaaacgg  | catctaaggc  | cttgctgtct  | tcgtatcgga  | tggaaagccc  | tgtgtgacta  | 2700 |
| agtattcggg  | cttgaaccct  | tttcgtatgg  | cttcgtcgtc  | gaaaccgacc  | tcttttcagg  | 2760 |
| agcatagccg  | agttggaact  | tctgcacagt  | ctcggacgaa  | tacctctttg  | gcgggaagtat | 2820 |
| gtcatcccaa  | tggtctggcc  | ttgatggtat  | tgagaagggt  | gtttttgaa   | agtcatttgg  | 2880 |
| caaactcatt  | ggaatgaaca  | tactttctct  | atcgctcttg  | agtttcttct  | cctcatcggt  | 2940 |
| agctcccgtt  | cgtgaatctt  | gatcccgtac  | ttacgtgcca  | aatagcgcag  | gcttcgctat  | 3000 |
| agctgagctg  | ttctattttc  | atgatgaaat  | gaacaggtag  | cctccttcgc  | cacaggcgaa  | 3060 |
| gcattttgcag | aggttttttg  | ccggcgaaca  | gagaacgaag  | gattgcgatc  | gctatggaaa  | 3120 |
| ggacacaagc  | cgaggtgttc  | actccacgct  | tacggagcga  | aaacaaagtcg | cttacgcact  | 3180 |
| ctacgtattg  | ccgcgatcga  | gtatcctttc  | tcgagtcaga  | tcgtcaatca  | tctctcctat  | 3240 |
| atactctatt  | acatataatg  | tcgcagatgt  | gtcattccat  | tctgcgaac   | ggagataggc  | 3300 |
| tatggccttc  | tccatatcct  | ccggcgtatc  | gatcctatcg  | tactctgctg  | tgtttgcagc  | 3360 |
| actcgaatcc  | gatagccgta  | tccagccagc  | gaagctgttc  | gagactttcg  | gcttgctctg  | 3420 |
| ccgtactttg  | ggcagtgagg  | ttatcttgcg  | gaggacggtc  | gggcgaaaagg | catagatccg  | 3480 |
| atatgcttgt  | agtaagtatg  | ccgacggcac  | caagatcag   | gctgtacccc  | ctgagatatg  | 3540 |
| ggataacgga  | gcggctgaaa  | taaagggcag  | agctcctcga  | tccaatacga  | tcttcgggtg  | 3600 |
| gtttggattg  | ttcaaacgct  | cgaagctacg  | tcagacgaga  | aaacttctgc  | taacgtagct  | 3660 |
| atatcggttt  | ctgggtgtcg  | aaggccgaaa  | tcagcagatc  | gatctgttcc  | ttttggataa  | 3720 |
| aaggctcatcg | ccttgacgat  | tcaggacgat  | cttttctccc  | cgacctactt  | tgtgaatgcc  | 3780 |
| tcccgacagc  | gttctgtacc  | actactgcac  | tctggggacg  | tctcaccacc  | tctcctccga  | 3840 |
| agtcctccac  | ggcctgacgg  | atacgttcgt  | ctcgggtggt  | acgacggccc  | gggggacgac  | 3900 |
| accgactatt  | cgctcatgta  | ccgttgatc   | atagacttgc  | caagcatatc  | ggccagtggc  | 3960 |
| ttgcccggga  | tcggctggaa  | gcaaactcgag | ccggaatgat  | ggctattacc  | tctgtattat  | 4020 |
| tctcctttga  | taaagcggag  | ataggcttcg  | cagttggccg  | gcagcattcc  | ggcaggcgag  | 4080 |
| gattgtagga  | atcgtagcag  | gcattgtagc  | cggtgatcga  | gcgcgcagga  | aagcagctat  | 4140 |
| ccgctcgaat  | acattcaagt  | agcttgacgc  | gtgtggcatt  | gctgtgctcc  | ttcggcaaaa  | 4200 |
| gctgatttgg  | gtgacccgag  | gagactgtcg  | cacagatttc  | tttaccctcc  | atcttgtctc  | 4260 |
| cacggcacca  | tagggccagc  | cctcagtaaa  | gacctcgtcc  | ttccacttct  | tcgcagatag  | 4320 |
| ggagctgcat  | accaatagag  | ggggaatttg  | aagacgatgc  | gtcatgagcc  | tccagcaggg  | 4380 |
| cttgttcatg  | tgctagatcg  | atttgtccgt  | cggatactgt  | tcgtagagat  | ggtggatagt  | 4440 |
| ggctgcacct  | tcgatggctt  | ggcccaagcc  | ttgttgataa  | cggatttggt  | caaactcggg  | 4500 |
| tgaacgacat  | tacgagcgtt  | tttttcattg  | ttgaaaagga  | tattactaag  | tagtgtgcga  | 4560 |
| atccccaaaa  | gagaagtctc  | gaattggaaa  | gaggtctcat  | tttaggttcc  | aaagaaacaa  | 4620 |
| tttataagcc  | aaaaaagcaa  | gggagatttc  | tccgaaaaag  | ctgtttttcc  | gtcctcttga  | 4680 |
| atagaagata  | gaccgggaatt | gtattatggc  | ttgagattct  | gccgagggtc  | tgctatatcg  | 4740 |
| gcatatgcaa  | atgaatacca  | tgatctttta  | caatctatgc  | aggcaagcaa  | ttcaacgtgt  | 4800 |
| gtggtagtaa  | tgctggagtc  | tttagcggat  | ggaaggtagt  | tgaccccata  | cagcagattt  | 4860 |
| gcaggaaaaag | gaaactgacg  | attagcaata  | ccaaagaatg  | gcaaaaagctc | gaggacgatg  | 4920 |
| gagccgggtga | tgatgttaga  | gcaagtagcg  | aatacggtta  | ttgcagccca  | tgtttctttc  | 4980 |
| ggatcccaat  | tccaatagtg  | ccccatgcaa  | gtttggccca  | aatagcgctc  | aatagcagtc  | 5040 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| cogtcataaa | aaagcaaadc | ccgtgtagac | cagattgtca | gtcgtatgca | tcatgatatt | 5100 |
| gcattcacct | ctttgtgttt | gcgcttgcaa | aagagggaag | agccgctacg | agcagtgccg | 5160 |
| ccccagcat  | ggcatatgca | aagatgtagg | agatacgtgg | ggtagcaaga | acggactttc | 5220 |
| gagagccggc | atcaatgtct | tgtgtggata | tccggtttgg | ctatgtttat | aatcatgaag | 5280 |
| accgtggaca | agcgttgcca | aaagaaagga | tccaccgata | tttccatcgt | atataaatga | 5340 |
| taggcctgca | atgatcacaa | aaaaagaata | ccaaagtcgg | gtttctccca | cgttcttaga | 5400 |
| ggaggtcggt | ccagagaatg | ccacatgcct | ccgataaaaa | catcagtaen | caagctgctg | 5460 |
| cgatagcgat | gcaaatagcc | cataccgcg  | ttggtacaaa | gcgaatagag | ctgacactat | 5520 |
| aagcagtagt | actgctgtat | cgcaa      |            |            |            | 5545 |

## (2) INFORMATION FOR SEQ ID NO:592

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...3292

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| cttgccgcta  | aactcttcgt  | ggcgagagag | atcgaagtca | gtccgactag | gatgccttcc | 60   |
| acttctttga  | agccgaacgg  | catctcgaa  | tcaatatcgt | ggcagcattg | gcatagtgtg | 120  |
| ccagcttgct  | atgatcatgg  | aaacggtttt | gtcgtctccg | aagccgaggg | cgcggtgcca | 180  |
| ctgcatacgg  | aggtttttcca | cttctcgaa  | cattgcagct | cttcccccgg | tcgtacgaag | 240  |
| aactgatctc  | catttggttcg | aattcgcgca | tccggaagat | gaactgacgg | gctagatctc | 300  |
| gttccggaaa  | gccttgccga  | tctggcaaat | tccgaaggg  | atctcattcg | tcccgtcttc | 360  |
| tgcacattca  | ggaaattgac  | aaatatgcct | tggccgtttc | gggacgaaga | tataccttca | 420  |
| tggcaccgtc  | ggccgtagag  | ccatctccgt | ggcaaaccac | aggttgaact | ggcgcacctc | 480  |
| tgtccagtta  | gcgtaccgct  | gatcgagacg | acgatctcgc | agtcgaggat | aatctgacga | 540  |
| tttccctccg  | attgttgctca | ttcagtgacg | tagcaaacgg | ttcgtgtact | gatctcgctt | 600  |
| ctgttgatat  | tcgactcacac | gggcgttggt | ggctcggatt | gagcctcgct | gaatgcctcg | 660  |
| ccgaagcggt  | tggctgcttt  | ggcgactctt | ttgctatttt | ttcatctatt | ttggccagat | 720  |
| gatcctccac  | gagtaatccg  | cacgataacg | cttttttgaa | tccttggtgt | ctatgagcgg | 780  |
| atcatgaacg  | catccacgtg  | tcccgaagct | ttccagatcg | aaggatgcac | gaaatggcag | 840  |
| agtcgatgcc  | caccacatta  | tcatgcagca | gggtcatact | ttccaccagt | agcgtttgat | 900  |
| attgtttctc  | agttcagaac  | cgtattgtgc | aagtcgtaca | cagctgccag | accgtcgtat | 960  |
| atctcgagac  | aaggaaagac  | aagcgtatt  | ctttgcagtg | tgagactatt | tttttgaa   | 1020 |
| gatcttctct  | tgtgccatgc  | tatcttgatg | tgtgaatctt | attgtattcc | tacattttcc | 1080 |
| tcgcgaaaat  | aactcttttt  | cttcaatagt | ctctaaacg  | atttgagtac | acatcccaca | 1140 |
| aacaaatgca  | acactaagat  | aaatttagca | agaagcctcg | aaaggagttc | taaagttag  | 1200 |
| ttttttctgg  | gtctatggtt  | cagttggctg | tattgttgtt | cgacctgacg | aaaaaggcct | 1260 |
| tcctatccga  | aaaacatcac  | actatcattt | tctccttgaa | ttcgggtttc | ataaagggga | 1320 |
| ttactggaat  | gattcccaat  | tctctcctgt | cgttgaaaac | ttttggcaca | taaaacattg | 1380 |
| atgcatgcgg  | acttgatttg  | ccacaaaaaa | gagcaccgaa | aagaagtccc | ggtgcacctt | 1440 |
| aataatcaat  | atggaaaact  | ccacttactt | ttgccaagca | gcatacgag  | gttgcgctgc | 1500 |
| gcatttgcat  | ctccttctga  | acggccttac | ggaagaaggt | ttcggcacga | gcaaaatctc | 1560 |
| ccgtacgaca  | taagcagctc  | caaggatatt | gcttacaccc | ttttctgtct | gaatcggtc  | 1620 |
| aacagagcaa  | ttgcctgttg  | aacgtctcca | ccattaaaag | cggctaagcc | aaattgattc | 1680 |
| ggcccgttac  | actttcaggg  | aaatacttaa | gggtctattc | agagcaaa   | aacgtctctg | 1740 |
| gtgcccctca  | ggataagaca  | ttgcacacgg | tacatttcgg | cctcactaag | ttctttcgga | 1800 |
| gcagtcttaa  | tgattcacga  | gcttcttcga | gggtataatc | acgaacgata | taccccatgg | 1860 |
| tttcgtattg  | cgacgcaaat  | tcggatagat | ctgatccaag | ataaacgat  | agacgaaagt | 1920 |
| tgccttcagag | cctgttcacg  | tgcacatcat | tcggcatatt | atcggagttg | attatctcca | 1980 |
| atacgcggtc  | acgatcggct  | atatcaactc | ttcगतagcc  | agtttcagcc | ccttccaatc | 2040 |



|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ttcaccgccc  | aattcagtg   | tatatccggc  | aattgttttgc | catactttacg | caccaattct  | 2100 |
| tccgcgatct  | tttagcacgg  | cgctccgaca  | aagccttatt  | gtgggctatt  | gaagcccggg  | 2160 |
| agaagcaaac  | ccttcgatga  | tcatttttatt | gaccgaatag  | tttggttagc  | cttaacgggtg | 2220 |
| cttacaaatt  | ctttgatatt  | ctctaactcc  | gcctattgtt  | gcgatactca  | ggaaggacat  | 2280 |
| ctgccttatt  | gactttgaag  | ttgtataaag  | atcgaagctg  | gactctcgct  | gtttttccac  | 2340 |
| ttcttctgcc  | gggtaattgtg | tgccaacaaa  | taaggagcct  | ctgccggatt  | gaagagtggga | 2400 |
| taaaaggaac  | aattattactc | gagagaccta  | cagggcattt  | agcacaacct  | gtacctcttc  | 2460 |
| acgaaccaca  | aacttggcat  | ccatcatcca  | tgatgcatag  | catgttctcc  | tgtaaaagca  | 2520 |
| aactgctcgc  | tcttccatt   | atgacggcaa  | tgtattgagc  | tgcatgtttt  | gcttggggca  | 2580 |
| aagccgaact  | aaatgcgttt  | cacgcttgag  | agcttttgtt  | ctattgcggc  | ctgtaatgac  | 2640 |
| taccgaggaa  | attccaccgg  | gctggtacca  | tcttctgaac  | gaagaatagg  | cgtaaaatga  | 2700 |
| tcattctgagt | gctcttgagc  | tttaaattac  | tcatactctg  | cgcacattca  | gtacaacctt  | 2760 |
| gtttccgggt  | ttgtccaacg  | aaattttata  | tgaattactc  | cctcgtaagc  | attttgagcg  | 2820 |
| accaaaccgg  | caacagcggc  | gagagagcga  | taagagttag  | ttgtattctt  | ttcatattaa  | 2880 |
| aagcctcttt  | ctttgagagt  | tcatttatta  | attaggaatt  | acttaaacag  | atagattaac  | 2940 |
| aaagagtggc  | tcgcgtcagg  | ccaaagtaat  | cggccttctt  | gtcaacacca  | ctttcttccc  | 3000 |
| acactctaca  | caactgatact | tgatcataat  | gaagtgaat   | aaccaccacc  | gatactcgct  | 3060 |
| tccagattcc  | aatgattgac  | caagatcact  | gacggcctat  | actgataccg  | ccgccataga  | 3120 |
| accatccttg  | ataacgtgat  | acctggcatc  | gtcgaagtcg  | ctcttaggat  | gaatggaacc  | 3180 |
| aacagaggga  | ccgatatccc  | tgcatatttc  | atgtgaccga  | catggccatg  | aagtcgataa  | 3240 |
| acactccatt  | gaattttctca | cagaaccaat  | agcgcaattc  | cgggtgggcaa | gc          | 3292 |

## (2) INFORMATION FOR SEQ ID NO:593

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic);

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...3592

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593

|             |             |             |            |             |            |      |
|-------------|-------------|-------------|------------|-------------|------------|------|
| caaatggaaa  | taataattct  | gtgtcatggc  | aaaagttata | aaacccaaaa  | aagcccttgc | 60   |
| acttaattctg | aaaggaaaac  | cgctgccgca  | gatgctggcg | aaccggggccc | aaagtcctac | 120  |
| ttacgcggtc  | gtgcccagcg  | attttgaggt  | gttatcccca | aggtgacggc  | tcgtccgggg | 180  |
| gataaggtgc  | gtgccgctca  | gcacttgatg  | caccacaagg | catatccgga  | gatgaagttt | 240  |
| acaagccggt  | tagcggcgaa  | gtgatcgcg   | tgaatcgcg  | tgccaagcgc  | aagggttgag | 300  |
| catcgagggtg | aaaccggacg  | gactgaacga  | atacgagtca | ttcctgtcgg  | ggatccgtct | 360  |
| gccctctctg  | ccgaacagat  | caaggagctt  | ttctgtcgag | cggtatgtgg  | ggttttatta | 420  |
| agcaacgtcc  | ttacgacata  | gggctacacc  | ggatatagct | ccacgcgaca  | tttatattac | 480  |
| tgccaacttt  | ctgcaccatt  | ggctccggac  | ttcgatttca | tcgttcgagg  | agaagaacgg | 540  |
| ccctgcagac  | tgccatcgat  | gccttggcca  | aactcacgac | aggaaagggt  | atgtgggcct | 600  |
| gaagccgggt  | tcattctctg  | gcttgcacaa  | tgcagaatcg | tagaagtaca  | cggacctcat | 660  |
| ccggcaggta  | acgtgggcgt  | gctgataatc  | atacgaaagg | aatcaatcgg  | ggcgaaacgg | 720  |
| tgtggacgct  | caaggtaccg  | acctgatcgt  | gatcggacgt | ttcctgctta  | cgggcaaagc | 780  |
| cgattttacca | gaatgattgc  | catgaccggc  | tcagacgctg | cagctcacgg  | atagtcgcta | 840  |
| ttatgcgggg  | tttgcaatgtc | tttgcttctc  | tcccggcccg | acgacaataa  | aggaatctca | 900  |
| cgagcgtgtg  | atcgatggca  | atgtgctgac  | cgtaagaagc | tctgcgagaa  | ggagcctttc | 960  |
| ctgtcagccc  | ggtgtgacca  | atcacgggtga | tccccgaagg | cgacgatgtg  | gacgaactct | 1020 |
| tcgggtgggt  | gcaccccgct  | tcgatcagta  | cagcatgagc | agagcttatt  | tctcttggtg | 1080 |
| caggggaaaa  | acaaagagta  | cgtactcgat  | gcccggatca | aggggtggga  | cgtgctatga | 1140 |
| tcatgagcaa  | cgagtatgac  | cgcgttttcc  | cgatggcatc | tatccggagt  | atttgtctca | 1200 |
| ggctattata  | gcattcgaca  | tcgacagatg  | gaggacttag | gcataatga   | agtggctccg | 1260 |
| gaggactttg  | ccactgcgaa  | tttgtggata  | catccaagat | cgagctgcag  | cgtatcgttc | 1320 |

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| gcggggccttg | gatatgctct  | ataaggaaat  | gaattgacga  | atccctcaca  | cttaaagcat | 1380 |
| aagacattga  | aagcgtaag   | gaatcaactc  | aacaaactga  | acctcatttt  | gaagaaggcg | 1440 |
| gcaagctcca  | tggcctgcac  | tctgtcttcg  | cggcttcgag  | acctttctct  | ttgtgccgaa | 1500 |
| caggacatcg  | cagcatggct  | acatgtgcac  | gatgccattg  | atagcaagcg  | cacgatgac  | 1560 |
| gtcgtgtgat  | ggctcttttg  | ccggccctgc  | tcttcggtat  | gtataatgtg  | ggggtacaca | 1620 |
| ttatatggcc  | atcgatgctc  | ccgtagtatt  | ttggccggct  | tttctctcgg  | acttctcgcc | 1680 |
| gtactgcccc  | aactcattgt  | ctcctatgcc  | gtcggttggg  | gatagagttt  | gccgtagctc | 1740 |
| agtaccggaa  | ggaagaaatt  | caggaggctt  | cctcgtatcg  | ggctctgctta | tcccgatgat | 1800 |
| cgtgccggta  | gatctccgct  | gtggatgatc  | gccgtggcga  | cggcttttgc  | cgtggttttt | 1860 |
| gcaaggaggt  | gttcggcggg  | acgggacgca  | atatattcaa  | cgtggctctc  | ggacgcgtgc | 1920 |
| cttcctcttt  | ttcgccctatc | cggcggctat  | gagtggcgat  | aggtttttgt  | ccgcacgggt | 1980 |
| gataccttcg  | gcctcggcgc  | aggtagcggtg | cggacggctt  | ctccggagct  | acacctttgg | 2040 |
| ggcagatagc  | cacggccgtg  | ccaagatgcc  | tgaatacat   | aatgtggcag  | gcgacccctc | 2100 |
| ttccctgtgg  | atgctttcct  | cggctttata  | cccggctcca  | tccgtgaaac  | ctctacctgg | 2160 |
| ctatcctgat  | cggagctgtc  | ctgctgattt  | ggacggggat  | cgcgactgga  | agatcatgtt | 2220 |
| gagcgggttg  | gtaggagcct  | cagcaatggc  | tctctattca  | atgccatcgg  | cacgacggcg | 2280 |
| gcatgacaga  | tcaactccgt  | gatcacattg  | tctatggagg  | ctttgctttt  | ggcttggtat | 2340 |
| ttatggccac  | cgccctgtta  | cttctgcccc  | tacagaaaag  | gggaaatgga  | tcttcggttt | 2400 |
| ctcgtcggtc  | tgatggctgt  | attcatccga  | gtgctcaatc  | cgggttacc   | gaagggatga | 2460 |
| tgcttgcat   | cctgctcatg  | aacgtatttg  | ctccgctgac  | gactatttcg  | tggtggatag | 2520 |
| caacatcaaa  | gcgcgcaagc  | acgtatgcc   | agaaatccta  | accgctaaat  | atctcgataa | 2580 |
| agacatgaat  | agagataaaa  | ctcgtacacc  | attctctatg  | cctcgggtgat | ggttattgtc | 2640 |
| gtggcgcttt  | gtggccttac  | gtctctcagt  | cattgggcga  | caggcagcgt  | gacaagagaa | 2700 |
| gatagacaag  | atgcagcaga  | tcctccgctc  | tgtgaatgcc  | ggaaagaaga  | taagggcaaa | 2760 |
| gtaatagctc  | ggtacacgga  | cgtgatcaag  | caaaactgct  | catcaatcag  | gatggtagcg | 2820 |
| tagccaagac  | cttcgagggc  | gacagttggc  | acaaaatgaa  | gcattcacgc  | tcaatacgcg | 2880 |
| caatgcttct  | aatcggccgc  | taatgatcca  | agcatttcgc  | tccctctcta  | tatcgagag  | 2940 |
| tagagggtca  | gaagaaatac  | attgtcccga  | tgaacgggtgc | cggctctttg  | ggccgatctg | 3000 |
| gggatacatt  | gcactgaacg  | aagactgcaa  | tacgatattc  | gtgcagattt  | cagtcacgaa | 3060 |
| ggcgaaacgc  | cgggattggg  | agccgaatca  | ctcgtccgga  | gttttcgggt  | cagtttatcg | 3120 |
| gcaaagaaat  | cttcaagagg  | gcgaattccg  | atctgttgcc  | gtagtcaaga  | aaggccagaa | 3180 |
| agccgaggaa  | aggactatgt  | ggatggcatt  | tccggcggta  | cgtgacgag   | cgtgagtgga | 3240 |
| atgagatgct  | catatcctct  | ctccgtcctt  | atgctctata  | cctatgaaca  | acgtaaaaaa | 3300 |
| ataagggcta  | tgtcactttg  | gaataaaaaa  | aaaaggaaat  | tcttctcggg  | ccgctaagca | 3360 |
| gcaacaatcc  | cgttatcgtg  | cgatgcttgg  | tatctgctct  | gctctggcgg  | taacagccaa | 3420 |
| gctgcaaccg  | ctattgtcat  | ggccctgtcg  | gttactgctg  | tagtagcttt  | tgccaacgta | 3480 |
| ttatctctct  | cctgcgcaat  | acgatccccg  | gacgcattcc  | aattatcgct  | agctcgtcgt | 3540 |
| ggtcgcagct  | ctggtgacta  | tctgtagtca  | ggtactgaag  | ccttcgctta  | cg         | 3592 |

## (2) INFORMATION FOR SEQ ID NO:594

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...538

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| cccgcacatg | agacagctgc | tctgtccagat | actccactgc  | cttctccatt  | tagccgttgc | 60  |
| tttggctatc | agttctttta | tttccatata  | tctatatggt  | ttgttttgtc  | ttgtatttcc | 120 |
| tttcaagcac | tctgtattga | aacataatac  | cgtattttctc | tcctctcaac  | accttgagga | 180 |
| ggtttcccg  | cgtatcatat | cgaagacgac  | gatgggtagg  | ttgtttctcca | tacacatggc | 240 |
| cgtggagtca | gatccattac | tttcagacct  | cgggcataaa  | tctcatcgta  | tgtgtccggt | 300 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cgaacttcgt | agccgagggg | tccttctccg | gatctgccgt | gtaataccat | ccacgcgcgt | 360 |
| ccccttgagc | atggcatcgg | ctttctaata | tcattgccgc | gaaagccgat | gaagcccggg | 420 |
| atcccgtagg | tgaaagaaaa | ggattggcct | gtaccgcgaa | ggagaaaaat | gggtcaacat | 480 |
| aacccttggg | cgagccaatt | ctatgggcat | gccatttggt | tgagaaaact | ccccttaa   | 538 |

## (2) INFORMATION FOR SEQ ID NO:595

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2029 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...2029

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| cggttaccgc  | caagtattcg  | tggaagtcga | tgttgaaaat | acggcccttt  | tgatgtttgg  | 60   |
| aataactaact | cgcggcgtgc  | aaggacagtg | tatggtggta | gtttgactgg  | ggtgggtcgcc | 120  |
| tccaaaagcg  | taacggaggg  | ttctaaagta | ccctcaggcc | gattggtaac  | cggtcgcaga  | 180  |
| gtgtaatggc  | acaaggtgct  | tgactgggag | acaaacaagt | cgacacaggta | ggaaactaga  | 240  |
| gcatatgata  | cgggtggttc  | gcatggaagg | gccatcgctc | aaaggattaa  | agggtactccg | 300  |
| gggataaacg  | gttgatcaat  | cccaagagct | catatcgacg | gagggtttgg  | cacctcgatg  | 360  |
| tcggctcgtc  | acatcctggg  | gctggagaag | gtccaagggt | tgggctgttc  | gcccattaaa  | 420  |
| gtggcaacgc  | agctgggttc  | aaacgtcgtg | agacagttcg | gtctctatct  | gttgtggggcg | 480  |
| caggaaaattt | cgagggtctg  | acactagtag | gagaggaccg | tgttgagacg  | acccctgggtt | 540  |
| accggttgta  | ccgccagggtg | caccgcgggg | tatccacgtc | tggttaaggta | agtgtctgaaa | 600  |
| gcatctaaag  | acgaagccgg  | cctcaagata | agatttcata | aatagggtgg  | ttaaagacta  | 660  |
| tgaccttgat  | aggctgcagg  | tgtatgtttg | taacaattaa | gccgagcagt  | actaatagcc  | 720  |
| cgaaactttt  | gtgcacccga  | aggatgcggg | atagggttgg | ttgttgccgc  | aaagcttgag  | 780  |
| gaataatttgt | tggcctttcg  | atatgtcgat | tgccttttcg | aagtattcag  | gtgttataac  | 840  |
| gttggggatc  | cacctcttcc  | cattccgaac | agagaagtta | agccaacggg  | gccgatggta  | 900  |
| ctgcgtcaca  | gtgggagagt  | aggacgccgc | cttttttaag | aagcgtgaga  | gagagggggg  | 960  |
| gataggatct  | ccaccctcct  | cccggaaaaa | aagggtgaag | agagagtcct  | gaatccgagg  | 1020 |
| ctctctcctt  | tttattttct  | ctctctccaa | aaatcatttt | gcttttctct  | ctattccttt  | 1080 |
| tctccttttc  | cttctctcct  | ttctctcccc | ttgctgcgcg | ttattctata  | acgtgagttc  | 1140 |
| gatataagtt  | tatgcgacta  | aatctttaat | caactcgtga | agaagcccaa  | gttcaaagca  | 1200 |
| atccgaatga  | agttttttag  | taaccattta | catccaaaaa | cacgtaggca  | agaaaaactct | 1260 |
| gaagttggct  | ctggtctgaa  | gcatagaatt | gcatttttag | cactatgggg  | aagagctaaa  | 1320 |
| taatcaaagg  | tccgtgaaaa  | agtctaata  | caaactctgt | aaaagcaaat  | ggcgattaat  | 1380 |
| agtttcaatc  | aaggcacagt  | gggtaatggc | caaaaagtga | ctttgttttt  | aagaatcaag  | 1440 |
| gataagccca  | tgatagctg   | tattgccgaa | agcccagtg  | ggggcgtgag  | atcgctgctg  | 1500 |
| tactcggtgc  | caccaaagct  | ataaaggcta | tatggagggc | aacggttatc  | aggtagacatg | 1560 |
| gactttcgac  | atctctgtgc  | cctcaaagaa | cctcacgact | atgcacccga  | atggaaggat  | 1620 |
| ggagtatcag  | ttctctaccg  | atgataccac | tgcgatttgg | catcaactca  | tcgatagcga  | 1680 |
| tagtattcgg  | gagcaattcg  | gcaccatcga | aaggctgtcc | atgaagcgga  | tatggtcgtg  | 1740 |
| aactgcggtg  | atgccggaca  | ggaggagagc | tgatccagcg | ttgggtattg  | cagaaaaacgg | 1800 |
| gctgcacatg  | tccgtgcggc  | gactttggat | atcttctctt | actgaggagt  | ctatccgtga  | 1860 |
| agcttttgca  | ggctgcgcga  | cagcgaagaa | tttctattcc | tatatgaggc  | cgactggctc  | 1920 |
| gtgccaatagg | cgactggcta  | ttgggtatga | acgctacgcg | ctttataccg  | cttccgcttc  | 1980 |
| ggggggcaacc | cgacaggtac  | ttttccatcg | accgtgtcca | gactccgac   |             | 2029 |

## (2) INFORMATION FOR SEQ ID NO:596

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2702 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596

|             |             |             |            |             |            |       |
|-------------|-------------|-------------|------------|-------------|------------|-------|
| tttgcgtcgg  | tttcggttgg  | tttcggccag  | ttggcggatg | gcctgttcgt  | atgacctccc | 60    |
| gatttttctg  | ccagctgaag  | cacttccatt  | ttttccggct | cttccgttgt  | atagcagaga | 120   |
| tacttctttc  | ggccgaagac  | ttcgggtgca  | tagacagccg | attgcgtgcc  | gcccagcccg | 180   |
| atccagacct  | ctttgtgagt  | ctggacggat  | cgttatccat | attgatggac  | aggatctgcy | 240   |
| acttccctta  | tcggtcagcc  | cgaggaggtt  | ctgtatctgg | tcgaatttgt  | tggctacttg | 300   |
| cgctggtcga  | gaagaatctt  | gcaatccgaa  | ttgttgatga | tgccctcctt  | accaccggcg | 360   |
| aagagatgat  | gtcgtccacc  | tcctgcgtca  | cccgattgcc | cccccgaaat  | acttgcgcac | 420   |
| cgttttgtac  | atatacttca  | gtagtccggc  | atattggccg | aggcgatcgc  | tttccaggct | 480   |
| tcctcgacga  | cagttgtttg  | cgaacgcctt  | tgagtcgcct | catcttattg  | atgaaagccc | 540   |
| catgatgatg  | atggttacca  | cggggaaaag  | ttcccggttt | tccttgatgc  | atcgatttcg | 600   |
| aagacgataa  | accgcttcga  | caggaggtcg  | atgttttgtc | cgaattgagc  | aggaagtcga | 660   |
| aacgaccgcc  | ccggtagtac  | tggcggggcg  | agtcagaaa  | ttgtcgatat  | tgaaatcttc | 720   |
| ccggctgact  | ttgattccgc  | gttttccagt  | tccggccggg | aggatatcgc  | catgaattcg | 780   |
| taaacgtatt  | gaagctcggc  | gttatccctc  | tgcccgaaac | gatcaggcgg  | ataaggccga | 840   |
| gacagcgctg  | ccgagctcgc  | ccgattccgt  | tttcgatatt | tttctctctc  | gcttttccag | 900   |
| agcgtcaaaa  | gcagcgtttt  | gatactgtct  | tcctttcgac | gtcgaacacc  | ccgtcatcgg | 960   |
| tataaaaagg  | attgaacgaa  | tcggctcctc  | ttccgtatag | gtaaaataga  | tgccgtcttc | 1020  |
| acctttcggt  | tcgggtggat  | gagcgaacaa  | agtccctggt | aggagttgcc  | cgtatcgaca | 1080  |
| gcaacacatg  | cgttccctgt  | tcgtaatact  | gccgtacgag | atggttctga  | aaaacgattt | 1140  |
| tcgccgaacc  | gacgggtccc  | ggacaaat    | gttgcgttcg | tgataatccc  | gcgtttcatc | 1200  |
| ggcaagtccg  | aaatatcgag  | atggacgggt  | tgcccgtagc | gcggtcggac  | agtttgatgc | 1260  |
| cgaagggtga  | aagcagctgc  | ggtagttcgt  | ctcggccgta | aagaagcaga  | gagccggctc | 1320  |
| gataaggtgt  | agaatgtttc  | ttcggaggga  | aaatcgcccc | cattgcgggg  | cagcccggcc | 1380  |
| aatagagcgt  | agccgtgtcc  | gtcgtattgt  | gacggggacg | gactccatca  | aggccagcgc | 1440  |
| cgagccctaca | tcgtttttga  | tcgtccggag  | tcctcccggt | cgctcgctcca | tgccagcaca | 1500  |
| ttgaaatgcg  | cacggatgga  | gcgagtcctt  | gggagtgcgc | aacgttcagg  | tattctctga | 1560  |
| tcactcggga  | ttgatctgat  | tgagcggaga  | gaagcgtgca | agtgaagca   | tgtttcggcc | 1620  |
| tgtttctcga  | agcgttgag   | attttcttcg  | ctgtcgtcga | taaagagtag  | tggttataga | 1680  |
| tatggtttaca | cgggagcatc  | agcccagcgg  | gagcgcgaag | ctcagccggc  | agtcgctgcy | 1740  |
| atcggtggag  | agccgttcgt  | aacgccgtcc  | gttgcgacgg | cagcaggcag  | atcgctcccg | 1800  |
| atcggacaag  | gtagcaggca  | gaggatttga  | tcgccgatcc | gcacttcatc  | ggcgccgagc | 1860  |
| cgagggtcttc | gagcgtgcct  | gccgcacgtg  | cgcgtaacga | gaggtaacgg  | tgagcaagcc | 1920  |
| acgcttgctg  | tcctgtccctg | cgatctcctc  | cgccgaaaga | gtctgaggcg  | catatagccc | 1980  |
| gaatcggtga  | tgatccgttc  | gaactgatca  | cgccctccag | aaatttccag  | acggcatccc | 2040  |
| gtcccccggac | ttccttcgca  | gaagggttcc  | gcgacagagc | gtcgagaaat  | cgcttcgttg | 2100  |
| cgccatgggt  | gtttcgtcgt  | tttcgtcaga  | cagaggtaga | cggaaatggtg | caggaaggac | 2160  |
| gttcgttgaa  | atgccgttcg  | taagagcggg  | cgaggaacga | gagatgtcct  | tttccaactc | 2220  |
| cggacggtag  | cttttccgaa  | taaaccagtc  | ctgctgtgca | ggatgctgta  | aacgggcaag | 2280  |
| accttcaccg  | ccttgtgcc   | ggcgcatgca  | tcgcccgtga | ttcgggtgag  | gtcacggtaa | 2340  |
| agagtttcggg | cattcaagag  | agaaaagccac | ggtgatgtcg | gcacttttcg  | atacgatgca | 2400  |
| cggtttctcga | tggccagcag  | cggaacttcc  | tcctccagtt | cgcattttct  | cggatatttc | 2460  |
| tcattggcgtc | ggttcgtttg  | tcgttacagc  | ccggacggaa | gaatacggcg  | gacaggacgg | 2520  |
| cgagagagca  | ggtaacgggg  | atgccggcag  | cggtctcccc | tttcatcagc  | ccgtgttctc | 2580  |
| cgtacttgcy  | gttcatccga  | acgtttgcca  | caccacgagg | gtggcaccgc  | atacgcccat | 2640  |
| gcccagcaga  | gatactggtt  | catgccgcac  | atgtagcaga | tgacgacaag  | gatcacgtcg | 2700  |
| cg          |             |             |            |             |            | 2702. |

## (2) INFORMATION FOR SEQ ID NO:597

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 762 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...762
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:597

```

aaatatgaag ttagcatcgc caactttctc ggaagtaagc catagcactc ctgtagatga 60
agtcaaatcc tcgattatct atccactggg aaaaatcttc cggaagcact gctggagtta 120
ttcataaaat tctacaagaa ggtatcttac gaagcctaata tctcccatgc tcaacgagga 180
atattatatt ccggcttggc tttcttgatg aagtcgcca aagtgctcct tgcagaacga 240
atacgctgaa agagcgatac gagctgatgc tgcgcaatcg aatcggcaca aaggcgagga 300
ctttatctac gaacagacca atggcagttt acatcgcttc agcgcagatt tacgctcaac 360
accatactcg tcttttatga gccgggatgc caacatgttc cgagctgatt cgccaactgc 420
atcaggatga ttggctgcgt atttggtaga atccaaacaa ctaagtattt tattcatata 480
tccggataat ataaaaatgc atgggtggcc ggtttgtccg attttcccg tttcgtggag 540
taggaatcaa tagcgatagc agtatcacag atcgacaact gtatgatata aagcctcacc 600
aacgatctat ctgcttgata atcacggata tgtaatttaa aagatgtaca aataggagtt 660
ataaaagagt atctgaaaga gaaaaagaat actctctgct tacgaagtat ttatgcatta 720
cagggaaaaa ataccgagaa tcttctttgc agctctgcag at 762

```

## (2) INFORMATION FOR SEQ ID NO:598

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 831 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...831
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:598

```

cccctcgcat catacgagtc aagaaaaaact ttttacacaa cacctgatga tatgccacc 60
ggggaaaccc acaagtctcc cccttcttcc tcgcatcggg actgtccgat gccgaagtct 120
tacatagccg agctacccac ggctcgacga actgactccc cgcgagcgcg aatcgctctg 180
gagcaagttt ttcgagagtt caaagatccc atcatcatca tctgctcgt ggccatggtg 240
ctttctttgc cgtggcttgc tatcactact tcacggggcg agagggcngt ctctctttc 300
tggagccgac aggggtgctg ctgctgtcg tattggccac ggggtagcct ttttcttcga 360
gatgaaatcc gagaaagagt tcgagatcct gatcaggtca atgaagacat attatataag 420

```

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| gtatatcgca  | acggcatgat | cgcaggggtgc | tcaaaaaaaga | aatcggtcgta | ggcgacctgg | 480 |
| tcgtttctgga | acgggagagc | aaatttcggc  | cgacggccga  | ctcatcgaag  | ccatctcgca | 540 |
| cagatcgacg  | aatccagcct | gacgggcgaa  | cccgttgtaa  | acaaaaaccct | gaccggcagg | 600 |
| acttcgacgc  | ggaagccacc | taccctccg   | attacattgc  | cgaggcacca  | ccattctgga | 660 |
| cggccactgc  | actttcagg  | tggaaggtg   | ggcgagccca  | cggaatacgg  | acgggtattc | 720 |
| gagggtgccc  | gaccaacaac | agcgtacaga  | cggccctgaa  | cagacagctc  | gaccatctgg | 780 |
| ccggctgatac | acgaacgtca | gctatagcat  | agcagccttg  | gtactcatcg  | g          | 831 |

## (2) INFORMATION FOR SEQ ID NO:599

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| ggccgatacg | gtgggttatca | ttgatgggtac | tattctcggc | aaaccgcaaa | cagagaagag  | 60  |
| gccgctcgga | tgctacgtac  | gttaagcggg  | cgtagcgaca | ggtggtgacc | ggtgtgtgca  | 120 |
| ttagccaccg | gtgggagaca  | agggcttctc  | gtgttcagc  | ctggtaacct | ttgcgcattc  | 180 |
| gagtgatgag | gagatcatta  | ttatctcgaa  | cgctatcgcc | cctatgacaa | agccgggttcg | 240 |
| tacggataca | ggaatggata  | ggctacatcg  | ccattcagcg | agtggagggt | tcgtctacaa  | 300 |
| tgtcatggga | ctaccggttc  | atttgctcta  | taatgaactg | aaaacttttg | cgaatcaaat  | 360 |
| taaagtctct | atatttgac   | cccgaagtgt  | aggagagata | actaacaata | caatataaga  | 420 |
| gcaatgaaaa | gaacatatca  | acctctaacc  | gtaagagact | gaacaagcat | ggctttcggg  | 480 |
| ctcgtatggc | acggcaaatg  | gccgtcgtgt  | attggccgtc | gccgtgcaaa | g           | 531 |

## (2) INFORMATION FOR SEQ ID NO:600

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atccccgaca | ttttttgcag | ataggacttt | gaaagtaagg | cctcttttcta | atgaaaaacc  | 60  |
| tacctttaca | gacgaaacgt | ttcggggaaa | atatgatgaa | aagagagaat  | gaaaaagaatc | 120 |

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| aatatcacca  | tcggctttct | ctttataact | tcgtagtgat  | gtccgtattg  | ggatacccgc  | 180 |
| gcgaaaggat  | agctccgacg | gtgccgaccg | gctgggtgacg | tatctggttg  | tttgcgcttt  | 240 |
| ggagcggtcg  | tactcatcct | attacggttg | gtattgatcc  | ggcggtagaa  | gatggcgagc  | 300 |
| gtcgccggca  | cgatatggaa | cagtatgcc  | gatacgatga  | aaacccgacg  | aatagtcacc  | 360 |
| taacgctaca  | gtgaagtatg | acgaacacgg | caagctctat  | ccttacatat  | tcaatcccat  | 420 |
| tcttcgaccg  | gtcgtgtggg | gggccgcagg | atacgccctt  | tcaagggaat  | ggagcccgcg  | 480 |
| ccgacgaaaa  | atcggagaaa | gctgggagaa | tttcgcatgt  | gagcgacccat | taattcgggtg | 540 |
| ttggcacaacg | ggccttcttt | gccggtaaga |             |             |             | 570 |

## (2) INFORMATION FOR SEQ ID NO:601

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 780 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...780
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601

|             |             |             |              |            |             |     |
|-------------|-------------|-------------|--------------|------------|-------------|-----|
| cagaagaata  | aagggttaagg | gtaggtcaaa  | aaaggattatta | tagaatagac | tccaaacggtt | 60  |
| ttgcacaaaa  | ccgacggag   | tcgttcgttt  | gtaattgtca   | actccccttt | caagctttcc  | 120 |
| tgaaaaatga  | gttctatccc  | ctttctcaaa  | tgcgatggct   | aatttgtaga | gtgggtgcta  | 180 |
| ttggttcaac  | atgtctatag  | actgatgaat  | aatgaagggg   | tatgatgggg | ctttttaatc  | 240 |
| atgaaatctg  | caagtttctt  | gctataaaga  | taagaaaact   | tgagatttta | tcaaggtttt  | 300 |
| cgcaaaactaa | tcaggggcaac | cgcatcaaat  | cttttagtagc  | ttttgagata | gtctatatcc  | 360 |
| agagcagctt  | tgaacaacct  | cttcgtaag   | gaagtttgct   | tttatgccc  | gatacaatgg  | 420 |
| ctaaagcaaa  | ctttctcaac  | ggttttagatt | ggtggctgaa   | taatccttac | gagctcgaca  | 480 |
| agtatcctcc  | taaagggttac | atccaaatgc  | caatggagtc   | gattctcaat | tccccaatgc  | 540 |
| ctcgaatata  | ttgtccgatt  | aactgacaat  | cctcggtgg    | taaactgcga | tataatactg  | 600 |
| cctatctatg  | cgagtctctc  | cctctaaact  | actaatccac   | gctccacttg | aattaaactt  | 660 |
| ctcaagcctt  | gccattgact  | atattcccct  | cctcaaagac   | ctctgaagct | agtaatgtgg  | 720 |
| tataaagtcc  | tcttccaata  | cgaccatgat  | ctttctccaa   | ggttcataac | gatgacacct  | 780 |

## (2) INFORMATION FOR SEQ ID NO:602

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1069 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature

(B) LOCATION 1...1069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| tcgggacagta | ttttcagagt  | gatttggttc  | ttagtgaagg | aagatattcg | aagggccgat | 60   |
| acgacgagga  | aaatatgaag  | agtacggtag  | tgccctttgt | aacggcatca | tgctggcggg | 120  |
| agctgcgggg  | ttagccgaga  | gcaggggttg  | aggcggattt | atatcgccaa | tcacttcggc | 180  |
| gaccatgccca | tatacccgat  | tgctcgtgct  | catttattcg | tccgatgacc | gaagctgttc | 240  |
| ggtgcgtacc  | acgaacggcg  | tgctcataga  | agcaccttat | actgatatta | ctaaacagat | 300  |
| attgcacgga  | taggagcttc  | attgggtata  | gactatgccg | agattggagt | tgctacaagg | 360  |
| gggggggtgtt | tcattgtggc  | gtttgtggta  | ccgtgtagag | cgcagggagg | ctttgcacga | 420  |
| tgccggcatt  | ccggatgccca | cgagtagcaa  | ggttgagtat | acttcattcg | gcacgaagtt | 480  |
| atcaggcgcg  | tgaagaaaaat | agggtctgta  | tccgatacgc | atggctatat | cgacgaaaat | 540  |
| accggatata  | tttcgccgat  | tgcgatgaga  | tttggcatgc | cggtgacacg | gctctgtaac | 600  |
| ggtagcgac   | tatttgtcgg  | gtttggctcc  | gctgcgtctg | tctatggcaa | tatagacggg | 660  |
| caagacattc  | gtctgcagta  | tcccagagttc | tgcgcttttg | tggtgaagag | gtgaaagtgt | 720  |
| ttatgacgca  | tatcggggat  | accccggtcg  | gtacgaacct | cgtatatatc | gaatgctcgt | 780  |
| gcagacccac  | ctcgtctttt  | tgtctgtggg  | catagtcata | ttctcaaagc | tattaccgat | 840  |
| aagaagtttg  | atatgctgca  | tctgaatccc  | ggagctgcag | gtagtatggn | tttcatgctg | 900  |
| ttcgtactct  | gatgcgcttc  | gtgaatcgat  | ggccgagata | tacnggattt | acaggtgata | 960  |
| gaattggccc  | gatcgataga  | tattaaagat  | gaaacatttc | attcttcaaa | gcttgcatth | 1020 |
| tcttctcccc  | ctggtangcg  | gatggatatc  | ctcttcgtgg | tcgtgggtgg |            | 1069 |

(2) INFORMATION FOR SEQ ID NO:603

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| ataggggaat  | gtttggcccc | acgtatatca | gcaggtgggc  | aatctgctcg | agtcgtacgc | 60  |
| caatcgaacg  | acagagccat | ccctcaagcc | atcggccgtg  | cctcacctac | ttcggcgaat | 120 |
| actggggcaa  | tcggctcttg | gctgcagcgg | tgctctgcac  | gagctgcggg | acagtggagg | 180 |
| gtataggact  | tgggaaaaga | ggagagggct | gaagactgac  | cctcaagtac | tgccctatgg | 240 |
| catattaaca  | atagaatcat | ggtagccagt | atagataaag  | aagccgttgc | cggctggagg | 300 |
| cagagataatt | ccccggcacg | atccacctga | tcgacaaacc  | ccagccatcc | ccgaagccat | 360 |
| aaggctgcta  | tcggccagtc | gcacgatcgg | ctcgacacgg  | agacccgccc | ttctttcgtc | 420 |
| cgtggcgccc  | gtccgtccgt | actctgatgc | agatgtccac  | agaaacggac | tgcttctctt | 480 |
| tccgactcaa  | atgatagata | taccggagga | actgcaacag  | ttactggaga | atccccgcaa | 540 |
| ctcaaggtag  | gactgagcct | gagcgatgac | atgacgggtga | tcagacgggc | aaaccgatcg | 600 |
| aacc        |            |            |             |            |            | 604 |

(2) INFORMATION FOR SEQ ID NO:604

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...4479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604

|            |             |             |             |             |            |      |
|------------|-------------|-------------|-------------|-------------|------------|------|
| cagcagatcg | gactgaagac  | caatctgctt  | tattggggta  | cgacgactcc  | aatgcaggat | 60   |
| tggagtttcg | catgggaaag  | aagtggacac  | tcgatgttcg  | ggaggttaca  | acccttttac | 120  |
| attcagccac | catcgcaaac  | tcaagcatgg  | ctcgtggctc  | cggagcttcg  | ctattggacg | 180  |
| tgcgaagcct | tctccgccac  | ttcttcgggc  | ttcacggcat  | cggaggtgag  | tacaatgtaa | 240  |
| atgattcgac | atccccatcg  | gccgggtcaa  | aaagctcaac  | aactaccgat  | acgaggatac | 300  |
| gccatcggtg | cagggtctgac | ctatggctat  | cagtggctgc  | tggcaaaaaga | tggaaacttg | 360  |
| aggcatcgat | cagcggagga  | ttcgtccact  | tcattatgac  | aaattcgaat  | gtgccaaagt | 420  |
| cggcaaaaag | atcgcggaag  | gaagaacgac  | tacttcgggtg | tgacgaaagc  | cacactttcg | 480  |
| ctcatataca | cattaagtaa  | taccttattt  | atacagacaa  | gctatatgaa  | acagagtcgt | 540  |
| atatcatcct | gtcgtttctc  | ttcgggaatgt | ctacgcttgc  | cgtgacagcc  | agacccatct | 600  |
| cgggggcat  | aaggtgagcg  | agaagcacgt  | ggtcaagaaa  | cgggacatac  | cgccaacgta | 660  |
| aagatggacc | ttgatcttga  | cggccaaccg  | gatatgaaca  | gcaatctgct  | gatggtgggt | 720  |
| acccccatta | ttcgtccaat  | acatcgaaag  | atcaagtcgc  | tctccgccc   | ttcctcctga | 780  |
| tgggaacaga | cgttatcgca  | tcacgcagcg  | tcgtatcgct  | ctcgataagc  | acccatctac | 840  |
| aatcagcccg | acaccaagcc  | ttctgcatg   | gtaaagcgct  | gcacggcaag  | gaacagagca | 900  |
| tggactatct | tgcgctact   | ccatataggc  | ctggatgcgc  | cactcatcaa  | tgattctatt | 960  |
| ggctgagaac | tcgggctgtg  | cgactgccc   | ctcggatcag  | aagaaaccac  | acttacggac | 1020 |
| gacgctttgt | gccactgtat  | gaagcggact  | atcaatacga  | gatcattgta  | cccgaaggga | 1080 |
| gctgctgaaa | aaacgcgaag  | agactctctc  | cgctcactta  | gcctatcggt  | agggaaatat | 1140 |
| gtggtcttgc | ctcagttcga  | cggcaatccg  | gccgagtggc  | acgtatcgac  | agcaaactga | 1200 |
| aagaaatcgg | aaacgatagc  | gatataat    | cgaaaagctc  | tccatggtag  | gctatgcttc | 1260 |
| gccggaaggt | ggcgagaata  | caacgcgaag  | ctctccaagg  | ataggggcgca | ttcatttgca | 1320 |
| agcatctcgt | taacaagtac  | cccatcctaa  | aaagtccgatt | cgaatacgat  | tgaaagggca | 1380 |
| ggattgggca | ggtctgctgt  | cggctgtaac  | caagagcggg  | cctcgcaaaa  | ggatgccata | 1440 |
| ctggagatca | tcgaccaaaa  | gccggtcgg   | agcgtacagc  | cgactgcga   | gctatcgatg | 1500 |
| gcgggtctct | ctatgccact  | tgtctcggga  | ctattacccc  | ccgcttcgcc  | gaagcgagct | 1560 |
| tacattccta | tcgtggtcaa  | aggatttgag  | ttggacaaag  | cacgtgaaat  | tatcaagcac | 1620 |
| acccctctcg | tctgagtcgt  | gcagaggttt  | acgccgtagc  | gcagagtatc  | cggaaggag  | 1680 |
| ccacgaacgc | tacgaaacgt  | ggacgatagc  | agagaaactt  | tccgaaagc   | gatagagccg | 1740 |
| acagccaatg | cggctataat  | agacttcgtg  | ccggcaggta  | tccgcaggct  | ctggctcgac | 1800 |
| tcgaagcacg | caaagcgaa   | ccaaactatg  | gatgctgttg  | ggcttggcat  | atgcctacag | 1860 |
| cgaaaaatgg | ctgaagccga  | gagctatctt  | actcgcgtg   | cgagcaagg   | cggcccggag | 1920 |
| cacaacacaa | tctgaacgaa  | ctgcgacgct  | atatgcaaga  | aatctctaaa  | tggaaaaaga | 1980 |
| ttcttagaaa | acaatattca  | cttttaaaaa  | aaaacgagat  | gaaaaaaaca  | aagtttttct | 2040 |
| tggtgggact | tgctgctctg  | ctatgacagc  | ttgtaacaaa  | gacaacgagg  | cagaacccgt | 2100 |
| tgtagaacta | acgctactgt  | tagtttcata  | attaagagcg  | gtgagagccg  | cgctgtggcg | 2160 |
| atgaccttac | agatgctaag  | atcacaaagc  | tcaccgccat  | ggtcttgcag  | gtcaagttca | 2220 |
| agaaggtatt | aagacagtgg  | aagaggacgg  | cggatcctta  | aagtagaagg  | aattccgtgt | 2280 |
| aaatctggag | ccaaccgtgt  | cctgtcgttg  | tagccaatca  | caattatgag  | cttaaccgta | 2340 |
| aaagtttgaa | tgggttgagg  | ccttgacgac  | ttcttgacga  | ctgaaaacca  | aaatgccaaa | 2400 |
| acttgatcat | gacaggtaag  | tcagcagctt  | ttacaataca  | accgggctcc  | accactattg | 2460 |
| ctatcctggt | gggactgcat  | ccgacaacct  | tgtttctcgc  | gaactcctct  | tgccgttact | 2520 |
| cgcggtgcat | ccggtatctc  | attcgcagag  | tagaggtaaa  | tatggctaca  | cagtatcaaa | 2580 |
| actactatct | ttttaaacag  | ctgacgctaa  | aatcgcagcc  | cttgctcgaa  | agaaagattc | 2640 |
| taagattttc | gcaattcttt  | ggtctcaaac  | actaatgcat  | atgtgtatgg  | agtccaacgc | 2700 |
| ctgccggtct | ttacactccg  | gatgctgcag  | gagaaacata  | cgaatggagg  | cgtctttgaa | 2760 |
| tacgaattat | gctgtagggt  | ccggttctta  | tgcttggaag  | gtaaatatga  | tgcaagcaac | 2820 |
| gagcttcgtc | cgacgatcct  | tttatctatg  | gaaagctcgt  | cgataaggac  | ggcaaccctc | 2880 |
| tcacggaaac | accttgacgg  | atgctataaa  | tgccggattc  | tgcgacggag  | atggcacgac | 2940 |
| tactatccgg | tattggtgaa  | ctatgatggc  | aatggctaca  | tctattcagt  | gctattaccc | 3000 |
| aaggacaaaa | caaaatcgtt  | cgcaacaacc  | actacaagtt  | tcgctgaaca  | tcaccggccc | 3060 |
| cggtagcaat | actcctgaaa  | atcctcaccg  | gtacaagcca  | acctgaatgt  | tacttgccaa | 3120 |
| gttacacctt | gggttggtgt  | aatcaggctg  | ctacttggtg  | atcgacccgt  | caaacgacta | 3180 |

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| aaaaatttca  | tagtttgtct | atatcggaat | acagggagcg | gggttcgctc | cactcctgta  | 3240 |
| ttcatttctct | ccaaatcaaa | tagggaaatc | ccaatcacca | atcaagaatt | attgttatga  | 3300 |
| acgacgctaa  | gaaatatatc | gtatcggtgc | tgtcttactc | gtggccggaa | tgtttggcgg  | 3360 |
| atgtatcaaa  | gaggactatt | cgattgtccc | cgctcggttc | gcctgaccgt | cagggcttgg  | 3420 |
| gatgccgata  | gcaagatatt | accgaaaccg | gagccgtgca | gcgcgtcggt | attttcgttt  | 3480 |
| cgacgaaacc  | ggccgcccga | tcgaccgact | gatgatggac | gccgcacagt | ggctgcacgc  | 3540 |
| aaaccgatac  | cattggaata | cgacggcccc | actacgggtc | tttcgtggca | tgggcccaacc | 3600 |
| ccgacgatca  | catgctggaa | gaaacaccaa | tgtgcaaaac | gtcaaagact | tattcttcag  | 3660 |
| gctttcctct  | accgaggtat | agcccaatcg | cccggagacc | ttttttccgg | tgtactgacc  | 3720 |
| tgccaataga  | gtacggctct | atcgaacagg | gtacagacca | aactgtcgat | atcaccgccg  | 3780 |
| tacggcacag  | gtacatatca | tcatacgcg  | ctatcaagag | tgctggaagc | taatggcccc  | 3840 |
| agacaactgc  | cagactatgc | cgacatcctt | tgggagaaac | tcccgcactc | tataccggcc  | 3900 |
| tggccgagct  | catcggaat  | ccgtccaata | ccgtcccgc  | ggacagatac | aaaacgggga  | 3960 |
| tttcatttcc  | ccatcttcag | agtttatccc | acacttgata | ctactcctct | gcactctaac  | 4020 |
| tctatgcata  | cggacaagaa | ttgctgaata | tcagcacagg | ttcggatgag | taccattcat  | 4080 |
| acccgtcata  | ggcaaaatgc | tcaatatcta | catagactgc | gtggagcaaa | cctcaatgta  | 4140 |
| ctcgtatccg  | tcaccccttg | ggacgagtgc | aacaatatgc | agaataacta | tccgacagct  | 4200 |
| attatgaaaa  | tgaatatctc | catcatcctt | cgggactact | tccacgcctt | ctcctgttat  | 4260 |
| tgctttaacg  | atggggcggt | agcatgtacc | aaggaagata | atcccgatca | gccacctcgg  | 4320 |
| acgaagtggc  | aacagtaaa  | atgtcgcttg | acgatgtcga | atgcgagggc | gagacctcta  | 4380 |
| cagtggagaa  | aatctgatca | agaaagtgcg | atattcgtct | ttcgtgaagg | gctaaacggc  | 4440 |
| ctttgggttc  | tcgacaagca | aaactatttg | cttcggggc  |            |             | 4479 |

## (2) INFORMATION FOR SEQ ID NO:605

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1156

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| ggcgattatt  | tccttcgcga | caatttgtca  | cttggtatct | ccgttgcacc | ctgcgagtgg | 60   |
| gatggagaaa  | caattggacg | gccaacgtta  | agttgtcggt | tgtcttcttt | agaatctttg | 120  |
| tagaggacgt  | tttttcgcaa | ttgcagtttt  | tcagtacacg | tcgcttttct | caaccgttga | 180  |
| gaaaatcttc  | gtcttgacga | gggcgcagcc  | gtagatggct | gagaggcgat | ctcgcaggat | 240  |
| ggcgatcgt   | tgccgcgaag | gctgacggta  | agcctgcaat | tctcgacaaa | atccgcgagc | 300  |
| ggatggaggc  | tccggcatct | ttcaccagtc  | gcataccttc | tccagcaaa  | gatattcgaa | 360  |
| ggcgatagtc  | agttcttcat | acaggatctc  | ttcttccggt | cggtctgttc | gagggcttcg | 420  |
| cgagccgctt  | cgcgataagc | acgataagac  | cgctcgtgcc | cagcttgaca | cctccgaagt | 480  |
| agcgcactac  | gcgacgaata | cctgcgtaag  | ccccaatgag | gtgatctgcc | cgaggatggg | 540  |
| ttgcggcgag  | tccccgatgg | ctctccgctc  | tcattggatc | gtgtgcgtcg | cctttggctc | 600  |
| ccagctttgta | tgcccagcat | acatggcggt  | catcgaatag | cggcgcagca | gatcggccac | 660  |
| aagcgacagg  | gcctcctctt | ccgaacttaca | ggataggcga | aagccaggaa | gcggtctcgt | 720  |
| ttctccgtgt  | actgtcttcc | gagggagcac  | tgatcgtgag | gtaggaatct | tcggccatgg | 780  |
| ttcaaggaga  | gcctcatctg | taccttcttc  | ccgggcggca | aacttttccg | acagacggag | 840  |
| aggagcgtac  | tcatttgttt | gatactggcg  | agcgtctctt | cgctcacttc | tttttctgca | 900  |
| agcgaggggt  | cagcagaccg | tatatggcag  | taggcaagtc | tctatctctc | cogtattgct | 960  |
| ccctgcactc  | ttggctctaa | ctgtacgatg  | gcagggagca | cctgatagta | gagtccttga | 1020 |
| taaatcatcc  | tttgggggtc | gccatcagtc  | cgtgagtgtg | tctcttccat | ttgcatgagg | 1080 |
| ctatgcggac  | gatattgata | tgcccctgct  | cgcgaaacgc | cttgggtaag | catcatcttc | 1140 |
| accagcttcg  | gcatac     |             |            |            |            | 1156 |

## (2) INFORMATION FOR SEQ ID NO:606

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1076 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1076
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| attctcttct | tctctcttct  | gaatggccag | ggaaagtcag | ncgaaaaagg | aagggacttc | 60   |
| cctttaccct | ttattttccg  | gctgcgtatc | gnagggcact | cgcgtcctgc | attcagagct | 120  |
| tgaggttcat | atccaccact  | tcttgtcttt | gcggctgaaa | atagcttcga | taccgcctgc | 180  |
| cagatagtcg | aaaggatctc  | aatgaaggga | gaagcggctc | cgagcatcac | gaagttggat | 240  |
| gcacgacatt | gcctacctca  | tcacgggcca | tgctgtccgc | atcgatcaga | acgtatgagg | 300  |
| aagagattcg | atcttggaga  | taactgacgt | agtctcggga | tagtcgggat | gttgatgaac | 360  |
| ggaaccgtat | tggtcactac  | ataaccgtca | ggttcaaata | aggaagatag | cgcaatgctt | 420  |
| ccatcggtc  | cacggagagg  | aaagatccgc | tccccgata  | gggatcaggt | cagagtaa   | 480  |
| gggtgcatcc | acaggcgag   | aaaagactgt | acatcaccac | ctcgctggct | catgccatgg | 540  |
| tttcggcctg | cttcaaatac  | aaattgttgg | tcagagcagc | cgaaccgaag | ctgctgcaat | 600  |
| ggacaaaatg | ccttggcctc  | cgacaccggc | caaaatatat | ctgttttcat | ttctttat   | 660  |
| cctcctactt | caatggttat  | tccttgcctt | tgcacgtttg | gcagctttgg | cgtcgcgagc | 720  |
| atgcttttgg | atgcaacgcg  | acggggaatg | atgacggata | caccttcata | gttgatttcc | 780  |
| tccgatgat  | gctgcatagt  | tcgtcatgat | tcttgggtac | cggaacagc  | tcctgatgtg | 840  |
| atcggggatc | tactccgata  | ccgcgacaga | tggcctctac | ttgccgtatg | cagacgaatg | 900  |
| ctgacctcgg | tcattggagat | ggattcattg | tcgagataat | caccgtaatg | tgctattctc | 960  |
| attgatggca | tcgagaagac  | cgttattccg | aatgagtgaa | agtagagtcg | ccgattacag | 1020 |
| acacagccga | acaagccggc  | atnggcagcc | cttnggcata | gtgatagatg | caccat     | 1076 |

## (2) INFORMATION FOR SEQ ID NO:607

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1015 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1015
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607 .

aactggaaaa tgaacaaaac cctccaagag gggcttgcac tggcaaaggg ttggacgcag

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ctttgaaagg | gcgtacgac  | aactgtgacg | tgattatcga | acccattca  | tccatttggc | 120  |
| aagtattgcg | gcagccatcg | ataccaccgt | atcggagttg | cagctgaaaa | ctgtgccgat | 180  |
| aaggagtcgg | gtgcattacc | ggagaggtct | ctgctgctat | ggtagccagt | accggtgctc | 240  |
| ggtattgatt | ataggacata | gcgaacgccg | tgcttactat | catgaaacat | ccccatcctg | 300  |
| atggagaagg | tgaagttggc | tttgtccaat | ggcttgaccc | ccatttctgt | gttggcgaag | 360  |
| tcttggaaga | gcgcgaagca | ggcaagcact | tcaggtagtc | gctcgtcagg | tggaagaagc | 420  |
| cctgtttact | ttggatcaga | cgactttgcc | aaattgatcc | ttgcttacga | gcctgtgtgg | 480  |
| gccatcggta | gggtaagacg | gctacggcag | accaagctca | agagatgcat | gcacatattg | 540  |
| taagagtata | gccgctaaat | atggaaaaga | ggttgcgaac | ggttgttcat | tctctatgga | 600  |
| ggcagttgca | atgcagccaa | tgccaaagaa | ctctttaccg | tgccgatgta | gatgggtggc | 660  |
| ttatcggagg | ggcttctctc | tcggtaacaa | attcttgcc  | atcatcgaag | cattctgaga | 720  |
| ttgcttattg | tttcaaccct | ttcgggcgag | ttttatttca | aaaggagaaa | cgaacgagat | 780  |
| gaaacgattt | tctttttagt | ctcctattgc | tttcggttgg | ttgccattcg | tcacggaagc | 840  |
| tcaggtttcc | acatcggctc | atagcaaagc | cccgatcagc | atttcgaagc | tctcagtgcg | 900  |
| gagcacgaag | gagaaggcat | catcaccatc | ttcagcctgc | atccgtaaag | ctgccgtggg | 960  |
| caagtatccg | gacgttggcc | nttgatcgan | ggcgagagca | tatccgttga | tccaa      | 1015 |

## (2) INFORMATION FOR SEQ ID NO:608

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| gatccggctg | actatcgccc | gctattatac | gccttcggga  | cgtagcatca  | gaaaccttat | 60  |
| gcaaaaggga | atttcaaagc | atacgaacag | gaattgatgg  | tcgcttcaa   | cacggcgaat | 120 |
| ccatccacag | cgacagcatc | cgtttcccg  | ttctcttcgc  | tacaagactc  | tcgtcacggg | 180 |
| gcgcaccgtt | tatgggtggg | aggcattatg | ccggatcttt  | tcattcccaac | ggatacggcc | 240 |
| ttgttaacaa | gctgcatcgc | gagctgctga | acaagggtat  | ctttaatcgg  | gctgactcaa | 300 |
| atatgtggat | gcacatcgtc | agaagctgcy | ccaacgcttc  | cccacagaca  | gtcatacgcc | 360 |
| acgtttacat | tcccgaagaa | ctgactgaaa | gctgaaaagca | tttgccgaag  | ctgagaaaat | 420 |
| cacatggagc | accgaacttt | ngctcaagcc | gaagagctta  | tcaagtgtca  | gctccatgcc | 480 |
| tatatcgcac | tgatattctg | gggagaacga | cttcttctat  | ttcttcaatc  | gcatggatag | 540 |
| gatataataa | gcactcgatc | tctcatgac  | cgacgaa     |             |            | 577 |

## (2) INFORMATION FOR SEQ ID NO:609

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...850

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609

```

cgaagccgtc gtgatgcagg cacagctgga aatggaagcc aagcgtttgc caaggcgaag 60
tctatcctcg aaaaatttat tgccaagagt actcctcaca gtattggttg gcacgagggtt 120
tcacccctct gtccgatatt tataagaaga aggggatacg tttacggcaa ggcagtattt 180
ggaaagcttg gaaaagacta tcctaatacat gaggatgaca ttcacgaaca gatagcccaa 240
cggtcgaata atcttctgta cgattcatca ctctgagttg gaaataatga acagatcatg 300
aaatatcaat tatatacggc cgtcataatg gctctctctg tatatccgtt tgcggtcaaa 360
ccccacgaaa tacagaaacc aaacgccccg accgctgcgc agggagctta ctatcgttaa 420
tgaccagact gtggagatgg acatgcggat ccgcttccgg ctgcatacaa ggccatcgaa 480
cctcgattaa acccttccgt ccggaatata acaagcgtaac attcggattt gtccctgaat 540
ttcctcttca ggcaggaaca atcttccgaa tatcctgccg acggaaggca tatgaagcac 600
cgggggtacc tgaatatcgg tatcggccat accgtaacca gcgaatggat gccggctatc 660
gtctgataga tgcagagcag gagagatgaa tcttttcctc tcctatcgtg ggatgaaatt 720
ggctttcaat accgggactt cgacggcgac agaaaggata gacgaaatga tggcaggaat 780
ggacacgagc agcgcaggcc ttcctttgtg cttgctaccg gcttggatta ttcaaccatt 840
atttcaatac 850

```

## (2) INFORMATION FOR SEQ ID NO:610

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 680 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...680

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610

```

aggatcccc gccatgcggc gatcttatcc tgggctccta tgggcatcac tttgcatgtg 60
tgactgggta cataaggaac gcaaggaaat tattgacagg ggctgcaaaa aaggctgtgc 120
tcctcatacg agatcgcaat gtgcacctct tgaaagagac aatcgcccaa ctggacgaat 180
acttctctca caagaggaga ctttcgacat cccctgctt atggcaggaa cgagatttca 240
gcaaagggtat ggggcgagct gctgaatata ccctacggca ccacgatctc ataccactc 300
ttgcacgacg aataggaaac ccaaagccg tgagggccgt agccgtgcc aaggagccaa 360
tcccatatcc atcctcgtgc cgtgccatcg ggaattggaa gcgacaatac gctgacaggt 420
tacggtgggg gattggacaa aaggaattcc tgctttcgtc atgaaatgag tctgccggtc 480
taaagccttg aagcctctcg aaggctatct atatttgagt atatttgcaa gcataaaaca 540
gttatataaa aacaaagtag aatatggatt tcacttttct tcaaggccga ccacaagccg 600
gaggcctgtt cggaggctca agccagatga ttctggtctc gtgctcatgg tagtaattct 660
ttactttctc atgacaggc 680

```

## (2) INFORMATION FOR SEQ ID NO:611

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1992 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| gcaaagtctc  | caattcggca  | tcattcatag | cctcggcaag  | ggcatagcgt  | tcttggtact  | 60   |
| ctcaaaagct  | ttccagccgc  | tccagtcttg | tttggccttg  | ctctggctac  | gatctgacgc  | 120  |
| atcatagaac  | gggccgaatt  | gcctcccaag | ggctgaagct  | gtcaaaatcc  | atcgccaata  | 180  |
| taaagtaggc  | atagaaacga  | cggaggcaac | cagattactt  | tgcagatccg  | tctcattata  | 240  |
| ttcgagggat  | cgaactggtt  | gtattcgaag | ttcagttcct  | gatctcgcca  | aatagctgag  | 300  |
| gagaaaaata  | ggaggaattg  | taaatagggc | gacgagaagt  | aacaagagtt  | cggccttgta  | 360  |
| ttgactttcg  | tctttcactt  | cggtaagggt | gaggaaaaag  | gtgcagtcga  | tacgctctgc  | 420  |
| aaaactgaat  | gtggccggtg  | tcctcgagtc | agggttgagga | gatctgagag  | ctgacgctcc  | 480  |
| aatgtcttga  | tgtctccgca  | ttggcattac | tgcgagacg   | ttcgctattg  | atagttacct  | 540  |
| ggcattcaac  | tcctgactta  | cagcagagcc | gtatagaaaa  | acaggcagtc  | cacaggcccc  | 600  |
| accacaatct  | ccttctcatc  | ccaatccgat | tatatagcca  | caatatcttc  | ggccacctcg  | 660  |
| accttgcttt  | tgagcggata  | gtccgaggtc | ggccttcaact | gtcgaatatg  | gtgatcttat  | 720  |
| tcgtacctac  | tccaatccgg  | ctcccgcatc | ggaaagcgaa  | ttcagtacta  | tcgcatccaa  | 780  |
| gtgctggctt  | tcattcttgc  | catagcctct | tgctcccccac | tgctccgtctc | caagcaaaac  | 840  |
| ccaccaaccg  | ctgtcctgca  | cgtttgagtg | ctccgagcgt  | agcgctatat  | ccggattagc  | 900  |
| agtcaagcga  | agatcgaagt  | cgccttggtt | cctcgtttca  | tctttttctc  | tgctgtctct  | 960  |
| gccggacgat  | agtcagccac  | gctgcggaca | agacggttat  | gtcggccttt  | tcaaaagggtt | 1020 |
| tccgacaggt  | tcgagcatct  | ctacggcact | ttccacatcg  | atacggctcta | tcccttcgca  | 1080 |
| gttgcttgca  | tagtggttagg | gccggtgaca | agcgtaaccg  | aagccccaat  | tcggccaaac  | 1140 |
| gttctgctat  | gcagaagccc  | atccttccgg | aagagtgttg  | ccgagaaaaac | gtacaggatc  | 1200 |
| gagtttctcg  | tatgtagggc  | cggcttaacc | aatgctctct  | tcccaaggag  | gggcttacia  | 1260 |
| tcgtttctct  | tgaaaaagcc  | tccaatatct | ccacaatgca  | ctccggctct  | tccatccgcc  | 1320 |
| ccttctctacc | aaatgactgg  | ccaattcgcc | ttcaccgggc  | tctatgatata | gatgccataa  | 1380 |
| gagcgtagta  | tctccatatt  | gtgctgcgta | ctcggatgtc  | gaacatgtcc  | aatccatag   | 1440 |
| ccggagccac  | gaatacggga  | gccttggcgg | aaggtaagtg  | gttaccaaca  | tattgtcggc  | 1500 |
| tatgccatgt  | gccatcttgc  | tatcgtagag | gctgtggccg  | gagctatcag  | catagcatcc  | 1560 |
| gcccagagct  | gagatccaca  | tggctgttcc | atgtaccatc  | ccgtccggag  | aaaaattgct  | 1620 |
| gatgacaggc  | ttggaagtca  | gagccgagag | ggtgatggga  | gtaatgactc  | cttgccggca  | 1680 |
| ggagtaatga  | ctatttgcac  | ttcagcctcc | tttttatgag  | caggcgggtc  | aaaacggcag  | 1740 |
| ccttgtaggc  | tgcgatactc  | cccggacacc | gaggacgatg  | tgcttaccgg  | caaagatga   | 1800 |
| tttcatctgc  | acgagttctc  | ttgtacttgg | tttatttggg  | ctccggattg  | ttcagagaca  | 1860 |
| tagcaggcga  | gtaaattctt  | gctttggatt | cagcgtaaaa  | tccgcatcca  | tatccagccg  | 1920 |
| taataaccgg  | aatctgtacg  | caatacatcc | agagctttac  | gccgcgatac  | ttgccgaaat  | 1980 |
| gatgataacg  | ta          |            |             |             |             | 1992 |

(2) INFORMATION FOR SEQ ID NO:612

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

## (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...569

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612

```

ggatccccctt gcataacagt tgtttgcttc gtgcctatct gtgaatggag cgcgcaacgg 60
aaataaccgga ctttccatac agagaggaaa gggtagaaca gcaaaaagca gggtgaaaaa 120
tagtcgtttc atctttttgt cttatttttg tggaaattat gattgataag cccttcctttt 180
cccttcacatcg taaatgatag tcgtcccata aaggggggga taagggatga ctaaataatc 240
tttgcatcac ggtctccata tctttccaaa ctaaaggcaa tggaaattta ttgcctttct 300
tcgattcttt gctgttttta gtgttatgat tatagcttcc tgcaaggaaa cacatttttt 360
gcttttcaca aggcctgataa gtcttgattt tttgttttag aaattttatt cttcttggat 420
tttgctcggtt ggcattttat gtactctgtg ataccacttt atatcggtct gaatctctgc 480
ctgtgtggat ccagaaaggt ctgattttct atataatcgt cccttaaaaa acccgaaata 540
gccgagatgc catgggaata atggatatc 569

```

## (2) INFORMATION FOR SEQ ID NO:613

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...528

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:613

```

cgcgcatctc gccggtttgt gtcaggtcga gcctgcctgt ggcaacggta tacgcgtatt 60
ctccgtaacg cgcttcataa agagcaggat ggccaaaaca gtcctatctc tatggcaacg 120
gtcaagtcga ggatgacggg aagcaagaag taaccagcat gacgaggcta tcgctgcgag 180
ggccgcgacc gatattgcca ccgaacgcca tccgctcata ttgtaggata ctatgatcag 240
tactcgacca aacaagccat cgggatgtat gccgtcagag gcccgaggaa cagcggatca 300
gcagtaacac gaaggcgtgt atgatccctg caatgggaga gcgccgccgt tgttgatgtt 360
ggtcacgta cgcgctatgg ctccggtgac ggaataccac cgaagaacgg aaccactata 420
ttggccgcac cctgagcgat agctcggtat tgctgttggt ctttttcccc tatcacacca 480
tcgggctacg ttggctgaca agcagagatt cgatagcttc caacaggg 528

```

## (2) INFORMATION FOR SEQ ID NO:614

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...653

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614

```

tccgtgtcga tgcgatccat tcgaattttg gccggagtaa cctctccgat atcttcttca 60
tggcagccat atagttgttg atcttggtgc cacctccatg agaataatgc cggcgccgat 120
atcttcaagg aggcctgaga ggcgtagatg ttgaggtagt tggctgtgat ttcgtccatg 180
cgagccttgg ccaggcattg acttcggagg agcggaaactc tctttcggaa aatttgctcg 240
caaagtcatg cggaatgatc cgttggactt attgtcgttg atcatcgaca cgtgttgagc 300
ttcatgttct ccgcctcctg ttctgtcagt cgcaggctgg tcaatcgcgt gtgacgttat 360
aacctcccat cggaagtacg cgaagcatgg ccacagcctg tttttataga tagataccga 420
tgtacagccg gcacctatat tacgtagcaa catcccaatg tcaagctcgt cgtccgaaga 480
gcaatacctg gcttcgcaaa gcggtgtgac gaggatgcct gtcaagcgca atcccagact 540
tcttctatgg cgatgcggat attctgcttt accgaacggc gagcagtgtc aattggaagc 600
cgggcttcaa gtttcatgac aaaatacttc cttggccgta tcttcctgtt tcc 653

```

## (2) INFORMATION FOR SEQ ID NO:615

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...626

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615

```

cggtatgggg caaggtgccc aaacgtcagg gtacaggtta cgctttcgaa atactgccgg 60
agcacgaccg aaacaggacg tcggctttaa cggacttaga cggcagagga aaaagacttc 120
cctacatata cagagtacat atcccgttg cctcgatcgt atcgccggat gttttgaacc 180
aatggagtac agatccttca gtccgatcaa cgatccggga ggggataact tccaccaacta 240
tagagggcag attacgatga ggcacggaag tctattctcg atcgttataa gcagataacg 300
gagtggaaag caactcggcc gaagccacta acaacattac cggtaacaac tgtccagccg 360
tttggtgccc gatgtggaag acatcaatca ggcaatacgc tcaacgagat agagaagtat 420
ttccagtacc cgtgtggagc tcatccctct aaaatggttg tggggcaaaa ctatattgtc 480
gattctcgca caaagaggta gagttgcgca acggtaaaaa ggaaacgata acctggtata 540
gttcaaagtc cccgtgcggg aattcgagag aaagatagga ggcattacga cttcaagacc 600
attcgattca tgcgtggtct acctga 626

```

## (2) INFORMATION FOR SEQ ID NO:616

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| cgcccttag  | caggctgagg  | cactccggta | aaaccggcac | cgatcggctt | cgatatgcaa | 60  |
| gcaaacgtct | gaagcctctg  | ccagccctt  | ggcatgtcga | gcaaaccgaa | acccgtaata | 120 |
| tcggtggcac | cccttatccc  | gtatttcgca | tcaactccgc | ccctgctcta | ttgagcaggc | 180 |
| acatctgccc | gatggcgcc   | cataaacttc | actgccgata | agccccaac  | gggtggcagc | 240 |
| catcgtagc  | ctattcccag  | cggtttggtt | aggacgaggc | attgccctgc | acgtcgccgg | 300 |
| catttgtagc | cagatgctcc  | ggatgcacta | tgcctgtaac | ggcagtcctg | acttaggtat | 360 |
| gggatcgtct | atcgtagtcc  | ctcccatcgt | aaggcaccac | tctcgtctat | cgtctgctgt | 420 |
| cctccacgga | gaatagtncg  | caagacctct | acgggaatcc | cttcggaggg | gaacatggtc | 480 |
| agattgagta | caacagcggg  | cgcccttcca | tggcatacac | attcgagaga | gcattggcac | 540 |
| agctatgcga | ccgaagggtat | aaggatcgga | caaaccgcgg | gaagaaatcg | gggta      | 595 |

(2) INFORMATION FOR SEQ ID NO:617

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 556 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| ggatcagtag | cgatgaagaa | gagataagtc | gacttgagca | agaagtcttg  | ccttttataa | 60  |
| agagattgag | gccaagcat  | cgttgctgac | cgaagaacca | ttcgggcagc  | ctccgctttg | 120 |
| gaaacttctt | tgtgcgaatc | cttacgcagc | tcaatatgcc | tcatgtccgt  | tttgctcgtg | 180 |
| atattcgctc | gacagatacg | gccctcacgg | agcagacaag | gtcgtttttt  | tgttttcggc | 240 |
| gaatagcaga | tggagccgga | gccggtatcg | gagattgcct | caggaggaga  | gattctcgcc | 300 |
| tgatgtttg  | tctgaaagct | ctcattgcag | acaagcgttc | tttcgggcca  | tcgttttcga | 360 |
| tgagatagat | accggcgtat | cgggtgaagt | ggtgaccgta | tgggagagat  | tatggctcat | 420 |
| atgggacaag | gtatgcaagt | gtcnccatca | cgcattctgc | caaatagcag  | cccaggggga | 480 |
| acggcactac | ttgtctataa | agatgaaaca | ggcgaacggg | 'cacgcacctt | cattcgtgat | 540 |
| gactccgaag | agcgaa     |            |            |             |            | 556 |

(2) INFORMATION FOR SEQ ID NO:618

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...311
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:618

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gccttaacat tgaacaatct aggtctatta tacagcaata acaatgagca aagcaagcga | 60  |
| aagactgcca tcaagaggcc ttggtgataa gaagagaatc gtataaaaaa gtcctcaggc | 120 |
| ctacaatcaa gacttggcta tgacattaac aatttaggcc ttttactcgg caaaaacaat | 180 |
| gaattaaagc aagcgaagat tgctatcaag aggctttggt gaaatacaga gagcttgcaa | 240 |
| agaaaatcct caagtctata acccgaggtt agcctcagta ttgaacaatc tggggtctta | 300 |
| ctcaacgata a                                                      | 311 |

(2) INFORMATION FOR SEQ ID NO:619

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 566 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ggcaaccact gccttcggat agcgttgcag tacttctgcc gtattcttgg aagcggattg  | 60  |
| ataaagcgga agtgagccaa agccactttc ttgccggctt gcgcatacgc tccattgtct  | 120 |
| catagagggtg gccataggta ccgccccacc gatgatcaaa agctcggcat cgtctttatc | 180 |
| gccgtgtact tccaaacagg aatatcttgg gcaatagctt gaaccttggc ttcacgcgta  | 240 |
| gcgacatctt ggcgtgattc tccggattgg tgcgtgatgg accggtcaca tagtcttctc  | 300 |
| caaaccgccc aaacggtgct ggaagccttc ctgtccgggg ataccacaata gcgaacgtgg | 360 |
| gtctcttcat ttctgaagta aggtctccat ttgcttcgcc cttatactga tccacgtagg  | 420 |
| gaggacggat atcgggatat gttggggatc ggggattctc catgcagagg agccgttagc  | 480 |
| gatgaaagca ccgttagcag gataccggtg tcatatgctc aaagctatct tacatgcccg  | 540 |
| aaagcagaag tcgaagcagt ctgacg                                       | 566 |

(2) INFORMATION FOR SEQ ID NO:620

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 458 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620

```

ggagaagcct cccccgatgg agttcgagac aatgggttact tctactacag atggcgatag 60
cccttatcgg aggagtactt atgacccttt tgatgctgtg gccaaaggtc ccttcgtgac 120
catgttcagt cgcaatagcc ccgaactgtg gacttttact atagtatcgt ccccttggtc 180
gtcttcatgc tcttttgtct gtcttcgaac tctacgccac acaactgatg cgaatagccg 240
tgcccagctg atccgcgagg tagtgctcag gctgatgctg atcgtcgttt atctctctat 300
gcctttcgat gggtaagtc tggaagtttt catcgccata tttttgcagc ctatgccgca 360
tgtatgctct tgctgttggc ttatatccgg cgatcgggcaa ggtcaatctt cgtcacaatc 420
ggggctttct gacaccggag cgaagcgcaa ttttctcc 458

```

(2) INFORMATION FOR SEQ ID NO:621

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1626 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621

```

ggcatccgtc ggacgaagaa gccaagtccg tggtaagaa tacatgggtc atctcgggtg 60
taatagttgc gagcaaatcg tattttgtct caagcgtatg ccgagccgtg taagaagcat 120
gtggacaaca acctcaaatc cgctgccaaag gtctgtgtat ccgaatttct tgctgcacgc 180
gaaaaactca ttctcttata aaagaggcca agctgatcgt gtccaacgaa acggatgaga 240
tcttgatccg atgacttacc gcggcaagga catcaagaaa gagctaaagc agctcgcaag 300
acacagctta gccgcattca gcagggggag agcagtctga agattctctc gtctatctga 360
atctcttgca ggagtcgcag cagttgggtga attattggac gatctgatec acgccacgga 420
gaagctgttc gaccccgtag ccggatcggc acggacgaag aatttttcaa ctgacggccg 480
atagctctgt ttttctcac tggtcatccc cctgataaag ggtcttcoga atacattaaa 540
ggatgtaata acggaggatc agggataaat aattgataaa agcttgtgaa gagaaaaaaa 600
atgccttact ttgcaaccgg attatgaccg ctttatgtgc tacaagcagt cctaacgaac 660
tggaacgata ataaactaat aacgaatagc aatgtcaaag atttgtcaga ttaccggcaa 720
aaaggcaatg gttggaacaa cgtttctcac tccaagagaa ggacaaaacg agtattcgat 780
gtcacttggt cagaaagaag ttctattggg tagaacagga ttgctgggtt gtttgaggat 840
atcggctgcc gggctgcgcc tcatcaacaa aatcgggtctc gagctgccat caagcgcgcg 900
gccgagaagg gcttcttaaa cgcataatca aggagaattc tgtcatggca aagaaagtaa 960
aaggcaatcg ggtgcaggtt tccttgaatg caccgagcat aaggagagtg gtatgccggg 1020
tatttctcgt acatcaccac caagaataga aaaaatacga ctcagcgtct ggaactcaga 1080
agtacaaccc catcctgaga cgtatgacct ttcataagga aatcaaaaat aaagaggaga 1140
tcagacaatg gcaaaaaaat cggttgcaac atttaaaaag gtgatggccg tacctactcc 1200
aaggtaatca agatggtcaa gtctctaaga cgggtgccta taccttcag gaagaaatgg 1260
tcccgaacga agcttaaaag acttctttaa gtaaggtttt ttccttttga ataatataga 1320

```

|                                                                   |      |
|-------------------------------------------------------------------|------|
| gtggataagc attctcagtg aagccccctc tattacacta taggggcttt atttttatcg | 1380 |
| atcgatcaag attgacaatg aaaacaaaca cttattccct gtatttgtct ctatctctct | 1440 |
| tgtctttttg tegtcttttc cagcaaggc caggctatac acccgaggat tgaagcaggg  | 1500 |
| ctgggtttgt tgaaggaggg ctgcctcttt tctctatacc ttccataggg tggctttttc | 1560 |
| gaatgacgga aaactctgta tcgaaccatc ggtcggctat tatctatggg tagctccaag | 1620 |
| catcag                                                            | 1626 |

## (2) INFORMATION FOR SEQ ID NO:622

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2704

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gtccatttgc attggcctcg gtaacaaaag ctccgttggt gtctttcacg tattcagacc   | 60   |
| ccactcctgt gcttcgctgt atttggtgct ggccaggga gaccggcttg gagctggaag    | 120  |
| gacttgtagt cgaccttacc ttccagatga gaccgaatac tttggctccg ctaccgttga   | 180  |
| tacgcgtgta gcgtttatgc catcgtgctg atcaggctgc tctcgtttgg tgaatacatc   | 240  |
| cagcaacgag tatagaagcc ttccacaagg aagttggctt ggacgttacc gaaagatgat   | 300  |
| acatatcggc actcaaaactg aatgcatgag aaatttcagg cttaggttcg gatcgttgaa  | 360  |
| tactttctgt gcctcaccgc ctacaacccc tagtgcaagt cttcatcgaa tacctgcggt   | 420  |
| gcgcggaacc cttttgcata ttagcgcgca ggttgatgtc cgatttcacg ttgaaacgca   | 480  |
| gtgtggtacg ggactcagaa tcatatcctt gacttcgcta tgcttgcca agcgagcgca    | 540  |
| acaaggatgc tccatctgtc atttttccat tegtctgac cgaatagggt tagttgttga    | 600  |
| tattctgata caattcggga tagaggggaa tggatattcca ttggcatcct cgccggtctg  | 660  |
| ccatgaaagg atgggcatca cgtcatgagt tcatcacgcg tatattcggc tccgaacaaa   | 720  |
| agttgcgaag gcatgggagg aatttgtcca agtcgtagct gtactggata ccgccatat    | 780  |
| atgtttgcct ttggtcacgc cataattatt gccgtattga tcttgaggga taggtagcct   | 840  |
| tccgtaccac cgggggtggcc attgacgtca atctctccga tactccgtaa tagctcttgc  | 900  |
| gattttacgat ctgtccggaa gtataagcct gaagtgggtg tttagattgg aagagaagag  | 960  |
| atcgtatttc aagtttcocgc aaatacgtca tggctcgttt gttcagctac acccactacg  | 1020 |
| tgaggaggga atcgatacga tcgccaccac ggccggaattc actgatcgtg tgaaactccc  | 1080 |
| cgtaaatatt ctgtagtcgc tcaagcgcaa ataagaatgc gctcccacga gcgggcatct   | 1140 |
| atttttaccca attcgggaata accgtcattg ttagcaccca atgggttcgg taacgagcct | 1200 |
| gcccgaatac catggcaccg gcacgttggtc atcgtctgac atggaggcat tgaagtctgt  | 1260 |
| gttggttatcc agctgctgaa accggtaaag ctccagagatt cattgaatgt gaaagaattg | 1320 |
| tgaagggttc cttggtgatg atattcacca ctccggcaat agcagaagaa cctacaaggc   | 1380 |
| cgatcctcca ccacgtacta cctccacacg ttcgatcata tggcagggat ctgctccaga   | 1440 |
| ccgtaaaacac cggcaagggc actcatgatg gacggctgtc gatgaggatc tgtgcataac  | 1500 |
| gaccatccag tccattgatc gaacttgatt gaaaccacag ttctgacagt tgttctctac   | 1560 |
| acgaactccg gctggaatga caagccttga gccagggttag aagcattgac ttgcgagaga  | 1620 |
| ctttttcgtt caatacattt accagagtag gagcatctct ctgcttcgaa attcacctcg   | 1680 |
| ggccgaaatc acgacttcgt ccagattgat ggcattctct cttatagccc atgccacgca   | 1740 |
| atagtcttgt cctttttctac ggggtacgc gtcctgggt cttatagccc atgccacgca    | 1800 |
| taatcaaagt gattcacccg gacgcaagtt acgaagatag tagtgcccgg ttgcatctgt   | 1860 |
| agtgtaccaa aggtagtgcc tttgatagca atagtgtatc cgacaagggt tcaccgctct   | 1920 |
| tgctgtcttt gacgtgaccg atgatattgg catcggtcgg tacttgaaact cagtgtctgt  | 1980 |
| cgctgcgttc agcccactga acgcaatgac gccacaggga taaaaaagat tttttttccg   | 2040 |
| atcatgtttt tattgtatag gtgggaatag gttccctaaa gcattttctc cgattccgcc   | 2100 |
| caaaaaataa agaggatata gaatagaatc tgctcatcat ataaaagaga ggcgacccca   | 2160 |
| tattgttcgc ctctctttgt attcttagtt tatttttggg ctctccttac tttttcccg    | 2220 |

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| gcttgatccc  | gataagttcc | atctcgaacg | tcaggtagag | aacggttcga | tggatatagtt | 2280 |
| gccggtctcc  | ccataagcca | gctctgtggg | attaccacgc | gaactttctg | accgaccttc  | 2340 |
| atgagttgga  | gctctccgtc | cagcctttaa | tcacaccggg | aacggcaaat | tcgattcctt  | 2400 |
| ctcgtttttg  | tcgaactctt | taccatcgac | cagagtaccc | acataactga | acgtacagta  | 2460 |
| tcggccaaaag | agggagtagc | tcccgtacct | tcctgaagat | cttgtatgcc | agaccacttg  | 2520 |
| tcgtaacagt  | tacaccatct | tcttttttaa | ggatcgcgat | tattcattac | cctttttcgat | 2580 |
| gttctggcca  | aactgctcat | attgttttct | cgctgctttt | tggcttggat | tcgttgcgat  | 2640 |
| aaagccgtgc  | atctgcaggc | ttcatggcga | tagatacggg | gtcttaagaa | gagccgggac  | 2700 |
| cgag        |            |            |            |            |             | 2704 |

## (2) INFORMATION FOR SEQ ID NO:623

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...564

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| atccccagcg  | catcagccgg | atcgatgttg | ggatcacgta | taatattctg  | agatgccact | 60  |
| gggcattatc  | gatccaattc | ttcaaaaaca | aataatgccg | atcgtttgag  | gccgatattg | 120 |
| attgtttgcac | ggtgcgtcta | cgctgtcgtg | acgttatagg | cctgaatagc  | ctcgccgaaa | 180 |
| atcctattgc  | acaactgctg | atagtcataa | ttattattgc | cgcttaattt  | gtcaaaatta | 240 |
| taatgtatgc  | ggacaaagat | atataaaaaa | ccgattggcg | aactctgaga  | attagtcctc | 300 |
| caatcggttt  | tgtaaattgc | taaaaagcaa | caataatttt | aatagtcttt  | tttgactctc | 360 |
| ttttttattg  | cttatcagtt | gccttttctg | gctcttggcg | tgccgggcaat | ttcctgcttc | 420 |
| agctttgcct  | ttgccttcgc | agatttgtgg | ccgtgcttgc | tcttgacttc  | gcctttttct | 480 |
| gacttgtggc  | gtcacttttt | ttgcagtctt | tggatttgtc | cttgctacaa  | tctttgcgtg | 540 |
| gcaccccttg  | ccttatcctt | acag       |            |             |            | 564 |

## (2) INFORMATION FOR SEQ ID NO:624

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...426

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tagaggatcc  | ccgcttatgg | gacgaatgat | gggtagtata | atcaagggga | tccctccaag | 60  |
| atgcgtcccg  | tggcagatga | gttggccgct | ctcggacggt | cagccagatc | gggttcctta | 120 |
| cttattgttt  | gcggctcttt | cgcgagtgtg | tataagtaga | gtaggggttg | caaaactgaa | 180 |
| ctacctctct  | cccgagaaga | atccttcgtc | gatatgctca | gtggaggcat | tacgggacag | 240 |
| aacatcgacc  | ggtgatggag | gaggtggagc | tggctatccg | tcataattcg | cagatggaaa | 300 |
| cggtcgggatg | atttttttcg | atctctcctc | ccgccttacg | gccctcttgc | ccctgctctt | 360 |
| cgtgccaaag  | gccttaaata | agcaaccctg | tcttccccct | ttatacgggc | ttgtacatag | 420 |
| agggag      |            |            |            |            |            | 426 |

## (2) INFORMATION FOR SEQ ID NO:625

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...549

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| ggacgtattc  | cgctcaatga | aacggatcgc  | tgcgccaaag  | cgagtgtaga | ttttccatgc | 60  |
| gtgggactcc  | tacggatata | gagaagctgc  | agcgcaactt  | atggaaatgg | cttctcagct | 120 |
| caatatggat  | atttcgttcc | agcgggaagc  | atgttcgctc  | gcatgcgtcg | tctcatttgc | 180 |
| ttcgatatgg  | actctacctg | attcagacag  | aggatcataga | cgaactggct | atcagagccg | 240 |
| gagtagcgat  | cgggtaaaag | ccattactga  | aagtgccatg  | agaggcgaaa | tcgatttacc | 300 |
| gaaagcttcc  | gccagcgagt | ggctctgctg  | aaaggacttg  | atgatctgtg | atgcaggaga | 360 |
| ttgccgaaaag | tcttcctatt | accgaagggtg | tgagcggcta  | atgaagatcc | tcaagatggt | 420 |
| aggcttcaag  | atcgctatcc | ttcgggggga  | ttcatgtact  | tcggcaacta | tctagccaag | 480 |
| aagttcggaa  | cgactatgtc | tatgccaatg  | aattggaagt  | aaaagacggt | aagctcacgg | 540 |
| ccgatatgt   |            |             |             |            |            | 549 |

## (2) INFORMATION FOR SEQ ID NO:626

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...524

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626

```

gggcttcctc ttttcgtgaa acccaatgtg ggaggttcca gcatcgcat accaagggtg 60
tggaagctgc acagctcctt ccggcaatag aacaagcctc tcggaaggcg aagaggtaat 120
gatagagcgt ctgatatgtg gtaccgagtt acctgcgggg cattcctcag aaaaaaagaa 180
gtggtcgcat tgcctgtaca gaagttgtcg cacataatga gtttttcgac ttcgatgcc 240
aatacacgga gctgtagagg aaatcacacc ggcgagaatc agcgatgaag ccaccgattg 300
atacagacca tgactgcgag catatacgag cttctcaacg ctccgggcatc atacgtgtgg 360
actatattca tcgaagcgga tggatttccc acctgctgga agtgaacacg acaccgggca 420
tgacccttac gagctttatn cccagcaggt tcgagcagcc cggaatggat atgaaagaag 480
gtgctttgca tattcattcg ggatggactt gaatgagacc caat 524

```

## (2) INFORMATION FOR SEQ ID NO:627

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1165

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627

```

ggaagttggt cagaactcca ctgataatgg agtccatctc tgccaattcg attcgtgttg 60
gctgtttact gctgcaatag agtcatactg catttttact ctttataggc actggagtgt 120
tttccacatg ataccaaggc aagagttgag ctgtggcgat aaacagtttc ttcttcattg 180
tcgtaatact tttattgcgt gacacttcat tcattcttaa cttattgctt ctcttctttt 240
ctcccttcgg ggcggtcca cccacgatga gaacgaatcc tccccttgga ggggtgttttc 300
gaagtgaagg agtaattccg cgagtgttcc gcggatcacc tctcgtggag ttgtctcagc 360
tcccggcatg cagcagctgg tcgatcgaga ccaaagtctc cacaaattgg gtcagagtcc 420
tgagcaccgg atggggcgac tataaaatat catcgtccgg agctcttcgg ccaattcttt 480
cattcgagtt ggcggccttt cttgacaggc agaaaacctt cgaaaacaaa cctgtcggcg 540
ggagtccgct tgctaccaa gcccgaatca atgctgtggg tccgggcaac attctaccac 600
tacacccaac tcggcacatg ctctgacaag caaaaaacgg ggtcgtgat cccgggagtt 660
ccggcgctcg agatcaaagc tatgctgcac ctccgatat ccgttcggcc aatgacttgg 720
ccgtacgatg ttcgtgaatt tatgatggct ctggagcgga cagtgaatgt cgtaatgggt 780
gagcatacac tgctggtacg cgtgtcctct gccaaaatca ggtctgcttc gcgagtacct 840
tcaaggctct caaggtaata tcctccaaat tgccgatagg agcggcacga ctgtcaaacg 900
tccttccatc gcaaactcta cggttcagtt cttctacgga agaaatccga cactacttcc 960
gcaaagtcac ttaccaccgg tcctctgcct cccattgcat ccgctgatgc aaatagatca 1020
tagcttcagc gctgacgaca gcaatccgag atgggcagag atgtctcgca taagcttgca 1080
tcgtcttgaa acaactcccg tctaaagcga aaaaaatcca acgtagaact atcttctgca 1140
aatcgaagcc tgcaggagag gtctc 1165

```

## (2) INFORMATION FOR SEQ ID NO:628

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1008 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

```

gatctatctt gatgtccaag tggagttctc ccgcgtttgt tggcctgagg atcacctctg 60
ggcataatctt tccggcatcg gaatagagtg cttcggaggc tggtcatgca ggtcttcgcc 120
gaagtgtcgg cgaaactcgt ccactctttt ttccagcttc tctgccggag cttcggttatc 180
ggcatagagg atattcccac ccgtcgatct cctccgtaa ggcgaagggc caaccatctg 240
ctattggcgt atcgggatga aagagccgga tggattcggc caaagaatcg atcccgatc 300
tatttcagta ccgatacttg tcagtcgatg cggagtacag cgaatatccc ttgggccacc 360
tcggacaggg ccgacaggag atcggatatg cctctcccga acgtgcactg gctcctacga 420
cagggatgcc cagcctgcgc ggagacctct caggtcgatc tctacgccgt tccgttcggc 480
ttcgtccatt gattggcaca taggacggca cgatccgtta ttccgaggat ttgcaggata 540
gattcatatt ccgctccagt cgggtagcat ctgccacgat gagggtaaat cgggcttgcc 600
gaagagaatg aagtcgcgag cgatctcctc atcctcgagg tagaaaggag agaataagggtg 660
cccgaagat ccactatctt gtatgagagc cggcatacga gaatgcacct tgggctttct 720
ctaccgtttt cccggccagt tgcccgtagt ttgtttgagc ccggtcaggg cattgaatac 780
cgtatcttgc ctgtattggg attgccggca agggcgatgg tgaagtcgta tcgtccgcat 840
cggtgcccat gcgccggagt ttatttcgcg tgtgtgcggg gcacccgttg caggctgaag 900
aagtggtagc actctttttc atcattcgat tgaagttggt ctgaacgtta ggtcttttac 960
ctggatataa ggatataacg gcttgatcgc gtcgcaaggc gatggccg 1008

```

(2) INFORMATION FOR SEQ ID NO:629

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629

```

cggcatcggt ctgtagcgac aggtacgacc atacggctac ggggatagtt tggctttgca 60
ccaaattctc ttttaatcat tcgactgacc tctcgataat gaggagaagc catttcatga 120
accgcacata tccgaaccgg ctctcaggag taagatatat ggtgaagtat atggcttctt 180
gctcaatgaa atccaatttg ttacaaatat actgacagac agtgattcta ccaaagcatc 240
cattcatata ttccgggctg tgagtgaac acaataaaca aaggccgggt agagtgaag 300
ccggatattg gagcggattt tagtagtttt gcgctccggt agaatactga atataaggat 360
gtttcaagat ccaagaaacg atcgtcaagc ccgacctctt cgacaagtat tttgtctgcg 420
attatgctac gtgtcagggg attgctgcgt ggaaggagaa agcggtgctc ctctcgaagc 480
gggtgaaagc gattttgct

```

(2) INFORMATION FOR SEQ ID NO:630

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggcaatgaca | atttgcaaac | gataacagtg | cgtcgcaata | tggccaaatc | agcttggcca | 60  |
| tgaataccgc | caagctgaca | gaggtggagt | actctcttat | aacacctttg | acaaaggcac | 120 |
| cttggtccca | ttcgacccct | ccgaaacaat | ccagacttag | cattcaaaaa | agattttgtg | 180 |
| accgagccgg | ccggagtgat | tttgataatc | agaaaggggt | caaacctgtc | ggtcctgaga | 240 |
| atttctttat | ggtttcgagc | gtaaaaattc | agttattgct | gcggggagaa | aaattcttgc | 300 |
| ctgatcataa | aaggcaaata | tcaaggtagt | aatgcctttt | cttctacaag | atagactttg | 360 |
| tccatcagga | cgacaagacc | aagcgttacg | actcatacgc | aatcacttct | ataaggtgac | 420 |
| gatcaatgat | gtatttaaag | cggatttccc | acaatcgagg | cggctctttc | aggtgctgct | 480 |
| gcgaacaaca | agctctctcc | gaggagctgc | aaatgtaccc | cgctctttct | tgacggaaa  | 539 |

(2) INFORMATION FOR SEQ ID NO:631

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gggttcaaag | agatattggt | accggccgat | aatttccggc | aggaggatgc | ggccgcttcg | 60  |
| gtattcggct | cgtgccggtc | agaaaggtgg | aggaagcctc | cgccatctgt | tctcgaaagg | 120 |
| aagagaatag | aaagaacgga | gaaaacacta | tcaggagaga | gctacaattt | ccaaaaacat | 180 |
| acaagtaata | atgaaaagaa | caaactattc | cgtatcggga | tacttgccat | cgttgccctc | 240 |
| ttgctacagg | atgcaagggg | agccgatacg | cattttatca | ccgatgcaga | cttcgcaaac | 300 |
| aggtgcaaga | agatctgaga | gtaaaacgcg | aagctctatc | cgaggcaatc | tcttcgaagt | 360 |
| gctggagcgc | gattcgctcc | gtaccgaaga | gccgaagcac | tggagttcct | gtatgcctac | 420 |
| atgacttctg | ccggacatcg | tgactactcg | ggcgacttct | acttgcagaa | tgtacgcgag | 480 |
| agcttccgcg | aagaagaaga | atgtcgtggg | gtaaggaagt | gcccgaactg |            | 529 |

(2) INFORMATION FOR SEQ ID NO:632

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3949 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| cgagagcgag  | ccgatagccc  | gcttcaccca  | gaaactggat  | cagcccaatc  | cgtaaccttt  | 60   |
| gtaggcaaa   | gcaaattgga  | tgagatacgc  | gcctatgtca  | ggagaacgag  | atcggcattg  | 120  |
| tggtgttcga  | cgacgaactg  | tcgcccagca  | gctgcgcaac  | atcgaaaaag  | aacttcagac  | 180  |
| caagatcctc  | gatcgctcgg  | tcttattcctc | gatatattcg  | cccgacgggc  | acagacggct  | 240  |
| catgcaaaac  | gcaggtagaa  | ctggcgagct  | accagtatat  | gctgcctcga  | ctgaggggct  | 300  |
| atggacccac  | ctcgaaaggg  | agcgaggcgg  | tgctcgcatg  | agagtcgggg  | agaaaagcag  | 360  |
| ttggagacag  | accgcccgtat | cgtcttttga  | caaatagcctc | ggctcaaaga  | agaactaagg  | 420  |
| gacatagaca  | agcagaaatc  | ctgcagcgca  | agaaccgtgg  | caagatggta  | cgcgttgctt  | 480  |
| tggtcggcta  | acgaatgtcg  | ggaagagtag  | ggtgatgaat  | gtcctctcca  | aaagtggagg  | 540  |
| ttcgccgaaa  | acaagctgtt  | tgccacgttg  | aatacgacgg  | tgcgcaagt   | atcatagaca  | 600  |
| atttgctttt  | cttgctgagc  | gatacggctg  | ggtttatcgc  | aagctgcccc  | cacagttggt  | 660  |
| cgaatctttc  | aaaagtacac  | ttgatgggtg  | cgagaggcgg  | atttggttgg  | gcacgtgggt  | 720  |
| gatatgtcgc  | atccgcattc  | gaagagcaaa  | tagagggtgt  | gaaccagact  | ctggcggaga  | 780  |
| taacgcagga  | gaagaaaagc  | cgatgcttct  | tctcttcaac  | aagatcgatg  | cgtctctttc  | 840  |
| acacccaaa   | acgaagacga  | ccttactccc  | cgaacaaaag  | agacataagt  | gccgaggagg  | 900  |
| tgcaacagac  | ctggatggcc  | aaactcggga  | agactgcctg  | ttcgtctcgg  | cgaagaaagg  | 960  |
| caccgggtag  | gatgctctga  | agctcttttg  | tacgagagag  | ctaaggcaat  | ccatatcacg  | 1020 |
| cgcttcccca  | caatgacttc  | ctgttccagg  | actattcggg  | ggagatggaa  | taagctgtct  | 1080 |
| ctttgggaagt | atgtgaaaat  | tccttttagt  | gttctccatc  | ggcttgccga  | aattctctat  | 1140 |
| ctttgataga  | ttgttgatct  | tgagaccata  | agttttgtgg  | ctctgtgcac  | cgacgacttc  | 1200 |
| gatcatcaat  | aacaataaac  | gatcatagca  | ctgtggacgt  | atctgcatat  | cctttttttc  | 1260 |
| gtcgcgatat  | gagtggtctt  | cctttaacga  | acgcgtgttg  | atggaggctg  | ccgaccggac  | 1320 |
| tttccgggtt  | acgacaggat  | caagttcctg  | tccatcttct  | cttccaatct  | ggggagttct  | 1380 |
| ataccgtacg  | ggtggcctat  | catcaggccg  | tcctacagaa  | aggcgcgaca  | ggagcgaggc  | 1440 |
| cgaagaggat  | tccgatgcgg  | atgctcatat  | ctgcaagcta  | ttcggggagc  | tgtaatcaga  | 1500 |
| caggacgaac  | tgtattatcg  | atctttttac  | atcagatcct  | gcccaccttg  | gaggaacncg  | 1560 |
| gtatccgatg  | cgtacggcat  | gccccactc   | atccggatca  | taaagcctac  | ctgcgtcttt  | 1620 |
| cttccacgag  | gagatttttc  | ctctgctcta  | tccgatgctg  | ttgctgcgag  | caaggtgcgt  | 1680 |
| acattttatc  | gttcaggtag  | ggtgtatctg  | gctgtcggct  | caaagaaaaa  | gagacggacg  | 1740 |
| aggcctacag  | ctatgcactg  | ctcatgtgcc  | taccgacggc  | cttctctcgt  | tcgtagagct  | 1800 |
| gccacggctc  | cagccgacac  | attttattac  | tactcttttc  | tggaagatat  | tatcaaaagag | 1860 |
| caactggatg  | agtcttcccc  | ggatacagag  | tgatggacag  | ctattcgatc  | aagtgtcgcg  | 1920 |
| cgatgccgat  | ttgctgttgg  | atgcacagcg  | tcctgaagat  | tgcccggaga  | gatccgcaag  | 1980 |
| aaggtgaaga  | ctcgcaagct  | cggtgctcca  | cgcgattcat  | gtatgacggg  | cgcattgccg  | 2040 |
| acgaggtgct  | gcgatacact  | gcagttcgtg  | cgacatcgat  | ccggaggagg  | cgattcggag  | 2100 |
| tggaacacag  | tcaatctgca  | agatctggct  | atgctgcccc  | atccgtttgc  | ccccagctgg  | 2160 |
| agacactcac  | gccggagcct  | ctcctctcga  | agcatttggg  | gcaggcccct  | ctctgatgga  | 2220 |
| aggcattcgt  | aggaaggact  | acctgattca  | tgtgcttact  | atacgtatga  | ctatgtcgtg  | 2280 |
| cgcctgctga  | tggaagcggc  | cattcaccgg  | atgtgtcggg  | aatacgcctt  | acacagatc   | 2340 |
| gcgtagctga  | aattcgtcca  | ttatcagtag  | attggaagcg  | gctgcacaga  | gtggaaagaa  | 2400 |
| gtatctgtct  | tcgtggagtt  | gaaagcccga  | ttcgatgagg  | aaaacaactt  | cgtttgtcag  | 2460 |
| agcgtatgcg  | ccgttcgggg  | attcggatcg  | tttacagtag  | ccggggctga  | aagtccatgc  | 2520 |
| caaaacggct  | ctcatcctct  | atcatacacg  | gccgggtgaac | gtccgcaagg  | catcgctttg  | 2580 |
| ctctctacgg  | ggaattttaat | gagaccactg  | ctcgcattta  | ctccgacact  | acgctgatga  | 2640 |
| ctgccatacg  | gacattgtgc  | atgatgtgta  | ccgccttttc  | cgcatttttg  | acggaatccc  | 2700 |
| gaaccggcac  | gttttcagtcg | tctgctcgtg  | gctcgttaca  | acatgggtgaa | gccattacca  | 2760 |
| acctgatcga  | acgcgagata  | gaaaatgtga  | agctggtaag  | cgtggctata  | tgctcctgaa  | 2820 |
| gatgaacggc  | ctgcaggaga  | agatgtcatc  | acacagctct  | atcgggcttc  | cgaagccggg  | 2880 |

|            |             |             |             |            |             |      |
|------------|-------------|-------------|-------------|------------|-------------|------|
| gtggagatcg | actgatcgtg  | cgagggtatct | gctgttttgg  | acccgatatg | ccacagagtc  | 2940 |
| caatatacgt | gtcactcgat  | tgggtggatat | gtattttggag | catagccgtt | ctgggtgcttc | 3000 |
| cacaacgggg | ggaaagaaga  | ggtattcatc  | tcttcggcga  | ctggatgaag | cgcaatctat  | 3060 |
| acaaccgcat | cgagactgcc  | tgccctggct  | ggatcctgct  | ttacgaagag | agattatcga  | 3120 |
| catattggag | atccagttcg  | cgacaatatc  | aaggcttgcc  | ggatcgattc | ttctctcaac  | 3180 |
| aacattacaa | acacaatagc  | gatgagaaac  | cggtgcgagc  | acaagctgct | atctccgcta  | 3240 |
| tctcaaaggc | aaagaagagg  | ccactcctgc  | tgcaaaataa  | atgtgaataa | gacccgtttc  | 3300 |
| ctccgtatcc | tgtgtgctact | ggcagccgtt  | tgtttctcgtc | tctattcctc | gtggctcaac  | 3360 |
| gacattcgga | agcttcgagc  | gtggcatcgt  | gacaaattca  | gccttttcat | tcattacggc  | 3420 |
| ttctacagtg | gcttggaggg  | gtttggcaag  | gcaaaccagt  | gaagaacgga | tatagcgaaa  | 3480 |
| gatctactct | ttcgggaatac | gcgacatgaa  | gcaatacgag  | ccggtggcaa | gcggttccgc  | 3540 |
| cccgacagat | gggatgccga  | tgccatagta  | gccttagtcg  | gaaagcaggg | atgaagagta  | 3600 |
| tcgtgtttac | ttccaagcat  | cacgatgctt  | ctgcatgtat  | ggctcggctg | agactccatt  | 3660 |
| caatatagtg | gaggcactcc  | ttcgcgtcgc  | gatgtgatga  | aggaattgag | cgatgcttgt  | 3720 |
| gagcttcggg | tatgaagttc  | ggcgtttact  | tctctcttat  | tgattggcat | ttccggaagc  | 3780 |
| caatccgata | agcgatcaca  | atgctgatcg  | gattactccg  | gccatcacca | atacaatatg  | 3840 |
| cgtcagggtc | gagagatcct  | cacgggctac  | gcctgtcag   | cgagttgtgg | ttcgatatgg  | 3900 |
| gatcgcttac | gccgaagcag  | gtgaagagtt  | gtattgtttg  | gtgcatgag  |             | 3949 |

## (2) INFORMATION FOR SEQ ID NO:633

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2096 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...2096
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| tccgaactta | tggtctctgag | gtaactccac  | ttgtcgccca | cagtgcggag | agtctttctct | 60   |
| ttaccatcga | aaacgatggt  | cagagggttcg | gccagagggt | cttctcatcc | accatcaggg  | 120  |
| taatgagtac | atagtccttt  | tccagcagct  | ctttactgta | ggatcgatcc | aaacggcatt  | 180  |
| ctccatcttt | ctacagtcac  | gcagccgtga  | cctgagaagt | cgaggaggac | aggtttgttc  | 240  |
| tcttgcgagc | aaaagccata  | ccggcctcat  | aatccgtaaa | gtgagcatga | acttgccact  | 300  |
| atagagattg | aaatcctgcg  | tgtggagcgg  | cgagcaaaa  | gcattacagc | cttgagcgga  | 360  |
| gccccccaca | aaccggggat  | catatataca  | gcaaagccaa | agagacagta | gccatcataa  | 420  |
| agcgcgggac | agagagatgt  | gccattcgct  | atcatggctg | aaacggatcc | atcccaagag  | 480  |
| atagcaaccg | gcagagcgaa  | aatgacaatc  | cagagagcga | ggaaagtctc | acgatcgaga  | 540  |
| tatgccagcc | atatgccaa   | tctgccacgg  | agaggaaact | gagagcaaa  | ccaattcgag  | 600  |
| gaagccgagt | accaccttca  | ccatattcaa  | ccatcctcgc | tcttaggcat | accctgcaac  | 660  |
| cagctgggga | agaccgcaaa  | aagagtaagg  | gcaaagccaa | tgaagtggca | aagccaagca  | 720  |
| tgcccatggc | cggagcagtt  | tggagccggc  | tgtagcagcc | tgtaccaaga | gcgtaccgat  | 780  |
| aatagaccgg | tacaagagaa  | ggacaccaaa  | gccagcgtaa | aggccataaa | gaaatactga  | 840  |
| gcaaaccggg | cgtagagtcc  | gccttgctgt  | ccagcttggt | agccaagatg | acggcaacac  | 900  |
| cagctcgaat | gctccgaaga  | aagagatagc  | gagactacca | acagcaggaa | gaatatgatg  | 960  |
| ttgaagaccg | cattcgtggc  | aaactgttca  | gagaattgac | accgaaaata | cccgtaatga  | 1020 |
| gcaagccgac | actacgtaga  | taacgatgat  | ggaagctccg | taggtaaagg | catctctccg  | 1080 |
| gctttcttct | tgtccttatt  | acgcttaagg  | aagaagctca | ccgtcatggg | atcataggcc  | 1140 |
| atacgcaagg | agtaagcaat  | gcaacaaaac  | cgtagagaaa | ccatagagga | aaatcttcca  | 1200 |
| cggagcactc | tctgcctgct  | tgagctatca  | tcaccgtatg | cacgcaactc | gctaacaacc  | 1260 |
| ggtgtccaca | agtcgccttg  | gacgaaagag  | cttcggcagc | atcggtctgc | gatgtagtat  | 1320 |
| ccgtgcggtc | tcggcagcaa  | ccgcttcagc  | agcttcagct | tcggtatcag | gactgcagcc  | 1380 |
| ttgctcttga | tcacggaagc  | atcgaaaag   | aagtcgctcg | tcgggtgggc | agacagtttt  | 1440 |
| catcattaca | agccatgaag  | cgaacaccac  | tttgatagag | aatttggcag | ggtccgtcac  | 1500 |

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| ctgaattttc | tgacggaaaa | gacagtcttc  | tcgtaccatc | tcagatccat | ttcgaactgc | 1560 |
| ttgtcgtacg | gttgacagga | gctttgtcag  | gaatagcctt | accgacaagt | ttggctccgt | 1620 |
| cattttatcg | aacaggaatt | ctgtggatgt  | agggccatcc | tcgggcgatt | ttggtcataa | 1680 |
| aggtgccatc | cgggtttgat | cgtggccgta  | aacacaatgt | tttctcaggc | gtgtcgctat | 1740 |
| cctgaagaga | ggtttttcaa | acgatacatc  | cttgataatc | tgagcagatg | ccccgatggg | 1800 |
| caacatagag | agaacagtag | ggctaaaagct | accgtccatt | tgetgtttct | gtggttcttg | 1860 |
| ttgtcattat | tatatgttgg | attattaaaa  | ttagtcagct | acctatttgg | acgttttttt | 1920 |
| gtctttgata | ttgtttggtc | tgetgcagtg  | ccttcttcga | atgtatcagg | cggcgaaaga | 1980 |
| gtttgggcaa | aggcaactta | tattcctgct  | atctcccgtt | tcaggatgac | ggaatacgaa | 2040 |
| tcgcgttccc | tgtagggcag | acagtcacga  | tggcggaag  | aactaccctg | cctcaa     | 2096 |

## (2) INFORMATION FOR SEQ ID NO:634

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 650 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...650
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| tagaggatcc | cctgtagatt  | tctcgtcatt | gtatagctgt | ctgaaaggga | taccgctgtc  | 60  |
| atgttctgtg | aagtggctaa  | ttctccggcc | aaagtaataa | gcagtttaca | aaggatacca  | 120 |
| aaggagaagg | aaagccttgg  | ctaaaagtgc | atacgtgcag | gaaagcttct | acattgggag  | 180 |
| ggaaaatctc | gatgcttggg  | ttcgatcaag | agcaaaaacg | aactcatcgc | agatgttgtg  | 240 |
| gcattctgca | gtctccggcc  | aagaacgtta | ttgcatcttt | gcagtcagca | ggtcaacgat  | 300 |
| ccatggtgtg | ttgaagacct  | tggaagaaaa | ataattcaac | agttaattga | aaacttttaa  | 360 |
| tactcaaaaa | taaaatggca  | gacattaaag | ctttgctgaa | caactgggta | acttgacagt  | 420 |
| aaaagaagtt | agcgaactcg  | cactatcctg | aaagaagaat | atggcattga | gccggcgagct | 480 |
| gctgctgttg | tgtagccgct  | gctcctgggt | ctgccgggtg | tgcagctgaa | gaggagaaac  | 540 |
| ttctttcgac | gtagtcttta  | agagtgcctg | agctgcaaaa | ttgcagggtg | gaaagctgta  | 600 |
| aagaacaatg | cggctcttggc | ctgaaagaag | caaaggactc | gtggacgcag |             | 650 |

## (2) INFORMATION FOR SEQ ID NO:635

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 623 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...623

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:635

```

ggccagttcg atattgcttc ggtctgtcat gctctctgcg acaagctgac tatcggcatc 60
cgcatatcta tggcaatgta caggtggaga atgctgccaa gtggtacgca actgggagca 120
actcaaaactc cgcgaaaagg atgggaaaag tccgtcctct ccggcgtgcc gaagtctctc 180
cctgcttttg tgaagactat cggatgcagg agaaagccgc aggcgtaggt ttcgactggg 240
agcaagggag caggtatggc cgaaggttga agaagagctg aacgaagtcc gagggctatt 300
gtcagtgaag atccccgatgc catggaagca gagttcggcg actgctcttc gccgtggtga 360
atgccgctcg tctctacggt atcaatccgg atatgctctc gaacgtacca atagaaaatt 420
cgacagccgt ttctcctatg tgagcagcgt gccaaacagc agggcaaagc tctcagagat 480
atgaccctct ggagatggat gcgctgtgga atgaggcaaa acagaaagga ctctgacctg 540
ttccaagcgg aaaaagctat ctttgtaagc acgatttagc attattacat aatgaacgaa 600
gacattaaaa agaatacctc ggc 623

```

## (2) INFORMATION FOR SEQ ID NO:636

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...753

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:636

```

agcggggcca aaccttttct ccacccttgc caaaaaccag cttccctttt ctaagttttc 60
tattatagca gaaataaatg cattattttc cagctccaag attattccgg gtataatggg 120
tggtgctttt attgttttca tataagatcg accactctat ctgcggataa ttgctctta 180
gcgtaatctg taaattgagc ttacaccaac cttttatcct gtaggctgca atggaggaac 240
aattttgagt ctgcactcag gattatattg attgattgct ttgcaaagat tttcgttcca 300
agaacatttg attgataata ttctttcttt gttgttcgtg aaattgtgcc gccaaagtga 360
caattacatc ttgtcctttt acaaaatcct cggagattcc aagttcgata aatctccttt 420
gataactttg actttatctt cattgtttct atattgctac tttccctgtt caaacagggt 480
attggtgtgt tgtttttgac aataattcaa cgagtctgtt tccaagaaaa cctgttcccc 540
ggttatgcca attcttatca tttttatc attcataaaa tatttcttat tattatcgnt 600
ctctccaaag agtgtagtag gcgtacngat atccatgcgc angaaagcaa gtatggggtt 660
ttcggcctga ttgggaatcg gagactaact aaaagaactt tttctttttt gtgttttcgt 720
ctgaaattcg agaaagctct aaagactacc tat 753

```

## (2) INFORMATION FOR SEQ ID NO:637

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 855 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| tcagtccatg | aagaataggc | agcggatcca | ctccgacaaa  | cgaacggcat | catcttgtaa  | 60  |
| gatgggacca | tccacgtagt | cgttcgggtt | cggccgatag  | taacgatcag | ctttttctgc  | 120 |
| tcctcggcac | aagcctccat | cacataggca | gcgtactgat  | ataagtaaag | aagcgaagtcc | 180 |
| cgacatcctg | catatcaata | gcagcacatc | gacgtcggcc  | aacattcgag | gagtaggttt  | 240 |
| cttgttttgc | cgtagagcga | aacgataggg | attcccgtec  | tgacatcccg | ttcaccttga  | 300 |
| ccgttgcccc | ggcatcggca | tctccacgga | agccgtgttc  | aggcctaaga | tcttgacgac  | 360 |
| attgactccc | tgccgaagca | gattgtcaag | aaatgttccc  | gctccgtccc | caccacgctc  | 420 |
| gtagcattag | ccaccagtgc | ccacgcttgt | ctctgagaag  | aggcaggagc | agctctgtcc  | 480 |
| tctctgcacc | acaactaccc | gtacctcttc | tcttgggggt  | gcgaccgaaa | tctcctgctc  | 540 |
| gaatgagcag | tctgactccc | gacttctctc | ctcctcgacg  | aatgcgctcc | cctgcaactt  | 600 |
| ggcaaccggt | ataggccgaa | aacgacatta | gcccgcctatg | caggctaata | cgatagaata  | 660 |
| tttccggaaa | aagcgaggga | tcatttctct | cgtttactcg  | tcgatgatct | tccaagaaag  | 720 |
| ccttcaatcc | actatcgtaa | gaggggtgct | gagcagaccc  | tttgatggcg | ttgagcgggc  | 780 |
| aagtgccaca | tcggcaccgg | ctttcgaggc | actgaataat  | gtgctgcgta | tgggggatgc  | 840 |
| tggcagcaag | tacct      |            |             |            |             | 855 |

(2) INFORMATION FOR SEQ ID NO:638

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 687 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gaagccaaca | actgttatgc | aagcaattcc | tgaatacgat | gataccggtg  | actatccaaa | 60  |
| agtcaaagta | ttgcctgcga | gtaaactccc | aaacgaaact | ccggtttgcg  | tcataactca | 120 |
| gacaagcaaa | gggattaaca | ttaaggtagg | actgttgatg | cagtcgatga  | tgaaaaccta | 180 |
| aacggacgaa | taataggaat | ttttaccccc | atgatactct | tggccccgaa  | tcggaagaga | 240 |
| aactaaaagg | ttgggggttt | tactctccaa | agcctccgaa | gatttcgatc  | ttcgcaaacc | 300 |
| aatgaaatat | ccatcgactt | aactgttttc | aaagatttgg | ctgttcaatc  | accgaaaagc | 360 |
| attgtaattt | atacggtgag | acaatctcat | acgtgaaaaa | atgacactga  | aaaagggaga | 420 |
| cttaatgacc | aagccatttt | taaaggcctc | tataaggtaa | agaataaaga  | gcatggcaaa | 480 |
| gcgaataatc | cgaggatagg | agacgttttt | gaagtccaat | tagataattg  | caagaagtat | 540 |
| ttcagtacat | cgaaatgac  | atgacacagc | tcaacagtag | cgtaataacta | cttttgtgga | 600 |
| agaatacccc | ttggactgtt | ctccgatctt | agaaaattta | cccgcgggta  | agggtgattt | 660 |
| tatgcacata | cagtcctccg | atggggga   |            |             |            | 687 |

(2) INFORMATION FOR SEQ ID NO:639

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3856 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...3856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gccgtttgct  | gttttcgtat  | ttttgtaaag  | tggcagccgt  | tttattgac   | ccacctgggc  | 60   |
| ccggacatcc  | tcgttatgtt  | tatcgaaaag  | ttccactaac  | tgtttaatgt  | atccgtctgt  | 120  |
| ccgcagtatt  | ccgatttgat  | cctctccgcg  | tcaaatcatc  | tactgttact  | tccaaacggt  | 180  |
| tgtaaatggt  | cagaattcag  | ccctgatttc  | ttcgatcttt  | cgattgactt  | caagtgtctc  | 240  |
| tgcacatgtc  | ctttgacttt  | ttctttttct  | gaatcccata  | attgggcatt  | gacaacaggc  | 300  |
| ctgtagaccc  | cagcgacaaa  | cgctccttat  | tcagataaat  | ccgatgagga  | tgggcgtctt  | 360  |
| gccttctttg  | ttgatgtaat  | tgctgcgcaa  | gtaaaaactg  | aacgaaattg  | actcttcatt  | 420  |
| ttgctccaaa  | attagtgtaa  | catacggcta  | caaagtctga  | catatgattt  | tgaacacagag | 480  |
| caatttgtea  | tcgtctaaac  | atcgtcttaa  | cgctgtctgt  | ggttacaatt  | tttcagccct  | 540  |
| ttgttttttg  | taacccaaaat | ggaaccaccg  | gaggcatatt  | tacggaatta  | cgcttattcc  | 600  |
| gaacctcatc  | cgacgtgtgg  | ggtggcgaca  | aagaaaagcg  | ccttaattcg  | ttggaattaa  | 660  |
| gacgcttttg  | gattcgtttc  | taaaatgctt  | cagatgacct  | atagcctatc  | tttcagctat  | 720  |
| ttagcgggat  | ggacggactc  | gaaccgcga   | ccccctgcgt  | gacaggcagg  | tattctaacc  | 780  |
| agctaactac  | cacaccgttg  | cgaatgaatt  | tacctctttc  | agcgtcgcaa  | agaaagtttt  | 840  |
| ttcctcaata  | tgcaatagtc  | atcaaaaaat  | ctggacattc  | catcaccagt  | gcaacattga  | 900  |
| gtagctaagt  | tagttctaaa  | acttggcatg  | ggttagatgc  | cctagccctt  | ttcgaggctt  | 960  |
| tcgattaagt  | ttgtcttgta  | tcttccacaa  | tgtggagatg  | taacttatgt  | tttttaggta  | 1020 |
| ttaggatgta  | ataacagttt  | ggcaagggat  | agatcgagag  | gagtagtcaa  | tttgatattt  | 1080 |
| cgatattacc  | gacaatcaat  | gccaccggtc  | ggccaaaaatg | gtgttcaata  | ccgaacaatc  | 1140 |
| atcggtaaaa  | tactcttcac  | agggttgctg  | ataggctctc  | gaagccattc  | gctccgaag   | 1200 |
| gtctgtggag  | tttgtaccgt  | gacgtccgac  | tctgtccac   | tgcataattg  | ccatcatggg  | 1260 |
| cataatagcg  | aagcattcgg  | tcatagggcg  | acaaggagcg  | acagccccct  | tcaactctgc  | 1320 |
| aagtcgaaac  | aggcatcgat  | agtttcagca  | ctgacccaaag | gacgtacccc  | gtatgaacag  | 1380 |
| caacccaaaac | accatcaggg  | acaacctgca  | atccattccg  | acagaggcga  | aacgtgtatt  | 1440 |
| tcacactgca  | accactcgat  | gagagaccga  | aagtcatact  | tccggcacaa  | ttcctgccaa  | 1500 |
| taagcatgat  | gatctgtggc  | aataccaata  | caatagcatc  | gacatgaggg  | gcaaagcgat  | 1560 |
| tcagcgtagc  | atcagcaccg  | gtagaccggc  | caaaagcaaaa | aactgttttg  | gccgatcgcc  | 1620 |
| cccatacgta  | gcccatagac  | accggctacg  | atcagagcat  | agcgttttgc  | tccatgagag  | 1680 |
| tttgccatg   | agttcttcga  | tctgcttgtc  | ggctatgtca  | gtttctcag   | acagaaacca  | 1740 |
| atcagagcaa  | tagcctcttc  | ggccgcttgg  | tcagctcgtc  | cacatccggg  | ctttcatggt  | 1800 |
| cgatgacacg  | aacattttct  | cgaggcgtct  | catggcctcc  | gtataagtct  | tattctcact  | 1860 |
| caaataatgg  | caaaaataag  | gatttgcaga  | agaaaaccgta | aacgaatcct  | cggatcaaac  | 1920 |
| tctaaaaaca  | gatgagaaat  | actagaagta  | gccgaatgag  | aaaaaaaactc | gccctaagg   | 1980 |
| gaggagggtt  | ccgtttttgt  | gaactcacc   | aataaatcca  | aagatcaatt  | ccggtattgc  | 2040 |
| aagaccatct  | taacctgttt  | tcggccctta  | tatttcgatc  | tcaccacaag  | aaaaaactaa  | 2100 |
| aaaaataatc  | atcacggcat  | taacataaaa  | gccactatc   | atgtttttta  | caaaaactat  | 2160 |
| tattattgta  | gtagacaaat  | acaagaccta  | attatgatta  | atataatacg  | cgactaacta  | 2220 |
| tcctgacatt  | tcttggtatg  | gtctttatgc  | tctcgccaaa  | gagattaatg  | tagattccct  | 2280 |
| tttccaaata  | gcggccgacc  | ggatctttct  | gccacggaaa  | agaaaaaaag  | gtatgaggag  | 2340 |
| atggggcaaac | agtcgaactg  | catcaacaag  | tcggtagtgc  | agccgatgca  | tattccttag  | 2400 |
| catcaagttc  | tgccgtgatg  | gtggctcgac  | cgaagagctt  | ccattttctg  | tttaaagtat  | 2460 |
| gcaaccatgt  | cgactcatgc  | aggtcgttat  | agcaatgcat  | aatggctcta  | gaagaaataa  | 2520 |
| tgaggctgct  | taaagacaaa  | aacgacaaat  | tatattagcc  | cgcacttata  | tgcatagtag  | 2580 |
| catcgatttt  | ttctttcgga  | aaagtgggat  | gaccgcattg  | gtattctatg  | aacgtgcgct  | 2640 |
| acaaatgctc  | aaaaagaaaa  | aggaggaaaag | aggtatctct  | atagcctaca  | acaactggct  | 2700 |
| aacattttatc | aaaaaaaagg  | aaatactcaa  | gaagcctact  | cctatataac  | aaagctttgg  | 2760 |
| atatacaacg  | aaccaatggt  | gatagtgtaa  | gtagtgcac   | agtctcatga  | atatcggcac  | 2820 |
| aattatgac   | aatgagaaaa  | atctgaggat  | agctataagc  | ctttgaaaga  | agctcttaca  | 2880 |
| atagcatcca  | aataaatgat  | atcgagatcc  | aggccctatc  | ttatgcacat  | cttgcatatt  | 2940 |
| ttatgcatgg  | agaagcgaat  | acggcaaaagc | aatgaagtg   | ctcacaatcc  | agaaaatttg  | 3000 |

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| gcatgccatg | ccgggtataa | tcaaaccaga | ttggcaattt | ggatatagcc | agttccatat  | 3060 |
| atgccgaata | cggtttgtac | tcttttggtt | tgaatgcca  | aaaagatcca | aacttctggc  | 3120 |
| agactctatt | ccgcgaaca  | gatgcaagaa | aaaattacgg | agtttgacat | tcggttcaaa  | 3180 |
| agcaagagaa | agaggccgaa | atagcactga | aaaaccagga | attacattta | gctccaaatt  | 3240 |
| acatatggcc | cttatcataa | tatccacact | gttggtggca | acctcattac | ccttatcatc  | 3300 |
| catgcagcaa | ggagatacag | acaaaataag | agctgcgaga | aatgaatgac | accagaaaca  | 3360 |
| gactcctctc | cattatctca | ccgacatcaa | gggtccggct | atagcacaga | aaatggccct  | 3420 |
| cgacactata | tatcatcttc | atctgactgt | ggctctatga | ctcggaatat | gctttcttca  | 3480 |
| tacgcaatag | tgtagcaaca | gaattgactc | ttttacagaa | tttactcgtt | ggtctaatat  | 3540 |
| ccaaatcggg | aatttagctc | ccaaatttgt | ggttttcaca | ttgtggaaaa | cattggaaag  | 3600 |
| gtgatcaatt | tatactctat | ttctgccgga | ataaagatat | tagcttacat | ttggaagctc  | 3660 |
| ctaaacaatg | tttggtcatg | ctgaccaaca | aatgatcaat | accgtaatac | gcaattttact | 3720 |
| cagtatgcaa | tcaaattctc | taaagcagga | agcgtaatat | acatccgtgt | ggagaaaaag  | 3780 |
| agaaagccat | ggggatcaaa | gtgtctgtat | cagacaaaag | tatggcatga | gcaaaaaaca  | 3840 |
| aataaccgat | atcctc     |            |            |            |             | 3856 |

## (2) INFORMATION FOR SEQ ID NO:640

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| aaccggctgc | catccggcgg | atcaactcga  | caaagtcgga | tccgattcga | qcatgacgac  | 60  |
| ttccgtttcc | ggatctccca | tacggcaatt  | atattctaca | cataaggatc | tcctcctaca  | 120 |
| ttcatcagtc | ccacgaagat | gaatccggat  | aatcgattcc | ttcggctatc | agtcccagata | 180 |
| tcgtaggccg | gataatcgct | cttcacacct  | ccgcatgaat | gcttcacgga | cgaaaggtag  | 240 |
| tggcgaaacg | tccccattcc | gccgggtattg | agcccggtat | ctccatctcc | gattgcttat  | 300 |
| aatcttttgc | gactggaagt | atgtgatagt  | ctttgccatc | ggtgcaacaa | atacggagca  | 360 |
| ttctatgcca | tcgagaaact | cttcgatcac  | caacgacggc | ttgcagcacc | gaatttgcca  | 420 |
| ccgagcatct | cagccaaact | cgtttggctt  | cttctgcagt | cggagcaata | atcacccctc  | 480 |
| tgcggcgccg | aaaccatcgg | ctttcagtag  | ataaggagcc | tgcacgtat  | ctatgaatgc  | 540 |
| ttgcctgcat | ctgtttggtc | agccgtgaat  | gtctgataag | cggcagtaga | atcccgtgtc  | 600 |
| gtttcataaa | agacttgctg | aaatccttgc  | ttccttcaac | cgtgcaccct | tggcatcggg  | 660 |
| ccccacaatg | aggagatcgt | gcagtggctg  | tgatttcgga | agtagtccac | tatgccacgt  | 720 |
| acaaggggtt | cttcagcccc | actaccagca  | ggtcgataga | actcgcgctg | taccacttgc  | 780 |
| gcaacggca  |            |             |            |            |             | 789 |

## (2) INFORMATION FOR SEQ ID NO:641

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO



(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

```

ataaacaag ttttgaaca tatatccaaa gatttnattt atatatccga ggcttcggac 60
agagattttc cggccggaaa atttattttt gtcggttgcg ggaaaaattt tcccggcccc 120
gaagaaaaca atcgaccggc gatgagtaac cgatatagct gtacagaaga aatggccaag 180
tttgtgatga gagaaagccc gatatgcaag gcacggggcaa gcggacgatg tatccgaaaa 240
tgatcgccga ggcacgatgg ggctggacga gatagccgat ctgatttcct cccatcgaca 300
ttctccccgg gtgaagtcaa agggttggtt acggccttgg ctcgacgata gcccacggcg 360
tggcttcggg atatacgggtg aagatagagg agtcggctct ttctccgctt cgctcacctt 420
gcacaaaggc gtagaacccg agaggccgaa ggcggcacac gccgtaatgc cgccagcgtg 480
acgataggag tgtcaatttc cgccccgaca aggcattgat tctcgaggct cgtactcgct 540
tcactctggtg cgaactacgg tacgcccgtc ccgtcggccc aatttgaccg cgaagagcgg 600
ctggccttgg ccttgcgcca tctcgatggc catagtcgct caagggtggc gattattgca 660
gacttacggg gctgggacgt accgctccgc ggaagaattg cgcgctttcg atcgcgagg 720
tctgatcgac tccacgggag cggcacgcat aaggtatata ttataaggaa caaagccggg 780
atctacaagg cgggaagacc accgttacgg gctttttgcg ttcttaagaa ttggctattt 840
ttgtgtgtgc aaagaaagat gtgtcggata ggcgaaacct gccttgccca gttgagagtc 900
cgagtcggtg ccgggagaca gagagagaaa gtattcgccg aatttttttg tgcagtctaa 960
cctcataaca tagatttaat agtcttatct ttaccgccat tgcgtatatt cttttcatcc 1020
ttgctatata gacttgattg tgggtgtcag caacgatgcg gtcaacttcc tcaattctcc 1080
atcgagacca aggctgctcc attcaagatc atcgctgggtg tggcagcttg ggggtttttt 1140
gtggcgcgac catgaacaac ggcattgatg agatcgccga cacgggattt tcaggccgga 1200
acattacact ttcagcgaat tgatgtcgta tttctgtcgg ttgtgatcac cgatgtcgtc 1260
ctgatggata gttaatttcg ctcgcatgac ctacctctac gaccgtctcg ctcattttcg 1320
agcgttaggc ggttcttttt ttatggccat gaccaagggt ggcggtacgg tcgcttttcag 1380
gatctttctc atacggagaa agctcttttc gtcattattg gatcttcctt tcgggtggaa 1440
ttgctttctt cttcgggatg gtcgttcagt tctgagccgt ttgctcttta cttttaatta 1500
caggcggaat ctccgatggt ggccggcctt ttcggcgagg ttgcggttac atccatcatt 1560
tatttcattc catcaaaggg ctgaaggcgg tgtcctttat gaccgaagaa tccacggttg 1620
gatagctgcc aatacgggca ggctggatatt gtactgtctg gtcgttccat tatcctgatg 1680
cagggtgctg attggctacg ggtcaatgtc ttcaagtgat cgtcctcttg ggtaccttcg 1740
ctttggcgat ggcttttgcc ggcacgactt ggtgaacttt atcggtgtgc cgtggccgg 1800
ttattcctct tattggactt caatgccaac ggaaacgggc agtacgatac ttatctgatg 1860
gggcttgtaa cgaaccggct tccactcccc tatatttcct cgtggctgcc gtatcgtaat 1920
ggtatatgcg ctgattacat cgaagaaggc tcacaacgtg tcaagacttc ggtggatctg 1980
gcgcgtcagg aggaagggtg ggagatgttg gtccttcggg cttggccccg agtatcgtgc 2040
gtttcagcac cacgacggca atgccgtgtc ccgtataatt cctcgccccg taggccgggtg 2100
gatagacgtc gcttcaatca ggacgaactg atcatggcca agggcgcggc tttcgattgg 2160
tgcgcgcttc ggtcaatctt gttcttgccg gactgctcat cg 2202

```

(2) INFORMATION FOR SEQ ID NO:642

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| aattgctctc  | acgttccttt  | tgcacgcact | ctattcgtgt | ttggttcagt | cgcgaaaacg | 60  |
| ctgtagcaag  | tctttcagac  | gctcttcgtt | caagtccgtt | cggccataga | cgaagttgta | 120 |
| ctgtcggccg  | attctcctgt  | acgagccgct | ttttcttata | gaaagcactt | ttgtaggcct | 180 |
| ctacttcctg  | tcggcgggta  | gctcttctcc | ttggagtaat | atggccaagc | tgtcaagtag | 240 |
| ctcgactcgg  | tcatgtccgc  | caaacgggcg | tttacacttg | ttttactttc | ttcgctgatt | 300 |
| tggattcgtt  | ttccaaagga  | gtcggatctg | ccacttccag | gcttgagcct | ccggcaaccg | 360 |
| gtctgtttgc  | gtaggtttca  | attcttcgga | ttaggctgtg | ccattgaatc | cgtgagaggg | 420 |
| ttcgtagggt  | tttccatacg  | tactgcttta | atgttcactt | ccaccgaaaa | cctcctgtcc | 480 |
| ggagagatac  | attcgggtact | tttccaatac | aacggaaggt | aattatcaga | taatgattcg | 540 |
| ttttcaaaaag | accaaattaa  | agaaaaaata | ttgacagacc | ataatttgaa | ggtgtttgca | 600 |
| gggcaaggca  | ttcaaaaaca  | gcattctata | aagtttttag | tccgttgaat | gaagtcgctc | 660 |
| ggtcatgtat  | tcaagtcact  | atcgggaaaa | tcctct     |            |            | 696 |

(2) INFORMATION FOR SEQ ID NO:643

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 954 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| ggtctttcca  | ttcaattcgg | acttcgtgac | gatgaatcgg  | cggctcacca | atgcgactcg | 60  |
| gtaggtatcc  | actgcttcct | atccatctgt | acctctgtcc  | gatgaagctg | ctaatacccg | 120 |
| cagtattttg  | cggattggta | attacgaaac | cctgtcgttt  | tcatttagaa | ccgtatccga | 180 |
| atgtgccagc  | gaaatatgtt | ggtacgcgaa | tccattgtgc  | gcgaaatcac | gtagtcatga | 240 |
| ccttttagcag | ttggcggact | tccgctaatt | ttttggagaa  | aacggccgga | tttttacaac | 300 |
| cagagagagt  | gcgatagcct | gattatcatc | gttatgttcc  | agatgtccat | cttctctttc | 360 |
| tctttggcca  | cactgatctt | gaaaatagct | cgacgatcag  | catggacgca | ataatcccca | 420 |
| ccactccgag  | cggataagcc | aagcataacc | gagtggtgata | gtcggatcgc | cggttcccgt | 480 |
| tagatcatgg  | atgtctgtct | ggcagctccc | aggcccgggtg | tgttcgtgac | ggcaccggaa | 540 |
| gaattcctac  | cattgtggac | atggatatgc | ctgtcacgaa  | gtgcagaaca | ccgttgtcag | 600 |
| tacccccaga  | aagacgacgc | ccatagccag | taggttcagg  | taagccccc  | cttgcaaga  | 660 |
| gaggagaaaa  | aacccggggc | cacttgatcc | ccaccgagta  | aacgaatagg | atcagtcgga | 720 |
| actctttgaa  | gaaatatgta | cgtcaggatg | cagattcatg  | ccgaaatgtc | ctaagactat | 780 |
| tccgcaaaaa  | gaacgaaagt | aacccccaaa | gaaattccga  | agatctttat | cttcccaacc | 840 |
| aaatccctaa  | ggcaatcgtt | acggcgacca | agagaatgga  | gtccccactc | ctacaccgaa | 900 |
| aagcaagtca  | ttaagccatt | gcatttcat  | caaacaggtt  | atagtagtca | atag       | 954 |

(2) INFORMATION FOR SEQ ID NO:644

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 567 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| gatccccagt | tttcaagacc | aacggttgga  | agtatatagc  | ggtattttacg | tcctttattca | 60  |
| tttcgctgac | ttgctcgcgt | actatccggt  | acattttcca  | ttggcttccg  | cctgtttgtt  | 120 |
| ggccaaagct | tgtgtcatgc | tgagttcaat  | ctttggcctt  | cttcttgcat  | cttcaggatt  | 180 |
| ttctcctggt | ccactctgca | gcactcttcgc | tggtgaatgc  | attcgtccga  | agacggcggt  | 240 |
| ggaaacctcc | gcagctttct | gcatggcagt  | catcttggtg  | gccaagggtc  | tttgttctgc  | 300 |
| tcagcttcgg | ccgcaagttg | tttgttcatg  | tccccgaaagt | attatatattg | gaggccaggc  | 360 |
| tgtccatcct | tacgaaaagt | ataggcagag  | tgcggcagct  | tggttctgcct | tatgatttgt  | 420 |
| tgtcttggt  | tttgatgccg | agaacgcggc  | atcataatga  | agaggatgat  | gatggcaacg  | 480 |
| gccagtacaa | cctcgatgac | ataatggatc  | tgtttcattt  | gtgaatggga  | tatgtttttg  | 540 |
| gttcgtatta | ttcgagttct | ttgattc     |             |             |             | 567 |

(2) INFORMATION FOR SEQ ID NO:645

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1259
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| gcaatataac | cacggaagac  | aaatggctcg | gtcaggctct  | ttgtattgct  | cggctgaagg  | 60   |
| aggcccatcc | gcagacaatg  | gtgaaagtga | tatccagctg  | agaatataat  | cgccaatctg  | 120  |
| cttaccaggt | atggctatac  | caagatttca | aatgttatga  | tccgggagta  | actcctaaaa  | 180  |
| acattattga | tgctttaacg  | gaggaatctc | gttggccaac  | tatacgggcc  | acggaagcga  | 240  |
| aacagttggg | gtacgtctca  | cttcggcacc | actcatgtga  | agcagcttac  | caacgcaacc  | 300  |
| agctaccgtt | tattttcgac  | gtagcttggt | tgaatggcga  | tttctgtaca  | acgtaccatg  | 360  |
| tttcgcagaa | gccctgatgc  | gtgcacaaaa | agtggtaaac  | tgacagggtac | tggttgctatc | 420  |
| atagcgtcta | cgatcaacca  | gcttgggctt | ctcctatgcg  | cgggcaggat  | gagatgaacg  | 480  |
| aaattctgtg | gaaaaacacc  | cgaacaacat | caagcgta    | ttcggagggtg | tcaccatgac  | 540  |
| ggtatggttg | ctatgggtgga | aaagtataaa | aaggatgggtg | agaagatgtc  | gacacatgga  | 600  |
| ctgtattcgg | cgacccctcg  | ctgctcggtc | gtacactgtc  | ccgacaaaaa  | tgcagggttac | 660  |
| ggctccggct | cagattaatt  | tgacggtgct | tcagtcacacg | tatcttgcca  | ttataatggg  | 720  |
| gctattgcta | ccattcagcc  | aatggaaaga | tggttcgggtc | tgacagttgtc | gaaaatggaa  | 780  |
| cagcacaatc | aatctgacag  | gtctgacaaa | tgaaagcacg  | cttaccctta  | cagagttggt  | 840  |
| tacaacaaag | agacggttat  | taagaccatc | aacactaatg  | gtagccta    | ccctaccagc  | 900  |
| ctgtttccaa | cttgactgct  | acaacgcagg | gcagaaagta  | acgctcaagt  | gggatgcacc  | 960  |
| gagcacgaaa | accaatgcaa  | cactaatacc | gctcgcagcg  | tgatggcat   | acgagaactg  | 1020 |
| gttcttctgc | agtcagcgat  | gccccgaac  | ttcttcgcag  | cggtcaggcc  | gagattgtct  | 1080 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgaagctcac gatgtttgga atgatggatc cggttatcag attctttgga tgcagaccat  | 1140 |
| gatcaatatg gacagggttat acccagtgat acccatctct ttggccgaac tgtatgtccc | 1200 |
| ggccaatctg ttcgctccgt tcgaaatacg gttccggaaa agcagatcct tcttggtcc   | 1259 |

## (2) INFORMATION FOR SEQ ID NO:646

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...356

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| getgtccggt tccctatcct ccacgggcgc atggcttggg gtggagtatt tccgagagct | 60  |
| tggctcgcag gcatacggca cctcttacga ggagggtacg gcttcgtaga taatatcctg | 120 |
| tgggcggaag tagtagtaac cattgtcctc agcagggcac tgatggctcg acgctcttcg | 180 |
| tgcagctttg ccaaatgaac tggctcctt tctgatcaa agacggagtc tgcctgtaag   | 240 |
| ccagatgctg tcggggaaag tgctgatcgg taagggaatg atgctgtcgt aatgtaagga | 300 |
| gaggccatat ccaccgtata ggagattttg gctttgagcg agtctttttc agagtg     | 356 |

## (2) INFORMATION FOR SEQ ID NO:647

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2191 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...2191

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tagaggatcc cctggaaaaa attccttttc atttttgacc gcctgtcata ctgatcgcta  | 60  |
| tgccttttta gcaacgtttc cttcacttgg gcaaagaaat tatacttgaa gtgaacagaa  | 120 |
| cagccttttc gttttttaat atagagcgag cataatccga cctcggccat tctttcagaa  | 180 |
| aaagcgaaac gcaatccaga aataatggaa cgagaatctg aaaaatctca cgccacaaaag | 240 |
| ttttcttttg gtttgaaaat ttttcctttc cgacgcagga aaaaaatatt ttaccgcgac  | 300 |
| tttttgagtc ctcttaagta aggtattttt ttttaacatac ttgaccgaat tatgcatcta | 360 |
| accatagtgt agaatcctca tctgtaggta attgcaccga acaaccgatt tgtcagtaca  | 420 |
| ttatgtctga cgaaacgcgt attttgactt caaatgaaag aaagattgaa ccaaaccgta  | 480 |
| cgctattttc gcctatactc ttcgcagtat atgccggcct ggtcatatct ttcactcact  | 540 |

```

ccatatcatc aatggcggtga tcatcggtcca ctcccacgta cagtggggga caacgaaagc 600
gatccgcagg acaatccgca ttcggattcg gaattgatct gtacaatcag ctttcggcca 660
tattcacgac ttatttggat acgcccgcac agacttgaaa gaacctgtga ggggtgtcgg 720
cgtcgttcct ttctttgcga taatcttact gctctcattt cggagctaac tccttccaat 780
catccagggc tcctcccgtg gcctgatcca ttcttacctt atttcggacg atcattcatt 840
cggatggtat tgcgcgcgct tacaatgaga tccgttgcat cgcacttgta gatctgcctt 900
tctatgctga tttatcaagg ggatcgaatg tcatccatag ccgtgatgca aggattttca 960
tcctttcttaa taccgatctt tcgtgggata gggagtggga cacactctcc taacctcaaa 1020
aaccgactaa aaggatcgga ataaggatac cgaacagaca ctatatccat atcaagccat 1080
caaaccacaaa aataaaatga aacaactaaa cattatcagc ttcatcatgc tttcctattc 1140
ttaggaacga ggcgatcggc tcagcaatcg ggcggaccgt tacaggtacc gtagtggaca 1200
aaagctcaaa agaacctatc gcatagtaca agtattcgtc aaaggaacca ctctcggaac 1260
ttccacggat gcaacggaaa ctactcgatc aagggaatcc cttcgggtaa tcaaactatc 1320
gtaccgcgact catgggttac tccacttgcg aagaaaaagt acatatagaa aagggtggtc 1380
ccgccacgta gacctctatc tgaccgaaga gattctctct ccgatggggt agtggtatct 1440
gccaatagaa acgagacttt ccgccgtcaa caccctcggt ggtaacggtg ctgtcgccgg 1500
aacttttctc caaaaccaat ctaccaacct gagtcaggga cttaagttcc agcccggctc 1560
gcgcgtgggg acaactgtca gaactgcggt ttcaaccaag ttcgtatcaa tggactcaag 1620
gagcctattc gcaaattctt atcgacagcc atcccattct cagttccttg ccggtgtcta 1680
tggcttggag cagatgcctg ccaatatgat cgaactgtag aagtaattcg cgggtggagg 1740
tcggctctgt tcggctctaa tgcttgggag cgtttatcaa cgtaattacg aaagaaccgc 1800
ttcgcaattc ggcgagatca gccattctac gatgaccttc gaccacgcga aagggtgggg 1860
gacttccaaa atacgaccca gttcaacggt tctatgctga cggaagaccg caagccggtg 1920
tcatggttat cggccaacac aactaccgtc ccggacagga atagacggcg acaactttac 1980
cgaactaccc aatctgcgca accgctcgcc ggtttccgct catactataa gaccgggtcta 2040
tacagcaaaag caaccctcaa tatcacagca tgcaggagta ccgtcgtggt ggcgacagac 2100
tggacaacct cttttcgaag ccagatagc ggaatatctc cagcactata tcaatgcgga 2160
agtttcaaat tcgatcaggg cttcagcggg g

```

## (2) INFORMATION FOR SEQ ID NO:648

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...919

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

```

catcgaagtt ctattttcat caagcgctcct tacatctctg ttgtgggcat attcagaaga 60
agattctcgg agaactttcc aaaggtgaac gctccagtat ggcttttatag accgcattct 120
atttgtgatg cctaattcttc agcagaagcc cgatggagca gaaccgagct tccagatgat 180
acagagaaac gctgggagggt attattcgac ggtccataga cttaccatgt gccaaaggatg 240
aagaagggaa gttaccctctg agattattcc ctttgaagaa gatgccaaag ctgcctctat 300
atgtggcagg aagagcatgc tcgactatgc gatactgagg ctatgaagta cttgtaggag 360
tctattgtaa attagaaatc tacatcatcc gttttgtctc attattcagt tggctcgatg 420
ggtatgtggc gaaagtgaag atccgctata gacctgacat ctgtggagcg agccatcact 480
cttaccgagt tttccgccat tcggcacagc aagtacacgc agagatcgca ggtgttcagt 540
cactcagcaa cagcaacaac tccttgccga gctaccagca tcttttcaac tgccgaagcc 600
ctgagtattg cccaaaaatt ggggatgaaa gaaagagttt taaggatttt ctcagtcgta 660
atatcggaca cctctttgct aaggaagaca cggactttac cataaactca atatgtaacc 720
gagcgcactt tctgcttctc agcatttcgc cacccttat taaaccgaaa gtgtacaaag 780
tgcaatagtg tgccattcaa atcaatttta tcaatgagca attatagatt caattagaac 840
catacaaggg tgtgcggaca cggcatacct gccatcgtg cgacgtcctc gatgcttcgc 900

```

tcgctatatt gacacagag

(2) INFORMATION FOR SEQ ID NO:649

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 936 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| gaagacgatg | tgacggagga | ggaattgctg | gcctgcgtgc | atcgccctgat | caggatccga  | 60  |
| cggtagatgg | cttcacgta  | cagctcccc  | tcccgaagat | atcgacgagc  | agaaaaatcat | 120 |
| cgaagcagta | gacccgcgca | aggatgtgac | ggatttcac  | ccatcaacgt  | aggccgtctg  | 180 |
| agcatcggtt | tgcccgtttc | gtctcggcca | caccgaagg  | aatagtggaa  | ctgcttcgtc  | 240 |
| gctacatata | cctaccagag | gcaagcattg | cgtagtattg | ggacgcagca  | atatgtaggc  | 300 |
| aagcccgat  | cgcagcttct | gtccaaaag  | ggagagccgg | gcgctgcacc  | atcaccatct  | 360 |
| gccatagccg | taccctaac  | atcaaagagg | tagtctgacg | gccgacatta  | ttattgcagc  | 420 |
| tttggggcag | cccgaattcc | tacagccgat | atggtaaagc | ccggagctgt  | agtagtggac  | 480 |
| gtaggtacca | gcttgtagcg | gactcgacac | gcaaaagcgg | tttccgtctg  | acggggcgact | 540 |
| caaattcgat | gaagtggccc | ccaagtgcct | gtacatcact | cccgtaccgg  | cggagtaggt  | 600 |
| ccgatgacca | tcgtatcgct | catgtccaat | acccttcggc | aagtaaagga  | ttgtaccggt  | 660 |
| aaacctcct  | tcccttattt | gccaacacct | tatcgaagag | gcccgtcatc  | aatatcggtt  | 720 |
| cgtccggtat | gatgacggcc | tcttttctta | ttgacagtgt | gtcatcatgc  | gcaaattgct  | 780 |
| gcgtgcttgc | ggcattcggt | tcttagcgcc | ttgnacttta | cgcattctta  | ctccctaaaa  | 840 |
| tggggtatgc | caaaaccgaa | ttttgacacg | ggctccctcc | tgcgatactt  | tcaagaattc  | 900 |
| gcttcgtatc | ctttccgtta | ggaggtaaag | ggtact     |             |             | 936 |

(2) INFORMATION FOR SEQ ID NO:650

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3434 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...3434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650

tgcaccaacg gttcgccttc gttggaaaaa gaccttcgcg atggccttga tatggaaagg 60

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| ctcatgactg  | gaaagcgtga  | acagcgtacc  | tacgaaagtt  | gtttcatacg | gctgagttcg  | 120  |
| tccacggcat  | gtagtaagaa  | cgggctctcc  | cagatgcccc  | atacgccatc | gaaatcttca  | 180  |
| tcgtgggcat  | actctgcttg  | ccgaaataaac | gtttgtagcc  | ggcttggttg | acaaaagcat  | 240  |
| cgaagccatt  | gatccgtttg  | gtgcaccatg  | caagaaaatg  | gattgataac | cgatcgcccc  | 300  |
| agagccgtcc  | ccaatccttc  | aatctcattg  | cccgaatagt  | gagtgtaatg | aagtgtgagc  | 360  |
| ggaggggaagg | caacgagcct  | aatatggacg  | gctggcatcg  | atactcttgc | gcccgttggc  | 420  |
| aaaagcctgt  | tcgaaaaggt  | acccttttgt  | gaaatcgagt  | cgaagcaggg | tgtatatcct  | 480  |
| ttgtaatcgg  | aatgtcttgg  | ttcagccgtc  | ctacgtattg  | gcgagcaaag | ctttcgatgt  | 540  |
| tatcaccatc  | acgttgcgtc  | cacgcaactg  | actgaaaacga | gctgtcgttc | cgctcgccaaa | 600  |
| tgatgaatgg  | gattgaatac  | ttgtctcaac  | tcctttttgga | ggcataaaaa | cgcttttcct  | 660  |
| ccaatccctg  | tttgccaatg  | gtacgatgat  | gctgtagggc  | gtgttcagta | ccaaagccct  | 720  |
| atgttccact  | ttgtcaccga  | cagattggca  | taactcattg  | tcataggacg | ccacgacttg  | 780  |
| gcaaactgcc  | tnctcgtata  | ccccatacga  | taaatgcaat  | agcggcaacg | aggctaccaa  | 840  |
| cgtgaactgt  | ataataatgt  | aggctgtctt  | tcgcttcggc  | atggtgcgta | ccggcttgac  | 900  |
| ccgatgatat  | agccatacca  | tagcagcaac  | gggactatag  | ccagcaggct | catataccag  | 960  |
| taattcagga  | gaagatgcca  | atcagtcctc  | cgccctcatg  | gctgaattca | gagaaaaacg  | 1020 |
| tcgaggatgt  | cgtttcaagg  | tgtatggata  | gtaaaatacaa | tcggccagac | ctgccgccgc  | 1080 |
| cccaaagcat  | ttggcacgaa  | aaagggtccag | tcggtcagga  | ttcgatagat | cgcttggcac  | 1140 |
| gaaacctgaa  | cggcagaaaag | ctcaacagaa  | taaaaaggca  | ttcaaatata | aaacggaagc  | 1200 |
| cgtgtcgaac  | ctaagccctc  | ccatcatgca  | cgccatacct  | gctcggcagt | catgtcggca  | 1260 |
| aaaaagcgat  | agttaagagg  | tagaacagtc  | cacgggcaat  | accgaaaagg | aaataagcca  | 1320 |
| atgcatacga  | taggcaaaaag | cccaccagct  | gttcggtcgt  | atcgctccgt | taaaaatattc | 1380 |
| atatctcttt  | gtgtgtgttc  | tattcggatt  | ggaggcaggg  | acgagggtaa | tgaatgattt  | 1440 |
| cggtcacata  | cccccccaat  | tgagcctatt  | catgattcgg  | tgacagatgt | atcccgttgc  | 1500 |
| accggcattg  | gatctgatga  | gtctgctgtc  | gcgcgggatg  | cggcgtccct | ataggccttg  | 1560 |
| tcogtttgat  | tcgcttgatc  | aggttgccaa  | attcctctgc  | tgaggatacg | gagaagctcc  | 1620 |
| gccgacatct  | atcaattcac  | gggcttcctt  | gaatttctca  | tatcgtgtcc | gaaaataacc  | 1680 |
| ggtataccat  | agactgcggc  | ctcgggtgta  | ttgtgatgcc  | tttgccgaat | cctcctccga  | 1740 |
| taaaagctac  | ttgaccgtag  | cgataatgga  | ggataggaga  | ccgaagctgt | ctacaatcag  | 1800 |
| acaatcctgc  | cggcaatatc  | gctttccgta  | gcttccgaaa  | gtcgtatgaa | aggccgtcgt  | 1860 |
| attgcgatat  | gatctgaagc  | aaatgttctc  | tgctgatctc  | gtgcgggtgc | atatgagttt  | 1920 |
| gatcttggga  | tttcgattga  | agtagcgtac  | gagtatctct  | cgtcgggagg | ccaactgcta  | 1980 |
| ccgcccacaa  | tgaccaaacc  | gtcttccgga  | cggaagcagc  | aaaacgctct | atcagcggaa  | 2040 |
| gcgatttccg  | agcttcatta  | cggagatcac  | ccggtcgaag  | cgctatctc  | ccgctacgga  | 2100 |
| tacatggcta  | tcccatgctt  | ttcaagtagc  | aggcgtgaag  | ccttgctctg | aacaaaatgt  | 2160 |
| gtgtaaagca  | gtgtagcaaa  | cgtttgtatg  | ctcctccata  | ccagcgaaaa | acagctgtga  | 2220 |
| cggtcggaag  | atggatgaaa  | ccagataggt  | aggttctgcc  | tacgtcccaa | ttctgtcagg  | 2280 |
| aaacagggcc  | agaagtcgta  | tttatgaaaa  | tagccatctc  | aggcttgacc | agatccagaa  | 2340 |
| acttacgcac  | tcggcaaacg  | atctgccggc  | aaatacacga  | tcacgtcggc | accttcgtaa  | 2400 |
| tcttacgtac  | ctcatatccc  | gaggggctga  | agaaggtaag  | cacgatccta | agtccggata  | 2460 |
| ttcgcttcgg  | atgcgttcta  | tcacggtctc  | ccctgctca   | attcgcccaa | agaagctgca  | 2520 |
| tgaaaccata  | tatagcgccc  | gcccggcata  | tgccctcacg  | cagctgacgc | cacaccttcc  | 2580 |
| atcgcccacg  | aaccatctgc  | gggctttggg  | attgaacgga  | acggcaagtt | tgatcagcga  | 2640 |
| agaataacca  | atccgatcag  | gctgaaaagg  | aatcgcatac  | atttcgaaaa | aaattttgct  | 2700 |
| gtcagcctaa  | gacttcgatg  | gcacgacgta  | tgctgccaac  | ggtccttcac | gcccagcac   | 2760 |
| ttccatgatg  | tcgaagatat  | gaggtccctt  | gcttcgccca  | cgagtgccaa | ccgagtggca  | 2820 |
| ttcatgatat  | tgccgaggtg  | atgccattgg  | tctcgatcca  | attcttcaca | gtgggttcgg  | 2880 |
| ttgcttcggc  | tcaaacgatac | ggtgagagtc  | cagcaattcg  | gctagtctgc | ccaactgctt  | 2940 |
| gccgtatctt  | ctttccagcg  | tttttttca   | gttttttcat  | cataggatac | ggtgcgatga  | 3000 |
| agaagaatcc  | ggcttgctcc  | catagctctc  | cgataaagtt  | acacgttcct | tgacgaggga  | 3060 |
| gattacatga  | gctgttttct  | cgctgggtgc  | actactccat  | tttcgcgaag | gatgggacgg  | 3120 |
| aagagttcgg  | ccaactcgca  | ttgtccttac  | gctggatata  | ttggtgattg | aaccagcgtc  | 3180 |
| ctttccgtag  | tcgaacttgg  | ctccggcctt  | gctgcatttt  | tcgatgtcga | acagcggatc  | 3240 |
| aattcgtcca  | tgctcatgac  | atcctgatca  | ttgcccggtg  | tcgcccaga  | agcgcgagga  | 3300 |
| agnttaccac  | tgcttcgggc  | agataacccg  | cttcacgata  | acctttggat | atatctcccg  | 3360 |
| tttggggatc  | tttccactcc  | acggaaatac  | cggaaatncc  | aaacgatcgc | catcgcgttt  | 3420 |
| gctcagctta  | cggt        |             |             |            |             | 3434 |

## (2) INFORMATION FOR SEQ ID NO:651

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cctgcaaata | gcggtctctt | atatcaattt | gctcttccgt | caggaaatgc | tcgtacggca | 60  |
| gaaacacagt | tggcactgat | tcgcgagcaa | cgcaatcgac | ggccgaaatg | gttcgcgtag | 120 |
| gtaaaatggg | agagggtaag | ctcctcgcat | aaatgccag  | atggccaagg | acgaacaact | 180 |
| tctcgtaaaa | tatcgctcga | ggaggagctg | gctcgtctgg | acttggggga | agccctcgaa | 240 |
| ctggacacc  | cgaaagcatt | gcagtcaagg | ctcccgaac  | agacgttctc | gtagagaaag | 300 |
| gttgggatct | ctccttgctc | ccgaagagat | ctatcgacg  | gcttcgggct | gaaaccggca | 360 |
| ctgcattcga | gcgagctgca | aatagcttcg | gccgcgaagg | tctggcctcg | ctcgtgcggc | 420 |
| atacttcoga | cgctcagcct | cctgccggat | acagcaacgg | ttactttcog | cgacctcggc | 480 |
| aaggagtatg | cgccatcaac | cccttcttct | ccgaacagtg | gaagaacaa  |            | 529 |

(2) INFORMATION FOR SEQ ID NO:652

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 571 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| agagaaagat | tcttatgaaa | agaccttgct | gatgtctgct  | cgtaagcata | tattgtagcc | 60  |
| atcaggatat | tcgatcggcg | agaggccgat | ctgccaaagt  | agggttgatg | cgctttcgcg | 120 |
| atgcagagac | agggcagact | cattggggga | taccgctgat  | agctccgttc | ggaaagcgta | 180 |
| tgcggatgcc | tatgaggacg | gcaagtagca | cttgccgttt  | tgctcaaacg | atgtggtgta | 240 |
| gatacactga | gatacgtacg | gggcaggatt | tcgtgcagca  | gcttcttatc | ttattaaana | 300 |
| acgctcatga | gacactctct | tgccattcgc | tttgttcttt  | ctgattttgc | atgctctttg | 360 |
| tctcttcctt | tctgaaggcg | caagagcttt | cttcataaggc | aaactcgacc | gtgcagagat | 420 |
| gcaaatagga | gagcaggcag | tatagatat  | actatccgca  | cggcagattt | ggcgataact | 480 |
| catctgcaaa | acctactgat | tcgacgatga | gtcggatcga  | aattttggcc | tttggcattc | 540 |
| ggatacgttg | ttgtgaaaga | tccgatcgtg | g           |            |            | 571 |

(2) INFORMATION FOR SEQ ID NO:653

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 600 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular



- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...600

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653

|            |             |             |            |             |             |     |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| tatattgaaa | atcgggtgata | atataccttaa | catataggaa | gttattcgac  | aatatctacc  | 60  |
| atcttgacga | atagttgatg  | tttccacgat  | tgaaatcagt | acccgtcctc  | tgattttgta  | 120 |
| ttaaaaatta | agcaaccttt  | atccaagggt  | ttgtactcaa | gcctaactga  | ggtttgatgg  | 180 |
| aatattctcc | atcttctagg  | atacgggttaa | aaagctatct | ttagcttctg  | ttttgagaag  | 240 |
| cataatgcat | caactgtttc  | attgttaagc  | atgcaaccat | caatgtaaat  | tataaaaaact | 300 |
| caccattagc | aatattaggg  | tgtatgcttt  | gatcataaag | gtgctagcaa  | gattgttaga  | 360 |
| ttgttcaact | atatcatctt  | tgtcatcaaa  | ancttggtga | caaactctata | tgacggattc  | 420 |
| atgtctaaag | actctataga  | acaaactgac  | agaaaacatc | aaacttgaat  | gtgtttttta  | 480 |
| ctaattgttg | ataaatccag  | aagcaaacga  | catatcatct | gcttttagaag | aaaatgctaa  | 540 |
| ccttctctct | ttaacttatt  | gccaaccttt  | gtactgtggc | gattgtagga  | ctcctaatta  | 600 |

## (2) INFORMATION FOR SEQ ID NO:654

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 534 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...534

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| gaaagcagca  | aatgccata  | caggcatagc | aagaattgct | aagtctcgac | ccttcaacga | 60  |
| agaaggtcac  | tgcggtattg | ctacactcat | gatcaaagag | gacgatcagc | cgaagcagaa | 120 |
| acattttctgc | gcgaagctat | cgaagagtgc | cggttcagcg | caatctgatt | ctgatgctcg | 180 |
| tcgaaatatt  | ggagaaaaag | gacaaacgca | ggaagcagca | gaatggcgtg | ccaaactacc | 240 |
| ggaagagagg  | tggaagcgca | agcgggtta  | ttcaatgatc | tttacaaggg | taactctatt | 300 |
| aacttctttc  | aaattaacac | ctgacctcga | tggcaaagaa | gtgtatgtgg | tctggaccgg | 360 |
| gcatacaccc  | ggagtttatg | ataattggga | tgatgtcgag | cgcaaacaga | gggattcaat | 420 |
| aaagcccgtc  | acaaaagctt | tctaccgaaa | gcgatgccct | aagagcctat | gaagacggag | 480 |
| cagatgaatt  | taccgcagaa | gcatacggat | ccactggtac | cgcaccggag | cana       | 534 |

## (2) INFORMATION FOR SEQ ID NO:655

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 703 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...703
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:655

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| cgaccccttt | gatgtcggac | aaacgtgctg  | tcagttctgc | cagacgggtg | caccgtacag | 60  |
| gtcgaggccg | tagaaggtaa | gatcctgagc  | aatcagttga | actcccgagt | cccatgcttt | 120 |
| acgagcatcc | gtacctcttc | gactaagcct  | ccatcgggcg | cgaccgatgc | cggccggtga | 180 |
| taatcggtat | ggcgcatacg | aacagctgcg  | atcgagagcc | tcggataatt | tcagataggc | 240 |
| ataatccgcg | gagtggtcag | tttgcgccct  | ttctctgcct | cggcataata | agactcccca | 300 |
| aatgagaaat | gagttgcttc | cagtcgaatt  | tgccgtagta | agctccactt | cgggtatctc | 360 |
| cttcttcagg | tcttcccgaa | accgctcgct  | cagcagccca | ttacgtacag | gctgccgata | 420 |
| cgtcgggctt | tcttcgcctc | cccattctcca | gaatggtatt | gacagactcc | tcctgtgcat | 480 |
| cgcctatgaa | ccgcaggtat | tcaccaccac  | gatctcgccg | cataccgaag | ccggatcgta | 540 |
| tgcacggtat | agccggttga | caggaactgg  | cgcacagca  | cctcgctgcc | accagattct | 600 |
| tggagcacc  | aagcgtaatg | acgtctactc  | tgtttctctc | attcgccaaa | ggagagagtc | 660 |
| cacgaattcc | ttcttacgga | agatctcagg  | tcgtcttatg | ccc        |            | 703 |

(2) INFORMATION FOR SEQ ID NO:656

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1133
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:656

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgaaaaaggc | atccatccca | gcagagata  | gatgcctttc | cttttatcgt | ttgatccaat | 60  |
| tatttcgctc | cttttggttt | acacgtatga | tatctgctct | accgtattag | cttccatcga | 120 |
| tgtgtagtat | ttttctttta | cctgctttta | gcagcgagag | ccttgctgta | ttggttgagc | 180 |
| tcttcgtata | cgcgacggct | ttgatgagac | agcccggtgt | aatggcatcg | ttagaggctg | 240 |
| cggcccgagc | ttctcaaaat | agcctacggc | ctcttcatat | tttttgagct | gtactaacag | 300 |
| tcaccgataa | gacgagtgat | agatggtgct | accatatatt | cctggaggag | aatcccttca | 360 |
| gatgatcaat | ggctttctga | tattctccga | ggtgtagtag | caaagtccgg | cataggcttt | 420 |
| tgccagattg | gatgcattcg | accggagtat | tttttgatta | ctgtcaacaa | tcccatttcg | 480 |
| tttgcaccgt | tccatttaag | gctgcgctgt | ccaattcctg | aatgaatttg | tcttcggcag | 540 |
| gtataccttg | gcagcagctt | cacgagcttt | aggttcgctg | acgaaacgtt | gtaggcaaaa | 600 |
| atacctgcca | caatgataaa | aacgcccaga | ataaccagcc | gattttggtc | atgttctttt | 660 |
| ctatgaactg | ctctgagcgt | gaaacccttc | tcctacgtgg | ttgtccggtt | gttgattttc | 720 |
| ttttttagcc | atatttgtaa | taattattta | tttcttttcg | gtcgcacaaa | ggtacgcgtt | 780 |
| tggcgtgata | tacaaatgtc | ctgtccgaat | aaatatacga | tatgtaatgg | ttgtcgaaaa | 840 |

```

cgtttcttct cttcttgcc ccaatatccg atttacttgt ctctcttgag ccgtcaggta 900
gccgaaaaga gagctattgc caatccacta accgctcttt acggcatacc gtatcagttc 960
ggctgcattg gtgaatccca tttgtgcaga atattactac cgggtgtgtt ctaccgttcg 1020
gtaactaaag tgcattttt cggctgnttc tttggcagaa tagccatcgc acagatatgg 1080
actacttctt tctctcggtg ggtcaagctc gagaagtcgc ttctgctctg tgc 1133

```

## (2) INFORMATION FOR SEQ ID NO:657

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657

```

cgactctcga ggatccccga ggagacgacg gacagggtgtc ccgcttcggg ggggattgaa 60
ccctgctacg atcctccaga acgagtacgt agctgtctca ttattttcca tatactactg 120
cgattataag gttatcgag caaagatcgc gaggcaaaca ggaatgatga agatggggtt 180
cttagcggtt cttagatgga ttagaatgga aaagccgtgt atctgttcca atttctggct 240
tgccgatgca gatttatgtt gactgcagaa agaagactgt agtaatgaat gaattcttaa 300
aaatggaccg cgctatgggg aaggaaacca gctacggcaa aaaacaaagc aataccatgc 360
caatggctgt aatgctatat cggacgagtg gatataat 398

```

## (2) INFORMATION FOR SEQ ID NO:658

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658

```

ttgcaatagc aacacataga taagccgggg tttgagaaga agattcaaag tcgccatagt 60
gagagattat atattattct ttatcagatc aacgaatcaa ttttgcgatt attctctccc 120
gtcttggggg ctttacagcc ccagtctgaa tgaggcagta cgtgccgtta tgctttttga 180
tgctttcggt ttggcaccgg ggcagagtat cagctcctcc atagactcaa agaggtcgtc 240
cgggagacgg acacaccatg tgtgcaacta ttagggacga ctcccttgag cccaccatct 300
gccagacatt ccaagagata atataggcaa tatactcaat ggattgtcga ggggacgctt 360

```

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| accgaacttc  | tcctcataat  | actcgataaa | gggattagta | gtgcctcacg | agcaaggagc | 420  |
| aggttatcgc  | cttgccattc  | aaagcataga | tgtttttata | tgccttttga | gccatcttga | 480  |
| gccattcgcc  | gtgcttgaag  | tattctctga | gatgatgcga | agctttctgt | cgagcatacg | 540  |
| atacgttgag  | gaatagggat  | aaactcccc  | gtagtagtgt | catacctgtc | acaagataag | 600  |
| gagcttcgcc  | acaagtaatt  | tccatacgcg | tggagcaaca | tagtctttcc | atgtcttacc | 660  |
| ttcgggggaat | gtaatagggt  | cggtagtgc  | atccaagtct | ttgtctcggg | ttgctcaata | 720  |
| ttaaacacat  | ccttagacca  | aaccaagcct | catcgatcag | attattctga | gcgttgcaaa | 780  |
| cccagagggg  | gtgaataact  | ctgctttatc | cttggtgcgg | ttggcttggt | cttcttgac  | 840  |
| ttcagcactc  | tgggctgtat  | tacagtgtca | tgctccctg  | tatgctgtca | gtcgtaattg | 900  |
| gtgcacgtga  | tttggtagcg  | atctccsagt | gagtatagtc | atctgtagcc | caaaagatat | 960  |
| tcctctgagt  | cgtatgggtca | agaggagtct | ttgcagaagt | ccttcggact | gacgcagtag | 1020 |
| ttcattctcc  | taatgtcgac  | ccccatcttc | atctcgctca | cgagtaacct | ctttgcattg | 1080 |
| acaagcagtg  | gttgtaaat   | tactgtatac | catatagaat | tgccatttgg | gcacagatta | 1140 |
| gaaataggca  | cgacaaatct  | gcccctactc | ttagccccgg | ttggggacat | caccaggaaa | 1200 |
| aagggcctcg  | gtcttttata  | gtttttctaa | actcattaca | taagcaaagg | tactaagtta | 1260 |
| ggggcatact  | aacgagggaa  | atggatattt | ctttaccgag | tagatcaaag | tgcaacagat | 1320 |
| gggtaaacag  | cagagatttc  | cgggcattcg | ggttgggctt | tt         |            | 1362 |

## (2) INFORMATION FOR SEQ ID NO:659

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| gtccaggcat | tcaatagcat | tttatcttta  | tttaattgca | tcaatccact | ccattctctg | 60  |
| taaagtaacg | gtcattattg | atcatccatt  | taccaacgtg | taggcaaaat | cagcatctaa | 120 |
| agaaagtcct | ttccaagaag | cacctaaagag | aaaccacctg | taataggagg | agtaacagac | 180 |
| ttatcaattc | gtgtctcaag | tcagctgagt  | actggcttgt | tgtaacttta | ttaccatccg | 240 |
| catctacttg | accaggaaca | taccacaact  | gcttaccggg | ttttttgtcg | attnagcata | 300 |
| ttcagctcat | atagaacgaa | ttgggtacc   | caatttncca | tatgtaccgg | tattaggcaa | 360 |
| catgtactta | ttgagaccna | agaaaagctt  | ttttatttcc | tg         |            | 402 |

## (2) INFORMATION FOR SEQ ID NO:660

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...672

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:660

```

tagccattgc tgttatccga agcatgagggc tggctaataa gaccataaga attttcgtcc 60
tgatatggta atcgggtgtag gaggctatgc cagtggccaa ccttacgcag agcacattcc 120
ctcgggatcc ccacctcat tcaagagaaa acagctatgc cgggtgtaacg aataaactgc 180
tgagccgagg agcgcaaaaa tctgcgtggc ttatcccga atggataaat tcttctctcc 240
tgaaagatcg tttttaccgg caatccgatt cgccctgaaa tagaattcgg ccaccagcc 300
gctcggagtc tcttcgcttt ttccggcttcg agcagtcga atccctgtcg tcttggtggt 360
cggaggtagc ttgggtgccc tgactattaa cagagtatcg ccgacaagct cggcaaatgg 420
gcagaaagcg gtgtacacct ttatggcaaa cgggaaagaa ctatattgag acagccagaa 480
aagcagtaga aatcatcccc ggttgaaatg ctatgtcaat gattttatca ctogaatggt 540
tatgcatact gtgcagccga cttggtagtg tcacgagccg gagcttgccc atttcagagc 600
tttgcttgct gggaaaacct acgatactgg ttccctccca atgtggcaga agaccatcaa 660
acaaagaatg ct

```

## (2) INFORMATION FOR SEQ ID NO:661

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...556

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:661

```

agagcaagtt ttccatctcg ctgcctcgtc tgcgtcctgc caccggcggt gggagcctaa 60
agatcctatt gacgatgtcg gtatggtaca gcttattatg ccttcctgtc gttggataag 120
gatgtcgaga tcagcctgtc cacacggaga gtcgtgagtt tcgtgaccac gtgatgccgc 180
tcggatatcac ctccgtagtg ccggcagcaa gaccgaaccc ggaggatatg ccgaagagaa 240
tgccgtctgg agcaattcgc catcaacgat gcccgcagtc cggccgaaat ggctccgatc 300
ttcggcgact tggctacgag ccggtttgga aagactggga tgcttcatgt aacagaagat 360
tcttaccgta acgctcgcg tccgaagcga aggatcttca taagaataaa ggcttgctct 420
ccggtcgagg aaagcagcct tgtccgtttt tggttttatc gtttgaatcc ttacaagcga 480
atacctaagc tacgtggaaa gaggtattct ttcagcgtag cctncaagtt tttagtctcg 540
gtttaatggc tttacc

```

## (2) INFORMATION FOR SEQ ID NO:662

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1416 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| acttccggtt  | tatccagaat  | gttcttaatc  | ctcggatcgg  | attcgtagtc | gacagcagat  | 60   |
| gttctatgag  | tcggagcagt  | accacatatc  | cggtcgttcg  | tctccgtgca | tcgtagaagt  | 120  |
| atagagcacg  | cgaggctttt  | tccctgtttg  | gcagaggacg  | tcagcttgca | aatcatcagt  | 180  |
| ttacgatcct  | ttacggcttg  | ccaatgacgg  | aagtagtaca  | aagtgatgga | tactttgttt  | 240  |
| ggaaccttcc  | atcatgctga  | tataggcttc  | ataggtgggg  | taagcattcc | attctatttt  | 300  |
| tctcctgagc  | ggtagtcgaa  | catctcgaca  | gcgcgctgca  | tggtggagga | gtcaagaatg  | 360  |
| taggcttgag  | cccatagcgc  | aggaatgcct  | cgactcctct  | tcgctggcat | aggcaatggc  | 420  |
| ttcattgggt  | acgggggtcaa | atcgtcgtatg | gacatgatca  | gagccagctc | ttgtagaacg  | 480  |
| gccctatcag  | cactttgaat  | gagaagttagg | cctcgccccg  | ttcgtcaaag | ttgaaataac  | 540  |
| tttgccctgt  | tgtgcctgca  | tgtgcctgat  | gaaagtcagc  | aaagcaacaa | aatgccaaaga | 600  |
| agcaaaaaat  | tctttttctt  | cataaatagg  | ataattagtt  | tgttattgga | ttcttgacgt  | 660  |
| atccttttgc  | gagaaaaagg  | tgtcgttttt  | tgcataacgg  | tatggcagtg | ggagcatatt  | 720  |
| tttcgggcta  | aatgtctcgc  | aaagataaaa  | atattcctat  | gccattatct | ttttgagcct  | 780  |
| aaaagtcaat  | tgcataattcc | acttagttga  | tagtttcagg  | atgggatgtt | cccaaaggag  | 840  |
| attgtttgat  | gggagtttca  | ttgagctctt  | ttgtcgcaga  | gcgattctta | gtgtcttcgg  | 900  |
| gaaagggtcaa | accttcggta  | tatggacaca  | gaagcaaaaca | gaaatttcat | caagtttcca  | 960  |
| ttagagaagt  | actcctttcc  | cgtcaaatca  | atgcttgtag  | cgataggcga | gaaataagga  | 1020 |
| atgattgtcg  | ctgattcttg  | cttcctgcac  | gatgcaggac  | gcgattgtca | gctgattctg  | 1080 |
| cttcctgcac  | gatgcaggac  | gcaattgtca  | gctgattctg  | ctcccgtaat | gcgctaacta  | 1140 |
| tcagctattt  | gcaactattt  | tataggactt  | tcattgagtc  | ttttgccgca | gagttgattc  | 1200 |
| tttaagtgttt | ttcagattac  | ttgagtttgc  | agagagatcg  | catgaagctc | tcctttcttc  | 1260 |
| gtcaaatcaa  | tgcattatct  | gtcttgatca  | atatgagggg  | ggaaggggta | ttgtataacg  | 1320 |
| gtccaaaagg  | tgcctttccg  | gatcaaagtc  | caaataaaaa  | ccttgcaggt | ctacttctgc  | 1380 |
| aagggtttttt | tgttttgtta  | cgaaagctcg  | gatttc      |            |             | 1416 |

(2) INFORMATION FOR SEQ ID NO:663

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 589 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| tacacgtgtc | aagcccgtgc  | aactntccgc | tttgctcgta  | acgatacacg | tcccgaactc | 60  |
| ggcccaaacg | aatcggtaga  | tcgcgatagg | aatgtggatg  | atcntgaata | tctcgcagtg | 120 |
| gtgagggcat | tcattggctt  | tagcatgact | cttctccttc  | ctgcggcgta | ttgatcggac | 180 |
| ggaaagaatc | ctgtcctatt  | tggcatagtg | cccggagggtg | atgtagagat | tcttattgcc | 240 |
| gatatcggcg | tgattacctg  | ttggtagcca | aagtgcctct  | gtatctgctt | cagaagtctt | 300 |
| ccaaacgcaa | acggagctgt  | gtgcctcgcg | gtagccaaag  | cggaagccgg | cacctacatt | 360 |
| ttgggagaaa | cggaagagtt  | cgagctcctt | acgatctttc  | gatggtcgcg | cttcttagcc | 420 |
| tcttccaaaa | gctcagagata | tcatccaaca | tctttttctt  | tgggaaagag | attccataga | 480 |
| ttcgtgtcag | tgttttctct  | tttcgtcgcc | gcgccagtaa  | gctccggcta | cacttaaaac | 540 |

ttgatcgctt taatgtaacc ggtattgggt aagtgaggac cgcgacaag

589

(2) INFORMATION FOR SEQ ID NO:664

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aatgatccgg aagccgatga agcgcgtctt tacggcgcaa tcccgatatg caggcgtcat  | 60   |
| tcatttttgc tgcaagtaag cccgtaggcg aatcggtgag aagccgcttt tgtactacag  | 120  |
| gancaatata ctctcactgc tgaatatctc gaactgatgg agcgattcgg cactcgtggg  | 180  |
| atcgatattt cctcatctgt acggtgtacg gacagccgga ggtattgcc gtaacggaag   | 240  |
| aggctcgata caggaagctc tctctcccta tggcaatacg aagcaaatca acgagagatt  | 300  |
| atccgcgatg ctatccatgc cggagcaggg tacagggcta tactctgcgc tacttcaatc  | 360  |
| cgatcggggc acaccccacg ggcgatatcg gaagcttcct aacggagtgc cacagaatct  | 420  |
| gatcccttat ttgactcaaa cgcagcaggc atcagagccg aactgagcgt ctccggcgat  | 480  |
| gactacgaca gcccgacggc tcttgatcc gggactatat ctatgtggtg gatttggcca   | 540  |
| agcgcgatgtg gctgccatcg aacggatgct gaatgaagag aaagcgagga ttcgctcgaa | 600  |
| gtctttaata taggtacggg taggggcgtg agcgtgcgga gcttatccgt accttcgaac  | 660  |
| gggtgacagg cgttgctgtt cctcatggat agtaggaagg cggaaggcg atatcgaaca   | 720  |
| ggtatggggc gagccaagaa agccaatgag gtgttgggtt ggaaagcttt ggagtcgttg  | 780  |
| gaagcacact gctgagtga tggcgttggc agcaacgctt gtcggagaag taaccgcagc   | 840  |
| ccattaacgc acccgatacc ctatcttctg gcagatggac atctatcgac caaaatcact  | 900  |
| tacctgaccg gcgtagggcc gaagcgggcg gactactgaa ggaggaaata gaagtacgta  | 960  |
| cctatctgga tcttctccat attttccctt tcgctatgtc gataggagtc gattttatgc  | 1020 |
| catacgggaa tacgctccga tatgccctat atccagcttg cgcggtgtcc ttcgcaactc  | 1080 |
| tccgaggtgg gcgaaggacg gcgcaagcgg ctgacggcta ctt                    | 1123 |

(2) INFORMATION FOR SEQ ID NO:665

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2764

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:665

```

ggttcctccc caccatctat aaggcgcgcc agccagtaaa tagccgcgtg ggatcactgc 60
cccgaataact tttgataaag gcggatgcta tatcataggg agttcgccct ccttgtcgaa 120
agcagcggggg ttttcttgca agcgtgcgt atcttttctg ttgtaatgac gagccggtct 180
tccacttcgc ttgtggcaga aggtcgagga tgttcagcag ctttcgtgca tcgcctccgg 240
cataggaagc agagcttccg tctcctccag tacaggatgc ttggcagcca gcagtcgtcc 300
cgatcgatag ccctgtgtgc caagtagcag cagatcctca tcatttgggg tttgagcaca 360
tagacctgac agcgcgatag gagcggacgt atacttcnaa actcggattt tcggtcgtgg 420
caccgatcaa gcgtcactat tctcgtctta cggctgccag aagtgaatcc tgctgactct 480
tgctgaaacg tgtatctcgt cgatgaagag gatggcgcggt cctcctttgt cgaacagatg 540
ccacgattgg attcgatgtc ggctattact tcccgcactt ccttcacacg gagctaaccg 600
cactcaatgt atagaaaggt gcatccactt catgagcatg atttcggcca gcgtagtctt 660
gcctactccg ggaggccccc acaggacatg gatggcgctc gtccctgtct gatcatctgc 720
cggagcacag ccccatccg atcagatgct gctgcccac atagtcggcc agcgtttttg 780
gacgattctc tcggccaagg gtatttgggt catgccgcta aggtacataa ttggatacga 840
tccgcatgta cgcgagtggg aactgcatt aaacgggaaa gcagaggaaa gtctatagaa 900
gtatcatttc cttattttta cagagcagat catcgctaaa aagacgaaga ataccatgc 960
cacaccatct gttgtcattg cttccctgct gaggtgcaga cttcaccact tcttctata 1020
tattattata tagtatcggc aggtatttca gccacggcac aaacgggtgat caaaggctg 1080
tcctcgcagc ggacaatgaa gccccggtat cttatgcatc catctattcg ctgaaacaaa 1140
gagcggagta gtggcggacg agagcggacg atttatctcc gcctccatcc gggacgctac 1200
cggctggcca tccgttccat gggatcactc ctcttgagac agagtgtctc gtgggcgaga 1260
aaagcgagga gaagctttcc gactcagctc cgtcatctat gatctgaaag aggtggaagt 1320
gatggtaaac ggcctaaaga agatcctgcc tatcccatca tgcgcgaact caagcgcgca 1380
ctccagttta cgagcacatg gtaaagagct atcaggccaa atctatacca aggttccgat 1440
gcggtggat aaagctgcct tctggctacg gtcatagaga gccaaagcctc tctggaattc cggcatccga 1500
gatctggaga aaaaacgctc gctatagaga ctcttcgata ccggatgacc tcaaatcgat 1560
acaaatacac aagcaagtgc gcgcgatgcg ctcttcgata ccggtatgacc ccaaaggttc agtcttgatg 1620
acaacggatt atatgcagat tatctcgacc aacatatatg ccaaaggttc agtcttgatg 1680
gaatagtaaa catggcaagt cctatacggg cgggttactg gaatcgtaca cctacaaact 1740
ggaggggtacc agccgggaaa aggaagaaaa gtgtaccaca tcagcttcaa aggcagaaaag 1800
ggacgccatg agggcgaaat gtgggtgacg gatagcatct ggtgtctgca ggcactaaaa 1860
ttgaaattaa ggcttacgat atgattcggg acaaggtcga tataagtctc atccgctcga 1920
aaaggatgtg tacctgcccc ccacctatgc catcggtatg agatgcagtc gatgggactg 1980
aaactggagt accagtactt ttcgtccttg tgtacgatcc gcttgagatc gaccgcaaat 2040
tgctatccac tgcccgaagg ctgagggact tcgcttccgt acgaaccgag aagtaaacccg 2100
ccaccttga tgctcgaatc ccgattggat acgctgggct atcatctgcc cgacaatata 2160
tgctgcccga taccgaattg caggccaagg tccgattcga ttcacagctt tcgatcgcga 2220
ctcttcctac tgggacgctg tagtgacggc accgttaccg atgaagaagc acagagctat 2280
gccaatcggg acagtctgat gcagcttttg agaaaaagcg gcggttcggg ggcggtcggg 2340
aaggcgaacg tacggccgta cttccatcct cgggtgctatc ctcgcgggac atgactataa 2400
atgggagagg ggactacact cggattcaac ggccttatcc gcggatcgct tatgactacc 2460
gctatacggg tggcttttgg ttgggacaga gctttttctc cggcagaagt tttccaaagg 2520
tgtagacctg acgctgcgcc ctatactaata tatactactc ataggcggaa gctatactgg 2580
gatgtccgtg ccgatttcgc tacgctcctc tctcgggtgg actactctcc ctatcggcag 2640
gcaggcgagt gcagacctga ctggcccgtt tgccaatacg gactggcgca tacagctttc 2700
ctgaccacct tagtagacgg tcgtgggtcat ctgatgctat atgaaagaag tatctgcgct 2764
tgag

```

## (2) INFORMATION FOR SEQ ID NO:666

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS



## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...581

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ggctctaaac | ctgcaaacgg | ctttcgagca | gataagacct  | ccggacacat | acagaaatca | 60  |
| gcgtgatgca | atggatgata | tcttctatgg | aagcagcact  | gtgaatggta | gcacaagaga | 120 |
| ataatctttg | ccgagacagc | gaaaatcadc | tccgtgcat   | tatctttcga | ttccaatctg | 180 |
| cacacatata | aatgagttcg | ggcttcgtcc | ggctccatga  | aactccggct | cttgccaaac | 240 |
| cgcagaagag | atagcagcag | ctatctcttc | gcagtcgccg  | ttatagacaa | tagttgacaa | 300 |
| tggagaaca  | agcggagctt | ttcctccagt | ttcgttttta  | tatcgggaag | ttctcctgat | 360 |
| gagcacctcc | tatatctgta | atgataccat | acaggggcat  | attatgctct | ccaaacgttc | 420 |
| catttccccc | atttgcgata | tccggcctca | aataataccga | gagtgtgttc | ctccgccatt | 480 |
| gccatacgga | aggggtactc | ctatctgcga | gttatagctt  | cggggcgagc | ggacaatgca | 540 |
| tagtccttgc | gcaataactg | ataaaggaac | tctttgacga  | t          |            | 581 |

## (2) INFORMATION FOR SEQ ID NO:667

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...545

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgaacaaaga | agctctgtcc | tatcgttttg | ccggcaagga | cattgcagag | tgaatgcaat | 60  |
| ggacatcaag | actcttattg | aatgggtaga | ttctctggtg | aacatctggt | ggatacgcaa | 120 |
| cgggctattt | ctatagaaat | actgaaaaga | tacggacacg | cttgggggtt | cttaaagatg | 180 |
| tggggttga  | gtacttacga | tgaaccgagc | tgcagcatcc | ttatccggag | gagaaagcca | 240 |
| gcgtatcggt | tggctacgca | gatcgggagc | aaactgggtg | aggtcttgta | catatggatg | 300 |
| aaccgagtat | cgtcttcac  | caaagggaca | atcttcggtt | gatcattcgc | ttcaggattt | 360 |
| gcgtgatata | ggcaatacac | tggtagtgg  | gggcatgatc | aggatatgat | gctgcacgcc | 420 |
| gactatgtaa | tagacttagg | acacgagccg | gcagacatgg | tggtgaagtg | gtgtttgcag | 480 |
| gtagtccgga | gagatggtgc | aggctaatac | cctgactgcc | gattatataa | gtggacgaag | 540 |
| cgtat      |            |            |            |            |            | 545 |

## (2) INFORMATION FOR SEQ ID NO:668

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1088

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:668

```

gtcgagttgc atagcgaact cggcgggtgc cttgtctttt ggaatgagtt gggaacctta 60
tttcggacta ttcacatag gagaaaatgc tcttttgtcg aaaccggatt ggcatacggt 120
agataagaca aagataatag gagagtgggg gtaaggagca taaatggatg aatatacgcg 180
ttcattatta agccgtttta attcggatga taagtgttag gatagagata tttagcttcg 240
ttgaatcggt tgtgtttttg caaatgtagc caattcctgc gacttccaag aggctgatga 300
actatgtgtg tcatttgtgt ctgtcctgtc gattgctcat aagaggcgag gggatggccg 360
ttgctcgaca tggaaataag agagctttgc tgatgtaca taagggtgtc tatttggtac 420
gatgtacggg gataggcttt gttttttccg taagtttgta ttgatatgtt ttcttgcata 480
cacattcaaa ctattgacag catggcaagc gaaagaaaac tgaaaaagca gataaccggg 540
ccatttccga agtctttact gatgcattcc tgctcaaaact ctttgtgaag aggaaaaaaaa 600
cgcagaggtg gaaactatcc tcaatcgtat tctccaattc aagataccac cattgccaaag 660
attcgttgca acgacggtaa gcacaacctg cactcgtaaa gaaatattat cgcgggctcg 720
tggatgattt caaggagagc tgtccgagat cgtgaagagt atttcggcgt gtgcgtctga 780
taatgatttg tcaattacgt gcattaagca gaaatagcgt aacatataga ggtttttgaa 840
gtttttctca cgattgttgc tcaggatgat gggctggaaa gcctcgtccc atctgcaaat 900
ccgctccaaa gcgtcatttg cgtggctcct ctaccagcaa ttacgacttt ttgctgggca 960
aactctacta ttggtctatc gtcggaaagc cggcttcctg atgaaaaagg aatggttttt 1020
cttccttttg gaccgatctt cagggtatg ggaggtatcc cgatcgatcg ctcgaagcag 1080
gttccact

```

## (2) INFORMATION FOR SEQ ID NO:669

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1025 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1025

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:669

```

ccttagctgt cccgtcgagc ttggtcacgg caagggcatt cacttcagtg ctgcggtgaa 60
ctgccttgcc tgttcgaaag cattctgacc ggtggatcgt ccaataccaa taaaatctca 120
tgccgagcgt cgggcactac cttctgtcca cacgcttgat cttcgtcagc tcgttcatca 180
gattgacctt attgtgagac gtccggctgt atcgatgatc acgacatcga cgccgcttagc 240
cacggcgaaac tgactgtgtc ataagccacc gaagccggat cgctacccat ctgcgcttga 300
tgataggcac tctactcgc tcggaccaga tctccaactg ctacggcccg cagcacggaa 360
ggtatcggga gccccgagca cgacgtctt gggcctgac gaaagcgatg tgccagcttg 420
ccgatggtag ttgtcttgcc tcgccgttta cgccactac catgatcaca taaggtttgg 480
taccggaggg aggtcgaagc tgtcgccatc ggccgatccg ttctccgtga gcagcgaggg 540
atctcttgac ggaggatagt cgtcagctcg gaggtggaaa catatttgcg cgagccactc 600
gttcctctat acgtttgatg atcttcaatg ttggtatcaca cccacatccg aagtcaccag 660
cacgttttcc aattcgtcca agacctatcg tccactttgc tcttaccggc tacggcacgg 720
gtgatcttgg cgaatcgctt tctttggctc ttgacaggcc ttctgcaaaa gtctcttttt 780
tcttttcgag aataatccga ataatcccat atcgatatata ctgttatatc tctccttagt 840
tcattctgtt cttgtaatcc tcataatcga accggcgcaa cactctttct tcccgtcggt 900
gcgcagcagt acgatgtccg gatggcgtgc acgttgaaca tgtcgtcttc acccggttag 960

```

tggagcatgt ctgcaatata gtcacgcga ctgcacgcga tcgaaactca gtcaccgatg 1020  
aagcg 1025

## (2) INFORMATION FOR SEQ ID NO:670

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670

```

gcaaggagtt cggcttcggc tttcgctatg gaatcctgcc gagctgcttt atcgagcct 60
tacgctgcgc ttctatttcc tgcggatcgg gacgattggc catgaaaacc caaagatcac 120
cagtccgatc agaactaaac ctataacgta tttttatcca tatattttcg ttgcgtaggg 180
attcttcggc accgactcgg caccctatc ttgttgcttg ttcgctacgg tatgtcagag 240
gggagaaaaa tttcacaccc ccccaaagaa ccgacaggca aagcgattat tcttatcttt 300
ttttctcggt ttgattgctt cacgaatgaa agcoatgaac aagggttggg attgaccacc 360
gtactattgt attcgggatg gaactgtacc ccacgaacca gcggcaggca ggcacttcca 420
cggcttctac caagcccgtc tcggattctc gccacacat tgcataccgg ctttttcgaa 480
agcttcgcca actggctggt gaattcgaag cgatggcgat ggcgttcgag cacgaattct 540
tgccataggc agcagccaat ttcgatcctt tgcgcagagc acagtcgagc gcccaaacgc 600
atggaaccgc catatccgta accgctctgt cgtcatcggt cgtgacct 648

```

## (2) INFORMATION FOR SEQ ID NO:671

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671

```

atagggtgag cttatcgagc gcgttcggct gcccgatatca tggcttcacg gctcctatgc 60
cacgaatggc cagatagtgc aggatgatgg agactatcgc atgcagagcc aaaaacggaa 120
tccgaactcc aagttctcag ccgagcaatc tgccaaatct gcatccccag atagataaga 180
aaacctatcg tgacgagata ttgaagatac atagtctgat cggcaagatt cgctttttgt 240
agaggagatg gtagcaaacg agatcagtag gataatggca tcaagagcaa aaagcccaa 300

```

```
gtggacttga ccagcgcat ggtagccggt gcatatagtc ctatatggtc atcgcggtatc 360
cttgcccttc cggccttate aaaagc 386
```

## (2) INFORMATION FOR SEQ ID NO:672

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2443

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672

```

tggtttccac ttgactccaa gcgtattgac ggcttccctgc ttgtccacga gccgttgtat 60
ttgagcacac cccagctaaa tagcaggaca aaaactgcat aatggcaatg atgattactg 120
ttcctttttt catattcatt ctatgttacg ttactattag gtttatctga atgtactact 180
tacgacgtct gacagggttt tgtctttctt gaccgaccag ccgaaatagc cgagaaagtc 240
cccaacgaga agtattcgcc atgcgaatat gccagcaggt ttgctttctc catacgaaag 300
aacctgtctc cgggttgata tattgttcgt cggcaccgat attaccacat cggccataaa 360
catgtcatgg ctaccgagtg gaatgacctg tctaccttgc actctatgct gaccggcgat 420
tcggccacca aaggagcttt gtcagcttgg ccggctccac ggtaaggcct gtctcggcaa 480
acttgtcata tccttgcctg aacggacacc gcaccagtcg gtctgtctgg ccatgccgac 540
gtagtcaggt tcaaaccgaa ctgcaccctc tctttgatga gagcatagag tgacgctccg 600
ggcgaatact gacatagcac ataggcggct ggctgcaatc gtccccaccc aactggccgt 660
aagcaaatta taatcctcgg gccggggcca caactcacca atatggccgg tagcggatag 720
ataagtgtgc cgggttccaa tcttgtctca ttgtttcatt cttagaaaac ttacgcaaac 780
tatacaactc gatgcggtca ccggctagtt ttgcgtcgca gtagtcgcat cgagggtgca 840
ctgctcggca tctatcacac ggaatcgggt ttgcatcggt tcttgttcgt aatacacttc 900
ggattcggac aacggacgag acccacaatc tgtgtggtac ttccacctga cgtttttcta 960
caacttcata gtcccgaata tgttcaggcg cacattcggg gcaataagag cgatgcgggt 1020
caattcctct cttcgaaagt cttgtcctct atcttgataa ctcctttcga accatggccc 1080
gactgcgcaa attgttgccg atggtgatcc gcttgccaa atcatccgtt gcaggagagt 1140
agccaccttg aacagtttctg tcggggggat atggtcatca cgatgccgtt tctaatacgcg 1200
gcgacgagca tttcttcctt tttcatacaa tatctgctta gtttgcaacg tctatgccga 1260
gcacttcaca aatgtggact gcctcgtata aagcccgttc agtgcttgcc ggataaagta 1320
ggcttgggat tgtcatccac atcataggca atctccccc cagcaggtag cgatgcagta 1380
cgcgagatt cggaaggctg tcggacagca tagcgttggt cgcacataga catctttgac 1440
ccgttcatat tcctccagat ccgtaaaccg tcacgttgta ctctgtcat gtagagaatg 1500
tcgcagttgt tgatcacctt tcgtcgaaat gtttggtttc cgtataaggc agatcatgct 1560
ctcgacaaac tgcttgatt cttccggaag agacagctct tcgggagcaa cgaagataaa 1620
cgagggcgga agtgcgacat accctctatc agagaatgga tagtactcca tacttgagat 1680
ccctaccat agcgatagtc ctgtcatata gcgtgcctgt gttttgcgaa tggaatagag 1740
atccaataaa gtctgtgaag gatgtggttg gctccatcgc cggcggtgac taccggcaca 1800
cggcttacct ccgagcataa cgagccgccc cttccagata gtggcgcata ataatacagat 1860
cgcatagtgt cccaccatgg aaatggtatc cttgagcgat tcgcctttcg tgagctggag 1920
gtggatgcat ccgaaaaacc gatgatacgg cctccgaggg gttcacagcc gtctcaaaac 1980
tcaggcgctg acgggtagaa ggctcaaaag aagagtggct acgaccttac cctccaaaag 2040
gtgcccattc ggattcttcc gaatagtctt gcccgatcga gaatgcgaag aatgtctctg 2100
gccgaacctg gtcaatagat acgatatgct tcatctttta aggagtataa ttgattaatg 2160
atatggacgg aagcaaagct cacttcaaag cgaaagaagc cttaacgtta tgcttgccgt 2220
cttcatcttg gaagacgtat tgaacgaacc tcccagctat aatcttcgtt cgagttgagc 2280
cccactatct ggaacacgac catgaagaag atagcatctt acccagggag gaaccgctcc 2340
cctccgcaat gacgaagcac gattgaaagc gtcttcggag gcaattgcga gcatctccac 2400
ctcagatcat tgagcttggt gtagtaatag gcccgagcgg tcg 2443

```

## (2) INFORMATION FOR SEQ ID NO:673

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...582
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| cggtttggat  | ttggctctcg | gtgtaggcgg | ttaccctcgc | ggacgtattt  | cgagatatac  | 60  |
| ggaccggaat  | cttcgggtaa | gaccactctg | gctatccagc | cattgccgaa  | gcgcagaaaag | 120 |
| cagggtggctt | ggcggccatc | atcgatggga | acatgctttc | gaccgcacct  | atgccgaaaa  | 180 |
| gttgggcgtc  | aatgtgataa | tctctggata | gcacagccgg | acaacgggtga | acaggctttg  | 240 |
| gaaatgccga  | gcaactgatt | cgctcttctg | ctgtcgacat | tatagtcatt  | gacttgtcgc  | 300 |
| agccctcacg  | cccaaagcgg | aaatagaggg | tgaaatgggg | gacacaaggt  | tggtttgcat  | 360 |
| gcccgtctga  | tgctgcaagc | actgcgtaag | ataccggagc | catcagcaaa  | tccaatacaa  | 420 |
| cctgtatctt  | catcaaccag | cacgagagaa | gatcgggtgt | ttgttcggca  | atccggagag  | 480 |
| caccacaggg  | ggaatgcact | gaaattctat | gcatccatcc | gcacgcacat  | tcgcaagaga  | 540 |
| caccgatcaa  | ggatggcgaa | gagatcatgg | gacacctgac | ca          |             | 582 |

## (2) INFORMATION FOR SEQ ID NO:674

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1547 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1547
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:674

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| gccggcaaaa  | tcctgattcg  | aagcgatcta | aggaaaagaa | agaaccctcc | atcatggcaa | 60  |
| aaagcatcca  | ggcatagggtg | cctaatagat | agaaaggctg | cgcagggtca | gaacatcctg | 120 |
| tatggtttgg  | agcgtatggg  | tagagggtag | cttggcgaaa | tctggtacat | aggcatcccc | 180 |
| ccgaagagac  | tgttggccaa  | taggagtgtt | ctcctgtctg | tgccctccaa | tcgcgtacgt | 240 |
| cctgcccgtg  | ccgctggctc  | ccgctacgtc | gccctggaac | agtacacgcc | cgtcaatgag | 300 |
| gcgggataga  | aataggccaa  | agcgagggtc | atgaaaagga | gtagaccgca | gcataaggta | 360 |
| ggatttttgcg | ccaatcaggc  | tttgtcttat | cgtgggtggt | acgggttcgg | cagcagctgt | 420 |
| cggcttttgcg | ttttctttca  | tatgtcgttt | gtttttcgg  | tacaaagtta | aaaaaccatg | 480 |

|             |            |             |            |             |            |      |
|-------------|------------|-------------|------------|-------------|------------|------|
| tgattggctc  | gcctacgacc | aactgcttct  | ctgaacggtg | agcagagaag  | tatcctccga | 540  |
| cattgttatt  | gtagtgaaga | ggtcagaaaa  | tgagcagttc | aaaccttgga  | caagctctct | 600  |
| ccctattcta  | tatacatatc | tgaggacaaa  | gcgaaacatt | gaggaaagag  | gcggcatcca | 660  |
| tttgtttctt  | gccgggcat  | tggagcagag  | tatacgtag  | acccctttgc  | gtgtcatcac | 720  |
| gtcgaggttt  | ttctttccca | tatgatggag  | ccgaatcggc | ctctgtgtcg  | cggttctcgt | 780  |
| tctacacttg  | ggtacggtat | atthttcagca | cgatggactc | catccttgga  | cgagaagctt | 840  |
| ggtccaagct  | gtaggagcag | gcgatatgct  | gcggatgaaa | tttgtacctc  | ttcagccggt | 900  |
| ttgtcccaat  | cgatacggca | gtcgtctttg  | aaatcttcgg | agccgggtcga | gcatcaacat | 960  |
| agcccgggaag | ttgctcctga | gtatggagac  | gggttctcct | tcgagaaaca  | agtccactgt | 1020 |
| gtgcacaaaa  | cggatgcacc | gagagtagcc  | atacgttcgt | acaattcgcc  | gaaagtcttt | 1080 |
| catgtcctat  | aggcaacttc | tcttgacgca  | gtacttcacc | cgtatcttct  | catgccggag | 1140 |
| gcggaaggtg  | gtaactcccg | tttccgtatc  | gccatgcgta | tcgctgggtt  | gataggggct | 1200 |
| gtcctcgcgt  | acatgggcag | cagaggccat  | gcagattgat | tgttcccatg  | gggggcattt | 1260 |
| gccatacggg  | gcgagaagca | tacggaaaagc | cactacgatt | tgcaagtgcg  | gctgataagt | 1320 |
| ccgagttcat  | cgagaaaaga | ttcctcgttc  | agattgtccg | gctggagaat  | agcagacca  | 1380 |
| attcctgtgc  | gtatagtttg | accatactgg  | gacttacctt | agtcctcgac  | ccataggctt | 1440 |
| gtccggcata  | gtgaccacag | cttttacttg  | tatccgtttt | cgaccaaaagc | tcggagtgcc | 1500 |
| ggaacagcaa  | aatcggccgt | cccataaaaa  | tcaatcgtag | ttcttct     |            | 1547 |

## (2) INFORMATION FOR SEQ ID NO:675

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...626

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| gtggctccgg | aagcgatcac | agcttcttgg | actatatthtt | ttcgttagag  | gtggagtaca | 60  |
| ctttgagcaa | aagcgatatt | acacaagacc | ccaaaaacga  | ctatcaatag  | agtagacctt | 120 |
| tcattaggca | gtacatctcc | ttctcttgat | ttaatacttg  | gccactaatg  | ggagtcgtat | 180 |
| tcgaaatgaa | taagaacttg | atggcttcga | cattggtttc  | atttccaact  | ttgtggacta | 240 |
| tgatcccgtc | atgctgggtc | tgaaccgata | ataatagaag  | aagactgtgg  | atggctgatt | 300 |
| ttaatccttt | gngagcacta | agtatagaga | tccaaatgat  | gttgatgaca  | attcggataa | 360 |
| taccgtgggt | ggagaacgct | cccataactt | ccgatcactt  | acccggggcca | ttacgtatat | 420 |
| ccgaagcaat | ctttcaatta | tctcccggac | atacaccgac  | aaagaaagat  | ctggtcttta | 480 |
| aacactgtat | ggtattccgg | ctttggcata | ccgataagga  | aggcgatcgt  | tatctggaca | 540 |
| cttttcaaga | tcaccaatct | aatgagatac | agatgggatc  | aaatacgaga  | cattactctt | 600 |
| tttatggttg | gagttggnca | tatgta     |             |             |            | 626 |

## (2) INFORMATION FOR SEQ ID NO:676

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676

```

ggccgactgg gcttcctcac cgatgtcgat tgccacgagg ctccggagcg atcacacgcc 60
tgctggacgg cgacttcacc atcgagaccc gttccctgtg gaagtgaccg aagacaacgg 120
ctcctctccc tctacgccc tgaacgagca gccatactca agcgtgaaac cggttcgatg 180
attcgggtga atgcctcctc aacgacgact atctggcggc ttacgatgcc gacggcctcg 240
tggtgccacg cctccgggt cccacagccta ctgctgagc gggaaacgggc ctatatcatg 300
cctgcctgtc ggaacttcgt ccttacgccc atcgccccc actgctgaat atgcgtccgc 360
tggtcgttcc ggacgacacg gtgatccgcc tcaagtggat tcgcgcagtc ggaattacct 420
cttggtgctc gacggacgaa cagaacgttg cctgcgata cctccatcct gctcaaacga 480
gctcctcaca gctgcgaatg atccgtctgc gtccgcactc ctccgcccga accctgaggg 540
taagctcatg tggggagcag ccgtaagata aagacacttg cgacggtgac aacgagccaa 600
cggacactta ccatagacta ctcccataat ggaagaaata caaccatggt gctgcgcacc 660
gaagatctgg tcaaacgcta ccggaacgta cggtcgtgaa tcacgtatcg atagagggttc 720
ggcaaggaga gatcgtggga ttgttcgggc cgaacggagc cggcaagacg acgactttct 780
atataccacg gggctggctg tcccacagca aggacggata ttctcfaatg atcggacatc 840
acccaatacc ccgtctacaa acgagcgcgt gccggcatcg gcattctggc caagaggcat 900
ccatattccg caaaatgtcc gtggaggaca aatcctctcc gtccctcgaaa tggccggact 960
gcccagacc tatcagcacg aaagctggaa agcctgatag ccgaatttca ccttgagaaa 1020
gtacgcaaaa ccttggcgac cgcctctccg gcggcgagcg acgcctgccc gagatagccg 1080
ctgcttggtc atatcgctc gcttcacatc gctggacgaa ccctttgccc tgtcgatcct 1140
atcgccgtac aggacattca ggccattgtg gccaaatcaa ggacaaaaaac atcggcatcc 1200
tcataccaga ccacaacgtc caggaacgct tcagcatcac ggatcgcgct tacctccttt 1260
tcgagggcaa agtgtgtatc agggcacggc cgaagagctt ggctgcgaac gaagtcgtaa 1320
gggaaag 1327

```

(2) INFORMATION FOR SEQ ID NO:677

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677

```

gggtttctca agaagcacgg tggtagcat cgtagagcat caaggcattc cactgctatc 60
gtggatgtgt ccttcacctg ccacatgccg gactgtctga gatgccttac aaaccctgca 120
ttcgtggagc gcatcaggag ccggtaccgg cctgcccaca tacaggatag gcggatgcag 180
ctgtctgagc ggcgactcat cggtagctgg agtttcgata ggccgttgca ggtggggcga 240
gaactatatt cgaagacatg ctccactaca cgacggtgaa gaacgacatc gttcacggtg 300
cacgcatcc ggacat 316

```

(2) INFORMATION FOR SEQ ID NO:678

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| gctcgggacg  | gatttcgctc  | ggcacctgga  | aggtagcacc  | accgatacgc | ggctcttcac  | 60   |
| ttctacctga  | ggagtgatat  | tatcgagagc  | cgccttccaa  | tctcgagggc | agacttctct  | 120  |
| tcgtttgagt  | gcttcgctct  | cacgatgcc   | aagcaccgta  | gaagatactg | aaagctgtgt  | 180  |
| tcttctttcc  | atcataatta  | ggtgattaac  | gaacttagtc  | accctcacat | caccatagac  | 240  |
| gggatcggca  | ggatctgtct  | tttttaggt   | tttgcttttc  | tcattgtctc | aaaaatttcg  | 300  |
| tttttgtcga  | ttgggtgcgc  | tttcattttt  | gtcttcaacg  | ctccgccgga | gcatttactc  | 360  |
| aaccctgttt  | aagcctatcc  | aattgaactc  | aaaccggttc  | ttaaataatt | tggttggttg  | 420  |
| gcccttgatc  | gtagcgcgat  | ttagattggg  | gaagtgattc  | gtccttatcg | gtctccggcc  | 480  |
| tcgctcatcg  | ggccgacgag  | tccgcttagc  | ggctcttact  | tcttaccttt | agcggcaggg  | 540  |
| cctgtccggg  | cttcggacgc  | ttggcaccgt  | atttggaacg  | acgctgcgac | ggccattcac  | 600  |
| acctgctgta  | tcgagcgtgc  | cacgaacaat  | gtgataggca  | caccgggcaa | gtccttcaca  | 660  |
| cgacctccac  | gaaccagcac  | gatgcttggt  | cctgcaagtt  | gtgacctctc | ccggggatgt  | 720  |
| aggcattgac  | ttcttggaat  | tcgtcagacg  | cacacgcgcg  | accttacgca | tagccgaatt  | 780  |
| cggctcttgg  | gcgtagtcgt  | ataaacgcgc  | acacaaacgc  | cgcgacgctg | cggcacgaat  | 840  |
| tcaatgccgg  | cgatttgctc  | ttatccgcga  | aagattcacg  | acctttctaa | ccaactgttg  | 900  |
| aattgtaggc  | atttcttctt  | tctttaaaac  | ttgattataa  | ttatctcttt | cctaactctat | 960  |
| tacactgcc   | actatacgag  | agtggcgcaa  | aggtacatat  | atthttccaa | tccacaacag  | 1020 |
| tccccgcagt  | tttttttcac  | ggcaacgctc  | taatactcaa  | tagtatcaac | cgacatctta  | 1080 |
| ggccgaactg  | ttccgcccga  | gcgagagatc  | cgaaaagggtg | gatgcgcccc | aaaagaaaaga | 1140 |
| gaatacaaaa  | cagcccga    | aagtgcgata  | cagcgtcagc  | cacagaaaag | aaacgcactg  | 1200 |
| catatatcca  | cagaaaagaa  | acgcatgcat  | atattaatgt  | acgcgcgcga | gagatgtcga  | 1260 |
| gggcagcact  | attcgtccaa  | agagagaaaa  | cggaacggaa  | aaggacaacc | atccagcaaa  | 1320 |
| ccgttacgcg  | ccacaatttt  | ctgtttcgat  | gctccgcaaa  | acgtggcgcg | ggactttttc  | 1380 |
| gttttggttc  | gggaagtata  | aaattctcgc  | gccacgagga  | aaaattctca | taagactttt  | 1440 |
| cccgaaaaac  | cgcgccgcaa  | tcagagcaat  | atggttcgag  | aaaatcagat | cggaatatat  | 1500 |
| ccgcccga    | gcgagagggg  | agctatgaag  | ctgtaccgac  | agcctcgatc | gccacaataa  | 1560 |
| ctaccgcata  | agcgaagccg  | tcagagccaa  | gaagagcaag  | caatagacca | caacgagatt  | 1620 |
| gtccgcccaga | agctccgcca  | ccaagagcag  | aggaatagct  | gcttgtgtcc | cagcaaaaaca | 1680 |
| aaaggaatag  | gagcaatgca  | ggtagcccgt  | atagcacc    | acccgggcat | cgctgtagaa  | 1740 |
| aggtagggcg  | agaacgttca  | gcaaaatagc  | tggcaggcta  | tgtacgcctg | agcgataatg  | 1800 |
| tgctccgtca  | gatatatgct  | ccggctcctt  | tttgtcgaa   | agccgctttc | gtactcacgg  | 1860 |
| cggaatggga  | agaatactga  | tgatcctgac  | agccttggtg  | ccttgaaacc | attcatcagc  | 1920 |
| aggtccata   | ttcttgaaaa  | gaaagggagg  | gacttcaacc  | atthttctgc | tcggtgacaa  | 1980 |
| acctcatttg  | tttgtaaaaa  | aaggctcttt  | ccccgtgtgt  | cgctcggcaa | tcattttctc  | 2040 |
| gctatcgctg  | ccgactgctt  | attctccttt  | tgcaaggagg  | atthttcttt | ttgatccatc  | 2100 |
| cgatactttg  | acgcgtaagc  | tcttcgcca   | tgggcttttt  | ctgcaaggga | tcaggtcgat  | 2160 |
| cagttgtgca  | aagatgatgt  | acagagaggg  | cagcacgaaa  | agggctgaaa | gggacggaag  | 2220 |
| tagacaaccc  | tcttgcccac  | gataaagtc   | cgtacaataa  | acccgggcgg | tagagcagct  | 2280 |
| ccacgatagt  | acgcccga    | ccgtgtcgat  | attggtgaag  | ccgcctatca | catttcggat  | 2340 |
| catctgcggg  | aatgataccg  | tccggtgcga  | gagggttgct  | cgcagcgggt | gcagaaattg  | 2400 |
| ccgtatatcc  | atctccgcag  | ttttggcata  | tatgtatgta  | tgggtctgca | gtggagtgcg  | 2460 |
| tctgccacgc  | atcagtctca  | actcgaatgc  | gcggattcga  | cccgaagggg | aaagagaagt  | 2520 |
| gattgcaacc  | gctgatcgat  | ctttcttgca  | gtagtctcgc  | cttccgtagg | attgccccaa  | 2580 |
| aagccagccc  | ggtaatgcag  | atattcccca  | ttgtccgcaa  | gtggccaaat | cttctattgc  | 2640 |
| caaccaagga  | cggatgcaag  | catgaggatc  | tgcaatgagt  | tggpcatttt | tctctcgaat  | 2700 |
| gccccatgctc | cccggtttttc | tgthttcttcg | aagtactatc  | gcgcaacctt | ccattttttt  | 2760 |



cttcgttttg ctactcgttt gcattatctg aattcacttg cttgcgtaca aatatagtta 2820  
 tgacaaatgg agggcgtagc acctcggttc ggtagcttac gggtagagctg cc 2872

## (2) INFORMATION FOR SEQ ID NO:679

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...542

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:679

|                       |            |            |            |             |     |
|-----------------------|------------|------------|------------|-------------|-----|
| gtaagaacgg gatacaggg  | cgaaatagg  | tatgcttatg | gcgggtatgt | aaactttccc  | 60  |
| gtctgacggg gtaccacata | atactcgatc | gtacgctgcc | atcggcaccc | gaagtactta  | 120 |
| tgcgaaggct gctctcgcc  | ttggagtgt  | ttgttcgaag | ctgtcgggaa | atctcacttt  | 180 |
| gggatctccc atcaactgat | atttccgctt | ccgttaatta | cgagcttgag | tgttaagggt  | 240 |
| tcgttgtttt ggcctgacgg | tcattgaaag | aggctgagat | ccgataatta | ccaaagcacc  | 300 |
| atcgaatcct tggggtttcg | gttcaggcaa | gggagcgaca | tctttgtgac | cggattgggtg | 360 |
| gtcagagtcc tccgcacatt | ctcatacggg | tgagtacaaa | gaagtcatt  | atgtcgtcta  | 420 |
| tctcccgctg gaccgntact | agacacgaaa | gttgcccgat | ggaatagtca | gcttaccgct  | 480 |
| tttttgagga agagcaacga | ctgcttgaga | acggttgctt | gatagttccg | tccttcatac  | 540 |
| tc                    |            |            |            |             | 542 |

## (2) INFORMATION FOR SEQ ID NO:680

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...865

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680

|                       |            |            |            |             |     |
|-----------------------|------------|------------|------------|-------------|-----|
| gtcagattat gtgcagcctc | ctgtggtaac | aagaactgct | ccccctcgaa | gaaagggtgca | 60  |
| ctccatccgt atcggtacgc | agaagatgaa | atacggcacg | cggaagaaac | cgatggtttc  | 120 |
| tatctgccga tacaggctcg | caggctctct | tcgatgtgga | tcactctcac | atacagtcg   | 180 |
| tccggcagtt cgtcggatgt | actccttcca | cggattgcae | ttcgccctct | tccgtcggga  | 240 |
| tgggacgccg tgccgggtcg | aaagcggatt | gccaggcg   | agtgtatcc  | gctctgctct  | 300 |
| tcatcggaca gatagtgtc  | ctccttgca  | gcttggtgt  | gccttcgctg | ggttcatagc  | 360 |

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| cgagagtgttc | ggacagatac  | ttttccaaaa | gctgtggcgg | cgaatcacct | tgagcgcata  | 420 |
| tttccgtccg  | ctttcgggtca | gtgcgagtc  | ggaggcaggc | agtagccttg | tttgtgcagc  | 480 |
| agatcgagta  | atactgttgg  | ttgcttatct | tcagcccggg | cagggtctgc | agtcgggtctc | 540 |
| attgacgggc  | agaccgtctt  | cttccaaaga | atagatagct | ttgagcgttc | ttcggacaga  | 600 |
| cggcgtagcat | cgaagcgaaa  | cagaagattc | gagaataatt | catgcttcta | taacttctat  | 660 |
| tattaccgaa  | agtggtcggg  | ctggtgcctg | tggcacaacg | ttttcagtat | gacaaaagtg  | 720 |
| cttattttat  | cgaagatccg  | caaactgcag | gctctctggg | ctatttacct | gcattgagta  | 780 |
| tccgagcgga  | gtgcttctac  | aagacgggtc | catttcttcc | tgactattcg | gcatgacgac  | 840 |
| tgaaatcgctc | caaaaagttt  | cacac      |            |            |             | 865 |

## (2) INFORMATION FOR SEQ ID NO:681

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2502

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| ccgattgcgc  | tttgctttca  | aaaccacaat | ccgatactca  | agaccaaac  | tatgctccgg  | 60   |
| aatcgtgggn  | acgcgaacga  | acagatcagt | actaccggaa  | tgggcagata | tgccatgc    | 120  |
| cgaattggcc  | gaaggagctt  | atgtcgactc | ttttgtcgct  | cttcggctct | cgtagatgat  | 180  |
| tgcatgtgct  | tcaccgggaa  | tatcagatcg | tggggcgctc  | ggccctcttt | atgcggaaga  | 240  |
| acggagcctt  | cctcacgggc  | tcaaccgagc | tgcccaagag  | gccttcgcgt | tgtagatgat  | 300  |
| gcagattctg  | cggaagacat  | cgattcgctt | ctccaaaaga  | tagagagcgc | agaccgcgat  | 360  |
| cagtagccga  | taggcgtcgg  | gtcttcaccc | ggactatttg  | ctccctcccc | gaggggctac  | 420  |
| tgccctcagag | gtcatcatcg  | aactttgctc | acatcgcggt  | cgtaaaatcg | tcgggttctcc | 480  |
| acgcccacaaa | cgtggcgccg  | gaactttttc | gttttggttc  | gggaaagaaa | aaattcccgg  | 540  |
| cgagaacgaa  | aaaattccca  | cgccacttcc | tttcagcttt  | tggttcgcgt | tcgggcgact  | 600  |
| ttcggctcgt  | atttttccct  | gatcgactga | atgactcgcg  | ccttgatgcc | gtttttcttc  | 660  |
| tatttgatc   | ggttggtctt  | gccatagcat | ggcattgaac  | tttaatcatt | attttcgac   | 720  |
| cggactttga  | ttacatgtaa  | ttatgaaaag | aatagtattg  | attcgccacg | gcgaaagctt  | 780  |
| gtggacaagg  | aaaatcgctt  | tacgggatgg | acagatgtgg  | atttgctcga | aaaggtattg  | 840  |
| aagaagccaa  | gaaagccggc  | gagctcatga | agaaagaagg  | cttcagttta | ccaaagccta  | 900  |
| tacttcttat  | ctcaaactg   | ccgtcaagac | ctgaacgggt  | tcctcgatgt | aatggacttg  | 960  |
| gattggatac  | cggtggagaa  | acctggcgct | tgaacgagaa  | gcactacggc | atgctgcaag  | 1020 |
| gcctcaacag  | gcccagactg  | ccgagaagta | cggagacgaa  | caggtagctc | tctggcgtag  | 1080 |
| agctacgacg  | tccccccac   | gcctatggag | aaagaggatc  | cgcgctcccc | ttcatggatc  | 1140 |
| cgcgctacaa  | aggtgtgtgc  | gagaaagacc | tgccacgaca  | gaagctctnt | gcgacacggg  | 1200 |
| aaatcgatc   | ctccccat    | ggaacagacc | atattccccc  | acgctcaagg | agcatgacga  | 1260 |
| ggtattggta  | gcagtcacgg  | caacagtctg | cgtggatcca  | tcaagggtgt | gaaaaacatt  | 1320 |
| tcgacgaaga  | catcatcagc  | ctgaacctcc | cgacagccgt  | gccttacgtt | ttgaatttga  | 1380 |
| cgacaatctc  | cgtctgggtga | aggactat   | cctcggcgat  | cagaagagat | caaaaagctg  | 1440 |
| atggaggcag  | tagccaatca  | gggcaagaag | aataaccccc  | catcgccggc | cctttcctat  | 1500 |
| tctgcttttc  | gacagaagga  | aggagaaaaa | acaagaagag  | agcgttgac  | gaccgttagc  | 1560 |
| ggtgcaacct  | ctcttttcat  | ttcatctttt | tttgctcggt  | tgccgcagat | gttatttctc  | 1620 |
| cggaggtctt  | tctctacaa   | gaccttgctg | tacacatgca  | tcagggtcgg | gctacggctt  | 1680 |
| cgggtgagaa  | acgctctata  | taggtacgcc | cgctcgctatc | atcttctcgc | ggagagagct  | 1740 |
| gtcggagagg  | atgctgtcca  | gcatgatgcc | atcatttccg  | catcgctcgg | gtcgggtgac  | 1800 |
| agggacgaag  | ggctccggct  | tcttccagac | acgaacctcg  | ggccgcaacg | accggcacgc  | 1860 |
| ccaagccaag  | gcttcgacaa  | tcgggatacc | gaatccctcg  | aagcgcgaag | gtagacgaat  | 1920 |
| acctctgctc  | cgcatagat   | gcccggcagg | aaagcaaatg  | gacatcgctg | agcatgacga  | 1980 |
| gccgggtctgc | cacacctgat  | cgctctgcaa | ctgctgcacc  | tccgcacagt | atggcgtagc  | 2040 |